



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 156807

TO: Elizabeth McElwain
Location: REM/2A11/2C18
Art Unit: 1638
Friday, June 10, 2005

Case Serial Number: 10/029756

From: Toby Port

Location: Biotech-Chem Library
REM1-A59

Phone: 272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner McElwain,

Here are the results of your search. Please note in the sequence files, we don't limit by date. If you'd like this run as an STN search, please let me know.

Please feel free to contact me if you have any questions.

Toby Port

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STIC-Biotech/ChemLib

155007

From: McElwain, Elizabeth
Sent: Tuesday, May 31, 2005 4:26 PM
To: STIC-Biotech/ChemLib
Subject: sequence search

Please search 10/029,756 - for DNA encoding any of SEQ ID NO: 6, 12 or 20
Good dates would be prior to 1/28/1997.

Thank you,
Beth

Elizabeth F. McElwain, Ph.D.
U.S. Patent and Trademark Office
Tech Center 1600, Art Unit 1638
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mailbox Remsen 2C18
571-272-0802
elizabeth.mcelwain@uspto.gov

STIC
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Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
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OM protein - nucleic search, using frame plus p2n model

Run on: June 8, 2005, 11:36:25 ; Search time 122.105 Seconds
(without alignments)
107.204 Million cell updates

Title: US-10-029-756-6
Perfect score: 53
Sequence: 1 WIGHDAGH 8

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                Ygapop 10.0 , Ygapext 0.5
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Searched:      1202784 seqs. 818138359 residues

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Total number of hits satisfying chosen parameters: 2405568

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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| SUMMARIES | | | | | | | | | |
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| 86 | 38 | 71.7 | 486 | 4 | US-09-513-999C-1880 | Sequence 1880, Ap | c 159 | 38 | 71.7 | 51620 | 4 | US-09-949-016-12848 | Sequence 12848, A |
| 87 | 38 | 71.7 | 601 | 4 | US-09-949-016-143643 | Sequence 143643, A | c 160 | 38 | 71.7 | 51621 | 4 | US-09-949-016-16503 | Sequence 16503, A |
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| c 90 | 38 | 71.7 | 601 | 4 | US-09-949-016-171126 | Sequence 171126, A | c 163 | 38 | 71.7 | 97989 | 4 | US-09-949-016-13208 | Sequence 13208, A |
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| c 97 | 38 | 71.7 | 624 | 4 | US-09-543-681A-1128 | Sequence 1128, Ap | c 170 | 38 | 71.7 | 156942 | 4 | US-09-949-016-12227 | Sequence 12227, A |
| c 98 | 38 | 71.7 | 699 | 4 | US-09-252-991A-4810 | Sequence 4810, Ap | c 171 | 38 | 71.7 | 156942 | 4 | US-09-949-016-12227 | Sequence 12227, A |
| c 99 | 38 | 71.7 | 737 | 4 | US-09-252-991A-7908 | Sequence 7908, Ap | c 172 | 38 | 71.7 | 156950 | 4 | US-09-949-016-15946 | Sequence 15946, A |
| c 100 | 38 | 71.7 | 753 | 4 | US-09-270-767-11527 | Sequence 11527, A | c 173 | 38 | 71.7 | 177293 | 4 | US-09-949-016-16513 | Sequence 16513, A |
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| c 103 | 38 | 71.7 | 894 | 4 | US-09-252-991A-7643 | Sequence 7643, Ap | c 176 | 38 | 71.7 | 275110 | 4 | US-09-949-016-16070 | Sequence 16070, A |
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| c 111 | 38 | 71.7 | 1197 | 4 | US-09-734-237B-28 | Sequence 28, Appl | c 184 | 37.5 | 70.8 | 227979 | 4 | US-09-949-016-11842 | Sequence 11842, A |
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| c 113 | 38 | 71.7 | 1299 | 2 | US-08-125-462-6 | Sequence 6, Appli | c 186 | 37 | 69.8 | 312972 | 4 | US-09-949-001-34 | Sequence 34, Appl |
| c 114 | 38 | 71.7 | 1299 | 2 | US-08-891-848-6 | Sequence 6, Appli | c 187 | 37 | 69.8 | 312972 | 4 | US-09-949-001-34 | Sequence 34, Appl |
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| c 117 | 38 | 71.7 | 1356 | 4 | US-09-902-540-171 | Sequence 171, App | c 190 | 37 | 69.8 | 312972 | 4 | US-09-949-001-34 | Sequence 34, Appl |
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| c 120 | 38 | 71.7 | 1369 | 3 | US-09-260-889-3 | Sequence 3, Appli | c 193 | 37 | 69.8 | 312972 | 4 | US-09-949-001-34 | Sequence 34, Appl |
| c 121 | 38 | 71.7 | 1369 | 3 | US-09-347-878-11 | Sequence 11, Appl | c 194 | 37 | 69.8 | 312972 | 4 | US-09-949-001-34 | Sequence 34, Appl |
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| c 123 | 38 | 71.7 | 1417 | 4 | US-09-904-615-31 | Sequence 31, Appl | c 196 | 37 | 69.8 | 312972 | 4 | US-09-949-001-34 | Sequence 34, Appl |
| c 124 | 38 | 71.7 | 2316 | 4 | US-08-252-991A-6950 | Sequence 6950, Ap | c 197 | 37 | 69.8 | 312972 | 4 | US-09-949-001-34 | Sequence 34, Appl |
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| c 126 | 38 | 71.7 | 3219 | 4 | US-09-016-434-1348 | Sequence 1348, Ap | c 199 | 37 | 69.8 | 312972 | 4 | US-09-949-001-34 | Sequence 34, Appl |
| c 127 | 38 | 71.7 | 3219 | 4 | US-09-895-652A-17 | Sequence 17, Appl | c 200 | 37 | 69.8 | 312972 | 4 | US-09-949-001-34 | Sequence 34, Appl |
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| c 132 | 38 | 71.7 | 4615 | 1 | US-08-188-582-1 | Sequence 1, Appli | c 205 | 37 | 69.8 | 312972 | 4 | US-09-949-001-34 | Sequence 34, Appl |
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| c 134 | 38 | 71.7 | 5140 | 3 | US-09-333-214-2 | Sequence 2, Appli | c 207 | 37 | 69.8 | 312972 | 4 | US-09-949-001-34 | Sequence 34, Appl |
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| c 141 | 38 | 71.7 | 6799 | 2 | US-08-891-848-5 | Sequence 5, Appli | c 214 | 37 | 69.8 | 312972 | 4 | US-09-949-001-34 | Sequence 34, Appl |
| c 142 | 38 | 71.7 | 7080 | 3 | US-09-380-190A-21 | Sequence 21, Appl | c 215 | 37 | 69.8 | 312972 | 4 | US-09-949-001-34 | Sequence 34, Appl |
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| c 144 | 38 | 71.7 | 15027 | 4 | US-09-949-016-12660 | Sequence 12660, A | c 217 | 37 | 69.8 | 312972 | 4 | US-09-949-001-34 | Sequence 34, Appl |
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| c 148 | 38 | 71.7 | 22339 | 4 | US-09-949-016-14777 | Sequence 14777, A | c 221 | 37 | 69.8 | 312972 | 4 | US-09-949-001-34 | Sequence 34, Appl |
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| c 150 | 38 | 71.7 | 23496 | 4 | US-09-902-540-5645 | Sequence 5645, Ap | c 223 | 37 | 69.8 | 312972 | 4 | US-09-949-001-34 | Sequence 34, Appl |
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| c 152 | 38 | 71.7 | 30068 | 4 | US-08-474-933-1 | Sequence 1, Appli | c 225 | 37 | 69.8 | 312972 | 4 | US-09-949-001-34 | Sequence 34, Appl |
| c 153 | 38 | 71.7 | 37068 | 4 | US-09-949-016-12543 | Sequence 12543, A | c 226 | 37 | 69.8 | 312972 | 4 | US-09-949-001-34 | Sequence 34, Appl |
| c 154 | 38 | 71.7 | 44353 | 4 | US-09-949-016-17376 | Sequence 17376, A | c 227 | 37 | 69.8 | 312972 | 4 | US-09-949-001-34 | Sequence 34, Appl |
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| c 156 | 38 | 71.7 | 47698 | 4 | US-09-949-016-16243 | Sequence 16243, A | c 229 | 37 | 69.8 | 312972 | 4 | US-09-949-001-34 | Sequence 34, Appl |
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| c 158 | 38 | 71.7 | 51354 | 4 | US-09-902-540-1270 | Sequence 1270, Ap | c 231 | 37 | 69.8 | 312972 | 4 | US-09-949-001-34 | Sequence 34, Appl |

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| 232 | 37 | 69.8 | 1236 | 4 | US-09-402-532-17 | Sequence 17, Appl | C 305 | 36 | 67.9 | 325 | 4 | US-09-614-124B-1202 | Sequence 1202, Ap |
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| 234 | 37 | 69.8 | 1332 | 4 | US-09-402-532-18 | Sequence 18, Appl | C 307 | 36 | 67.9 | 325 | 4 | US-09-658-824-1202 | Sequence 1202, Ap |
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| 238 | 37 | 69.8 | 1448 | 4 | US-09-903-840A-16 | Sequence 416, App | C 311 | 36 | 67.9 | 472 | 5 | PCT-US92-10284-16 | Sequence 16, Appl |
| 239 | 37 | 69.8 | 1550 | 4 | US-09-023-655-101 | Sequence 101, App | C 312 | 36 | 67.9 | 474 | 4 | US-09-902-540-1884 | Sequence 1884, Ap |
| 240 | 37 | 69.8 | 1580 | 4 | US-09-023-655-101 | Sequence 101, App | C 313 | 36 | 67.9 | 478 | 4 | US-09-270-767-3656 | Sequence 3656, Ap |
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| 252 | 37 | 69.8 | 3296 | 4 | US-09-949-016-1456 | Sequence 1456, App | C 325 | 36 | 67.9 | 601 | 4 | US-09-949-016-167941 | Sequence 167941, A |
| 253 | 37 | 69.8 | 3299 | 4 | US-09-949-016-557 | Sequence 557, App | C 326 | 36 | 67.9 | 729 | 4 | US-09-489-039A-4962 | Sequence 4962, Ap |
| 254 | 37 | 69.8 | 5483 | 4 | US-09-949-016-61 | Sequence 61, Appl | C 327 | 36 | 67.9 | 750 | 4 | US-09-902-540-5834 | Sequence 5834, Ap |
| 255 | 37 | 69.8 | 5487 | 4 | US-09-949-016-4997 | Sequence 4997, App | C 328 | 36 | 67.9 | 771 | 4 | US-09-583-110-2399 | Sequence 2399, Ap |
| 256 | 37 | 69.8 | 5599 | 2 | US-08-477-451-9 | Sequence 9, Appl | C 329 | 36 | 67.9 | 801 | 4 | US-09-252-991A-1075 | Sequence 1075, Ap |
| 257 | 37 | 69.8 | 5599 | 2 | US-08-477-451-13 | Sequence 13, Appl | C 330 | 36 | 67.9 | 866 | 4 | US-09-620-312D-682 | Sequence 682, App |
| 258 | 37 | 69.8 | 6608 | 4 | US-09-949-016-13960 | Sequence 13960, A | C 331 | 36 | 67.9 | 930 | 4 | US-09-107-433-464 | Sequence 464, App |
| 259 | 37 | 69.8 | 7710 | 4 | US-09-949-016-738 | Sequence 738, App | C 332 | 36 | 67.9 | 946 | 4 | US-09-904-615-24 | Sequence 24, Appl |
| 260 | 37 | 69.8 | 8242 | 4 | US-09-949-016-4620 | Sequence 4620, App | C 333 | 36 | 67.9 | 963 | 4 | US-09-248-796A-3965 | Sequence 3965, Ap |
| 261 | 37 | 69.8 | 8252 | 1 | US-08-046-585-15 | Sequence 15, Appl | C 334 | 36 | 67.9 | 984 | 4 | US-09-489-039A-890 | Sequence 890, App |
| 262 | 37 | 69.8 | 8252 | 1 | US-08-393-703-15 | Sequence 15, Appl | C 335 | 36 | 67.9 | 1143 | 4 | US-09-252-991A-1032 | Sequence 1032, Ap |
| 263 | 37 | 69.8 | 8252 | 5 | PCT-US93-11721-15 | Sequence 15, Appl | C 336 | 36 | 67.9 | 1257 | 4 | US-09-489-039A-1557 | Sequence 1557, Ap |
| 264 | 37 | 69.8 | 12061 | 4 | US-08-477-451-16134 | Sequence 16134, A | C 337 | 36 | 67.9 | 1341 | 4 | US-09-372-425A-7 | Sequence 7, Appl |
| 265 | 37 | 69.8 | 19332 | 2 | US-08-477-451-25 | Sequence 25, Appl | C 338 | 36 | 67.9 | 1350 | 5 | PCT-US92-10284-1 | Sequence 1, Appl |
| 266 | 37 | 69.8 | 21170 | 4 | US-09-949-016-12480 | Sequence 12480, A | C 339 | 36 | 67.9 | 1353 | 5 | PCT-US92-10284-1 | Sequence 1, Appl |
| 267 | 37 | 69.8 | 2166 | 4 | US-09-949-016-16072 | Sequence 16072, A | C 340 | 36 | 67.9 | 1353 | 5 | PCT-US94-01321-1 | Sequence 1, Appl |
| 268 | 37 | 69.8 | 2630 | 4 | US-09-949-016-16362 | Sequence 16362, A | C 341 | 36 | 67.9 | 1369 | 4 | US-09-205-258-174 | Sequence 174, App |
| 269 | 37 | 69.8 | 37475 | 4 | US-09-949-016-12299 | Sequence 12299, A | C 342 | 36 | 67.9 | 1410 | 4 | US-09-489-039A-1920 | Sequence 1920, Ap |
| 270 | 37 | 69.8 | 37492 | 4 | US-09-949-016-13198 | Sequence 13198, A | C 343 | 36 | 67.9 | 1410 | 4 | US-09-489-039A-1936 | Sequence 1936, Ap |
| 271 | 37 | 69.8 | 40512 | 4 | US-09-949-016-16612 | Sequence 16612, A | C 344 | 36 | 67.9 | 1410 | 2 | US-08-244-205-6 | Sequence 6, Appl |
| 272 | 37 | 69.8 | 43102 | 4 | US-09-949-016-16355 | Sequence 16355, A | C 345 | 36 | 67.9 | 1429 | 2 | US-08-244-205-8 | Sequence 8, Appl |
| 273 | 37 | 69.8 | 47727 | 4 | US-09-949-016-12904 | Sequence 12904, A | C 346 | 36 | 67.9 | 1429 | 2 | PCT-US92-10284-6 | Sequence 6, Appl |
| 274 | 37 | 69.8 | 49301 | 4 | US-09-949-016-16296 | Sequence 16296, A | C 347 | 36 | 67.9 | 1429 | 5 | PCT-US92-10284-8 | Sequence 8, Appl |
| 275 | 37 | 69.8 | 52789 | 4 | US-09-949-016-12130 | Sequence 12130, A | C 348 | 36 | 67.9 | 1429 | 5 | US-08-244-205-4 | Sequence 4, Appl |
| 276 | 37 | 69.8 | 53790 | 4 | US-09-949-016-16641 | Sequence 16641, A | C 349 | 36 | 67.9 | 1525 | 2 | PCT-US92-10284-4 | Sequence 4, Appl |
| 277 | 37 | 69.8 | 53260 | 4 | US-09-949-016-14298 | Sequence 14298, A | C 350 | 36 | 67.9 | 1525 | 5 | PCT-US94-01321-11 | Sequence 11, Appl |
| 278 | 37 | 69.8 | 57559 | 4 | US-09-949-016-13077 | Sequence 13077, A | C 351 | 36 | 67.9 | 1525 | 1 | US-07-932-915-1 | Sequence 1, Appl |
| 279 | 37 | 69.8 | 57560 | 4 | US-09-949-016-12536 | Sequence 12536, A | C 352 | 36 | 67.9 | 1540 | 1 | PCT-US91-05826-1 | Sequence 1, Appl |
| 280 | 37 | 69.8 | 60788 | 4 | US-09-949-016-16789 | Sequence 16789, A | C 353 | 36 | 67.9 | 1540 | 5 | US-09-489-039A-1971 | Sequence 1971, Ap |
| 281 | 37 | 69.8 | 61462 | 4 | US-09-949-016-17522 | Sequence 17522, A | C 354 | 36 | 67.9 | 1599 | 4 | PCT-US94-01321-9 | Sequence 9, Appl |
| 282 | 37 | 69.8 | 62728 | 4 | US-09-949-016-12539 | Sequence 12539, A | C 355 | 36 | 67.9 | 1645 | 5 | US-08-244-205-12 | Sequence 12, Appl |
| 283 | 37 | 69.8 | 63129 | 4 | US-09-949-016-16579 | Sequence 16579, A | C 356 | 36 | 67.9 | 1675 | 2 | PCT-US92-10284-12 | Sequence 12, Appl |
| 284 | 37 | 69.8 | 66213 | 4 | US-09-949-016-11803 | Sequence 11803, A | C 357 | 36 | 67.9 | 1675 | 5 | US-09-495-050A-229 | Sequence 229, App |
| 285 | 37 | 69.8 | 66213 | 4 | US-09-949-016-16739 | Sequence 16739, A | C 358 | 36 | 67.9 | 1776 | 4 | US-09-252-991A-1026 | Sequence 1026, Ap |
| 286 | 37 | 69.8 | 68213 | 4 | US-09-949-016-15601 | Sequence 15601, A | C 359 | 36 | 67.9 | 1836 | 4 | US-09-341-587-2 | Sequence 2, Appl |
| 287 | 37 | 69.8 | 79595 | 4 | US-09-949-016-15318 | Sequence 15318, A | C 360 | 36 | 67.9 | 2001 | 3 | US-08-244-205-10 | Sequence 10, Appl |
| 288 | 37 | 69.8 | 79634 | 4 | US-09-949-016-15642 | Sequence 15642, A | C 361 | 36 | 67.9 | 2169 | 4 | US-09-489-039A-1771 | Sequence 1771, Ap |
| 289 | 37 | 69.8 | 84156 | 4 | US-09-949-016-12388 | Sequence 12388, A | C 362 | 36 | 67.9 | 2181 | 2 | PCT-US92-10284-10 | Sequence 10, Appl |
| 290 | 37 | 69.8 | 90307 | 4 | US-09-949-016-16623 | Sequence 16623, A | C 363 | 36 | 67.9 | 2181 | 5 | US-08-410-784A-3 | Sequence 3, Appl |
| 291 | 37 | 69.8 | 102406 | 4 | US-09-949-016-14673 | Sequence 14673, A | C 364 | 36 | 67.9 | 2523 | 2 | US-09-372-425A-1 | Sequence 1, Appl |
| 292 | 37 | 69.8 | 112623 | 4 | US-09-949-016-14374 | Sequence 14374, A | C 365 | 36 | 67.9 | 2674 | 4 | US-09-731-166-15 | Sequence 15, Appl |
| 293 | 37 | 69.8 | 123863 | 4 | US-09-949-016-14202 | Sequence 14202, A | C 366 | 36 | 67.9 | 2700 | 2 | US-08-410-784A-1 | Sequence 1, Appl |
| 294 | 37 | 69.8 | 135667 | 4 | US-09-949-016-15051 | Sequence 15051, A | C 367 | 36 | 67.9 | 2712 | 2 | US-09-976-594-1031 | Sequence 1031, Ap |
| 295 | 37 | 69.8 | 148794 | 4 | US-09-949-016-12751 | Sequence 12751, A | C 368 | 36 | 67.9 | 2905 | 4 | US-09-919-039-381 | Sequence 381, App |
| 296 | 37 | 69.8 | 325034 | 4 | US-09-949-016-14957 | Sequence 14957, A | C 369 | 36 | 67.9 | 3195 | 4 | US-09-252-991A-937 | Sequence 937, App |
| 297 | 37 | 69.8 | 389504 | 4 | US-09-949-016-11774 | Sequence 11774, A | C 370 | 36 | 67.9 | 3778 | 4 | US-09-799-451-160 | Sequence 160, App |
| 298 | 37 | 69.8 | 767677 | 4 | US-09-949-016-12147 | Sequence 12147, A | C 371 | 36 | 67.9 | 4140 | 4 | US-09-248-796A-6403 | Sequence 6403, Ap |
| 299 | 37 | 69.8 | 767677 | 4 | US-09-949-016-17361 | Sequence 17361, A | C 372 | 36 | 67.9 | 4360 | 1 | US-08-470-350B-1 | Sequence 1, Appl |
| 300 | 37 | 69.8 | 786431 | 4 | US-09-751-389-3 | Sequence 3, Appl | C 373 | 36 | 67.9 | 5802 | 3 | US-09-341-587-4 | Sequence 4, Appl |
| 301 | 36.5 | 68.9 | 107458 | 4 | US-09-949-016-15687 | Sequence 15687, A | C 374 | 36 | 67.9 | 5943 | 4 | US-09-976-594-272 | Sequence 272, App |
| 302 | 36 | 67.9 | 266 | 4 | US-09-016-434-424 | Sequence 424, App | C 375 | 36 | 67.9 | 5943 | 4 | US-09-902-540-3951 | Sequence 3951, Ap |
| 303 | 36 | 67.9 | 325 | 4 | US-09-703-705-1202 | Sequence 1202, Ap | C 376 | 36 | 67.9 | 5973 | 4 | US-09-949-016-546 | Sequence 546, App |
| 304 | 36 | 67.9 | 325 | 4 | US-09-736-457-1202 | Sequence 1202, Ap | C 377 | 36 | 67.9 | 5992 | 4 | | |

| | | | | | | | | | | | | | |
|-------|------|------|--------|---|----------------------|-------------------|-------|----|------|------|---|----------------------|--------------------|
| C 378 | 36 | 67.9 | 5992 | 4 | US-09-949-016-2263 | Sequence 2263, Ap | C 451 | 35 | 66.0 | 601 | 4 | US-09-949-016-28118 | Sequence 28118, A |
| C 379 | 36 | 67.9 | 6776 | 4 | US-09-902-540-884 | Sequence 884, App | C 452 | 35 | 66.0 | 601 | 4 | US-09-949-016-69208 | Sequence 69208, A |
| C 380 | 36 | 67.9 | 12078 | 4 | US-09-799-451-835 | Sequence 835, App | C 453 | 35 | 66.0 | 601 | 4 | US-09-949-016-69209 | Sequence 69209, A |
| C 381 | 36 | 67.9 | 12308 | 4 | US-09-854-133-422 | Sequence 422, App | C 454 | 35 | 66.0 | 601 | 4 | US-09-949-016-69210 | Sequence 69210, A |
| C 382 | 36 | 67.9 | 18627 | 3 | US-08-961-527-113 | Sequence 113, App | C 455 | 35 | 66.0 | 601 | 4 | US-09-949-016-74405 | Sequence 74405, A |
| C 383 | 36 | 67.9 | 19566 | 4 | US-09-949-016-12096 | Sequence 12096, A | C 456 | 35 | 66.0 | 601 | 4 | US-09-949-016-83529 | Sequence 83529, A |
| C 384 | 36 | 67.9 | 19567 | 4 | US-09-949-016-14114 | Sequence 14114, A | C 457 | 35 | 66.0 | 601 | 4 | US-09-949-016-85332 | Sequence 85332, A |
| C 385 | 36 | 67.9 | 20870 | 4 | US-09-949-016-16017 | Sequence 16017, A | C 458 | 35 | 66.0 | 601 | 4 | US-09-949-016-85393 | Sequence 85393, A |
| C 386 | 36 | 67.9 | 21360 | 4 | US-09-949-016-12857 | Sequence 12857, A | C 459 | 35 | 66.0 | 601 | 4 | US-09-949-016-92668 | Sequence 92668, A |
| C 387 | 36 | 67.9 | 21361 | 4 | US-09-949-016-16245 | Sequence 16245, A | C 460 | 35 | 66.0 | 601 | 4 | US-09-949-016-92669 | Sequence 92669, A |
| C 388 | 36 | 67.9 | 21920 | 4 | US-09-949-016-15609 | Sequence 15609, A | C 461 | 35 | 66.0 | 601 | 4 | US-09-949-016-115233 | Sequence 115233, A |
| C 389 | 36 | 67.9 | 22156 | 4 | US-09-902-540-1195 | Sequence 1195, Ap | C 462 | 35 | 66.0 | 601 | 4 | US-09-949-016-115234 | Sequence 115234, A |
| C 390 | 36 | 67.9 | 22339 | 4 | US-09-949-016-14777 | Sequence 14777, A | C 463 | 35 | 66.0 | 601 | 4 | US-09-949-016-116738 | Sequence 116738, A |
| C 391 | 36 | 67.9 | 22598 | 3 | US-09-341-587-7 | Sequence 7, Appli | C 464 | 35 | 66.0 | 601 | 4 | US-09-949-016-116738 | Sequence 116738, A |
| C 392 | 36 | 67.9 | 22598 | 3 | US-09-341-587-6 | Sequence 6, Appli | C 465 | 35 | 66.0 | 601 | 4 | US-09-949-016-122594 | Sequence 122594, A |
| C 393 | 36 | 67.9 | 35524 | 3 | US-08-923-137-1 | Sequence 1, Appli | C 466 | 35 | 66.0 | 601 | 4 | US-09-949-016-122594 | Sequence 122594, A |
| C 394 | 36 | 67.9 | 35524 | 3 | US-09-949-016-15422 | Sequence 15422, A | C 467 | 35 | 66.0 | 601 | 4 | US-09-949-016-156172 | Sequence 156172, A |
| C 395 | 36 | 67.9 | 54420 | 4 | US-09-949-016-13047 | Sequence 13047, A | C 468 | 35 | 66.0 | 601 | 4 | US-09-949-016-164640 | Sequence 164640, A |
| C 396 | 36 | 67.9 | 63183 | 4 | US-09-949-016-13048 | Sequence 13048, A | C 469 | 35 | 66.0 | 601 | 4 | US-09-949-016-179055 | Sequence 179055, A |
| C 397 | 36 | 67.9 | 65986 | 4 | US-09-596-002-29 | Sequence 29, Appl | C 470 | 35 | 66.0 | 601 | 4 | US-09-949-016-179611 | Sequence 179611, A |
| C 398 | 36 | 67.9 | 72704 | 4 | US-09-902-540-1273 | Sequence 1273, Ap | C 471 | 35 | 66.0 | 601 | 4 | US-09-949-016-179612 | Sequence 179612, A |
| C 399 | 36 | 67.9 | 76164 | 4 | US-09-949-016-12288 | Sequence 1288, A | C 472 | 35 | 66.0 | 601 | 4 | US-09-949-016-184717 | Sequence 184717, A |
| C 400 | 36 | 67.9 | 76165 | 4 | US-09-949-016-14005 | Sequence 14005, A | C 473 | 35 | 66.0 | 601 | 4 | US-09-949-016-194510 | Sequence 194510, A |
| C 401 | 36 | 67.9 | 78157 | 4 | US-09-949-016-16466 | Sequence 16466, A | C 474 | 35 | 66.0 | 879 | 4 | US-09-252-991A-5795 | Sequence 5795, Ap |
| C 402 | 36 | 67.9 | 78157 | 4 | US-09-949-016-16467 | Sequence 16467, A | C 475 | 35 | 66.0 | 903 | 4 | US-09-602-787A-191 | Sequence 2319, Ap |
| C 403 | 36 | 67.9 | 100990 | 4 | US-09-409-800B-2 | Sequence 2, Appli | C 476 | 35 | 66.0 | 918 | 4 | US-09-328-352-2319 | Sequence 7, Appli |
| C 404 | 36 | 67.9 | 108924 | 4 | US-09-949-016-13834 | Sequence 13834, A | C 477 | 35 | 66.0 | 959 | 3 | US-09-067-800-7 | Sequence 7, Appli |
| C 405 | 36 | 67.9 | 137226 | 4 | US-09-949-016-13763 | Sequence 13763, A | C 478 | 35 | 66.0 | 959 | 3 | US-09-981-087A-5 | Sequence 5, Appli |
| C 406 | 36 | 67.9 | 141560 | 4 | US-09-949-016-16476 | Sequence 16476, A | C 479 | 35 | 66.0 | 959 | 4 | US-09-978-382A-5 | Sequence 5, Appli |
| C 407 | 36 | 67.9 | 190078 | 4 | US-09-949-016-12707 | Sequence 12707, A | C 480 | 35 | 66.0 | 1032 | 3 | US-09-193-503B-2 | Sequence 2, Appli |
| C 408 | 36 | 67.9 | 190078 | 4 | US-09-949-016-17026 | Sequence 17026, A | C 481 | 35 | 66.0 | 1032 | 3 | US-09-415-839-2 | Sequence 2, Appli |
| C 409 | 36 | 67.9 | 193303 | 4 | US-09-497-855A-37 | Sequence 37, Appl | C 482 | 35 | 66.0 | 1032 | 3 | US-09-328-352-804 | Sequence 804, App |
| C 410 | 36 | 67.9 | 193303 | 4 | US-09-497-855A-44 | Sequence 44, Appl | C 483 | 35 | 66.0 | 1092 | 4 | US-09-540-236-1362 | Sequence 1362, Ap |
| C 411 | 36 | 67.9 | 205163 | 4 | US-09-949-016-17009 | Sequence 17009, A | C 484 | 35 | 66.0 | 1104 | 4 | US-09-569-611C-19 | Sequence 19, Appl |
| C 412 | 36 | 67.9 | 209210 | 4 | US-09-949-016-15094 | Sequence 15094, A | C 485 | 35 | 66.0 | 1140 | 4 | US-09-176-666-54 | Sequence 54, Appl |
| C 413 | 36 | 67.9 | 250715 | 4 | US-09-949-016-13294 | Sequence 13294, A | C 486 | 35 | 66.0 | 1158 | 3 | US-09-176-666-53 | Sequence 53, Appl |
| C 414 | 36 | 67.9 | 254405 | 4 | US-09-949-016-14381 | Sequence 14381, A | C 487 | 35 | 66.0 | 1158 | 3 | US-09-176-666-52 | Sequence 52, Appl |
| C 415 | 36 | 67.9 | 256287 | 4 | US-09-949-016-14608 | Sequence 14608, A | C 488 | 35 | 66.0 | 1161 | 3 | US-09-176-666-51 | Sequence 51, Appl |
| C 416 | 35.5 | 67.0 | 156 | 4 | US-09-513-999C-18957 | Sequence 18957, A | C 489 | 35 | 66.0 | 1163 | 3 | US-09-176-666-50 | Sequence 50, Appl |
| C 417 | 35.5 | 67.0 | 601 | 4 | US-09-949-016-81525 | Sequence 81525, A | C 490 | 35 | 66.0 | 1170 | 3 | US-09-176-666-49 | Sequence 49, Appl |
| C 418 | 35.5 | 67.0 | 857 | 4 | US-09-270-767-28776 | Sequence 28776, A | C 491 | 35 | 66.0 | 1170 | 3 | US-09-176-666-48 | Sequence 48, Appl |
| C 419 | 35.5 | 67.0 | 1326 | 4 | US-09-543-681A-846 | Sequence 846, App | C 492 | 35 | 66.0 | 1173 | 3 | US-09-176-666-47 | Sequence 47, Appl |
| C 420 | 35.5 | 67.0 | 1740 | 4 | US-09-949-016-2873 | Sequence 2873, Ap | C 493 | 35 | 66.0 | 1176 | 3 | US-09-176-666-46 | Sequence 46, Appl |
| C 421 | 35.5 | 67.0 | 1767 | 4 | US-09-949-016-497 | Sequence 49, Appl | C 494 | 35 | 66.0 | 1179 | 3 | US-09-176-666-45 | Sequence 45, Appl |
| C 422 | 35.5 | 67.0 | 2862 | 4 | US-09-270-767-12914 | Sequence 12914, A | C 495 | 35 | 66.0 | 1182 | 3 | US-09-176-666-44 | Sequence 44, Appl |
| C 423 | 35.5 | 67.0 | 8801 | 4 | US-09-949-016-11791 | Sequence 11791, A | C 496 | 35 | 66.0 | 1188 | 3 | US-09-489-039A-4952 | Sequence 4952, Ap |
| C 424 | 35.5 | 67.0 | 8801 | 4 | US-09-949-016-14613 | Sequence 14613, A | C 497 | 35 | 66.0 | 1188 | 3 | US-09-176-666-43 | Sequence 43, Appl |
| C 425 | 35.5 | 67.0 | 12880 | 4 | US-09-949-016-16733 | Sequence 16733, A | C 498 | 35 | 66.0 | 1194 | 3 | US-09-928-881-25 | Sequence 25, Appl |
| C 426 | 35.5 | 67.0 | 19319 | 4 | US-09-949-016-14107 | Sequence 14107, A | C 499 | 35 | 66.0 | 1197 | 3 | US-09-543-921-25 | Sequence 25, Appl |
| C 427 | 35.5 | 67.0 | 93778 | 4 | US-09-949-016-15096 | Sequence 15096, A | C 500 | 35 | 66.0 | 1197 | 3 | US-08-798-000-2 | Sequence 5, Appli |
| C 428 | 35 | 66.0 | 28 | 4 | US-08-559-306-27 | Sequence 27, Appl | C 501 | 35 | 66.0 | 1197 | 3 | US-09-266-014-5 | Sequence 25, Appl |
| C 429 | 35 | 66.0 | 47 | 3 | US-09-338-907-261 | Sequence 261, App | C 502 | 35 | 66.0 | 1197 | 3 | US-09-491-759-25 | Sequence 1001, Ap |
| C 430 | 35 | 66.0 | 47 | 3 | US-09-218-207-261 | Sequence 261, App | C 503 | 35 | 66.0 | 1214 | 4 | US-09-023-655-1001 | Sequence 973, App |
| C 431 | 35 | 66.0 | 183 | 4 | US-09-248-796A-13029 | Sequence 13029, A | C 504 | 35 | 66.0 | 1225 | 4 | US-09-620-312D-973 | Sequence 913, App |
| C 432 | 35 | 66.0 | 249 | 4 | US-09-328-352-845 | Sequence 845, App | C 505 | 35 | 66.0 | 1236 | 3 | US-09-328-352-913 | Sequence 2, Appli |
| C 433 | 35 | 66.0 | 268 | 3 | US-08-928-881-20 | Sequence 20, Appl | C 506 | 35 | 66.0 | 1237 | 1 | US-08-798-000-2 | Sequence 2, Appli |
| C 434 | 35 | 66.0 | 268 | 3 | US-09-543-921-20 | Sequence 20, Appl | C 507 | 35 | 66.0 | 1272 | 4 | US-09-270-767-14080 | Sequence 14080, A |
| C 435 | 35 | 66.0 | 268 | 3 | US-09-266-014-2 | Sequence 2, Appli | C 508 | 35 | 66.0 | 1293 | 4 | US-09-252-991A-6028 | Sequence 6028, Ap |
| C 436 | 35 | 66.0 | 268 | 3 | US-09-491-759-20 | Sequence 20, Appl | C 509 | 35 | 66.0 | 1304 | 6 | 5179023-3 | Patent No. 5179023 |
| C 437 | 35 | 66.0 | 285 | 4 | US-09-621-976-17129 | Sequence 17129, A | C 510 | 35 | 66.0 | 1304 | 6 | 5179023-3 | Patent No. 5179023 |
| C 438 | 35 | 66.0 | 415 | 4 | US-09-621-976-17129 | Sequence 17129, A | C 511 | 35 | 66.0 | 1343 | 3 | US-08-928-881-18 | Sequence 18, Appl |
| C 439 | 35 | 66.0 | 422 | 4 | US-09-270-767-7856 | Sequence 7856, Ap | C 512 | 35 | 66.0 | 1343 | 3 | US-09-543-921-18 | Sequence 18, Appl |
| C 440 | 35 | 66.0 | 422 | 4 | US-09-270-767-23138 | Sequence 23138, A | C 513 | 35 | 66.0 | 1343 | 3 | US-09-266-014-3 | Sequence 3, Appli |
| C 441 | 35 | 66.0 | 435 | 4 | US-09-513-999C-295 | Sequence 295, App | C 514 | 35 | 66.0 | 1343 | 4 | US-09-491-759-18 | Sequence 18, Appl |
| C 442 | 35 | 66.0 | 464 | 3 | US-09-268-364-11 | Sequence 11, Appl | C 515 | 35 | 66.0 | 1393 | 1 | US-07-602-824A-1 | Sequence 1, Appli |
| C 443 | 35 | 66.0 | 465 | 4 | US-09-229-583A-20 | Sequence 20, Appl | C 516 | 35 | 66.0 | 1393 | 1 | US-07-983-451-1 | Sequence 1, Appli |
| C 444 | 35 | 66.0 | 465 | 4 | US-10-187-904-20 | Sequence 20, Appl | C 517 | 35 | 66.0 | 1393 | 1 | US-08-261-577-6 | Sequence 6, Appli |
| C 445 | 35 | 66.0 | 492 | 4 | US-09-602-787A-559 | Sequence 559, App | C 518 | 35 | 66.0 | 1431 | 4 | US-09-252-991A-5315 | Sequence 5315, Ap |
| C 446 | 35 | 66.0 | 492 | 4 | US-09-603-208A-299 | Sequence 299, App | C 519 | 35 | 66.0 | 1476 | 3 | US-09-930-872-1 | Sequence 1, Appli |
| C 447 | 35 | 66.0 | 525 | 4 | US-09-252-991A-5225 | Sequence 5225, Ap | C 520 | 35 | 66.0 | 1476 | 4 | US-10-217-774-1 | Sequence 1, Appli |
| C 448 | 35 | 66.0 | 601 | 4 | US-09-949-016-23751 | Sequence 23751, A | C 521 | 35 | 66.0 | 1482 | 4 | US-09-489-039A-1148 | Sequence 1148, Ap |
| C 449 | 35 | 66.0 | 601 | 4 | US-09-949-016-27713 | Sequence 27713, A | C 522 | 35 | 66.0 | 1566 | 4 | US-09-252-991A-6115 | Sequence 6115, Ap |
| C 450 | 35 | 66.0 | 601 | 4 | US-09-949-016-28117 | Sequence 28117, A | C 523 | 35 | 66.0 | 1569 | 2 | US-08-145-658D-23 | Sequence 23, Appl |

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|-------|----|------|------|---|----------------------|-------------------|-------|----|------|--------|---|---------------------|-------------------|
| 524 | 35 | 66.0 | 1617 | 4 | US-09-252-991A-5856 | Sequence 5856, Ap | 597 | 35 | 66.0 | 8912 | 3 | US-08-469-260A-11 | Sequence 11, Appl |
| 525 | 35 | 66.0 | 1669 | 4 | US-09-949-016-4250 | Sequence 4250, Ap | 598 | 35 | 66.0 | 8912 | 4 | US-08-488-446-11 | Sequence 11, Appl |
| C 526 | 35 | 66.0 | 1744 | 3 | US-08-961-083-131 | Sequence 131, App | 599 | 35 | 66.0 | 8912 | 4 | US-08-467-344A-11 | Sequence 11, Appl |
| C 527 | 35 | 66.0 | 1744 | 4 | US-09-536-784-131 | Sequence 131, App | 600 | 35 | 66.0 | 8912 | 4 | US-08-424-550B-11 | Sequence 11, Appl |
| C 528 | 35 | 66.0 | 1761 | 4 | US-09-252-991A-13349 | Sequence 13349, A | c 601 | 35 | 66.0 | 9173 | 4 | US-09-949-016-15206 | Sequence 15206, A |
| C 529 | 35 | 66.0 | 1814 | 4 | US-09-702-705-319 | Sequence 319, App | c 602 | 35 | 66.0 | 9267 | 4 | US-09-949-016-17441 | Sequence 17441, A |
| C 530 | 35 | 66.0 | 1814 | 4 | US-09-736-457-319 | Sequence 319, App | c 603 | 35 | 66.0 | 9273 | 4 | US-08-949-016-16184 | Sequence 16184, A |
| C 531 | 35 | 66.0 | 1814 | 4 | US-09-614-124B-319 | Sequence 319, App | c 604 | 35 | 66.0 | 10711 | 3 | US-08-961-527-145 | Sequence 145, App |
| C 532 | 35 | 66.0 | 1814 | 4 | US-09-671-325-319 | Sequence 319, App | c 605 | 35 | 66.0 | 11490 | 4 | US-09-949-016-14149 | Sequence 14149, A |
| C 533 | 35 | 66.0 | 1814 | 4 | US-09-589-184-319 | Sequence 319, App | c 606 | 35 | 66.0 | 11828 | 4 | US-09-949-016-15992 | Sequence 15992, A |
| C 534 | 35 | 66.0 | 1814 | 4 | US-09-658-824-319 | Sequence 319, App | c 607 | 35 | 66.0 | 12703 | 4 | US-09-949-016-16685 | Sequence 16685, A |
| C 535 | 35 | 66.0 | 1860 | 4 | US-09-949-016-2407 | Sequence 2407, Ap | c 608 | 35 | 66.0 | 12725 | 4 | US-09-949-016-14177 | Sequence 14177, A |
| C 536 | 35 | 66.0 | 1884 | 1 | US-08-307-382-3 | Sequence 3, Appli | c 609 | 35 | 66.0 | 13634 | 4 | US-09-949-016-16376 | Sequence 16376, A |
| 537 | 35 | 66.0 | 1884 | 1 | US-08-366-779-3 | Sequence 3, Appli | c 610 | 35 | 66.0 | 13935 | 4 | US-09-949-016-12247 | Sequence 12247, A |
| 538 | 35 | 66.0 | 1884 | 1 | US-08-478-727-3 | Sequence 3, Appli | c 611 | 35 | 66.0 | 14395 | 4 | US-09-949-016-16357 | Sequence 16357, A |
| 539 | 35 | 66.0 | 1884 | 1 | US-08-473-508-3 | Sequence 3, Appli | c 612 | 35 | 66.0 | 17198 | 4 | US-09-949-016-13776 | Sequence 13776, A |
| 540 | 35 | 66.0 | 1884 | 1 | US-08-789-936-3 | Sequence 3, Appli | c 613 | 35 | 66.0 | 17746 | 4 | US-09-949-016-12020 | Sequence 12020, A |
| 541 | 35 | 66.0 | 1884 | 3 | US-08-934-254-3 | Sequence 3, Appli | c 614 | 35 | 66.0 | 17750 | 4 | US-09-949-016-16909 | Sequence 16909, A |
| 542 | 35 | 66.0 | 1884 | 4 | US-09-685-775-3 | Sequence 3, Appli | c 615 | 35 | 66.0 | 20026 | 4 | US-09-949-016-13147 | Sequence 13147, A |
| 543 | 35 | 66.0 | 1902 | 4 | US-09-489-039A-6558 | Sequence 6558, Ap | c 616 | 35 | 66.0 | 20063 | 4 | US-09-949-016-14176 | Sequence 14176, A |
| 544 | 35 | 66.0 | 2086 | 3 | US-09-221-017B-188 | Sequence 188, App | c 617 | 35 | 66.0 | 20520 | 4 | US-09-949-016-14394 | Sequence 14394, A |
| 545 | 35 | 66.0 | 2202 | 4 | US-09-016-434-1443 | Sequence 1443, Ap | c 618 | 35 | 66.0 | 21978 | 4 | US-09-949-016-16646 | Sequence 16646, A |
| C 546 | 35 | 66.0 | 2214 | 4 | US-09-583-110-2414 | Sequence 2414, Ap | c 619 | 35 | 66.0 | 23260 | 4 | US-09-949-016-11985 | Sequence 11985, A |
| C 547 | 35 | 66.0 | 2292 | 4 | US-09-107-433-1007 | Sequence 1007, Ap | c 620 | 35 | 66.0 | 23260 | 4 | US-09-949-016-12907 | Sequence 12907, A |
| C 548 | 35 | 66.0 | 2346 | 3 | US-09-193-503B-5 | Sequence 5, Appli | c 621 | 35 | 66.0 | 23370 | 4 | US-09-949-016-12109 | Sequence 12109, A |
| C 549 | 35 | 66.0 | 2346 | 4 | US-09-415-839-5 | Sequence 5, Appli | c 622 | 35 | 66.0 | 23375 | 4 | US-09-949-016-15880 | Sequence 15880, A |
| C 550 | 35 | 66.0 | 2352 | 2 | US-08-922-837-1 | Sequence 1, Appli | c 623 | 35 | 66.0 | 27430 | 4 | US-09-949-016-13402 | Sequence 13402, A |
| C 551 | 35 | 66.0 | 2352 | 3 | US-09-351-550-1 | Sequence 1, Appli | c 624 | 35 | 66.0 | 34276 | 4 | US-09-949-016-12263 | Sequence 12263, A |
| C 552 | 35 | 66.0 | 2391 | 4 | US-09-252-991A-5812 | Sequence 5812, Ap | c 625 | 35 | 66.0 | 34278 | 4 | US-09-949-016-16103 | Sequence 16103, A |
| 553 | 35 | 66.0 | 2459 | 4 | US-09-799-451-853 | Sequence 853, App | c 626 | 35 | 66.0 | 36651 | 3 | US-09-738-89A-3 | Sequence 3, Appli |
| 554 | 35 | 66.0 | 2460 | 4 | US-09-328-332-1216 | Sequence 1216, Ap | c 627 | 35 | 66.0 | 36651 | 4 | US-09-964-469-3 | Sequence 3, Appli |
| 555 | 35 | 66.0 | 2478 | 4 | US-09-949-016-3640 | Sequence 3640, Ap | c 628 | 35 | 66.0 | 44608 | 4 | US-09-949-016-15604 | Sequence 15604, A |
| 556 | 35 | 66.0 | 2629 | 3 | US-09-392-184-17 | Sequence 17, Appl | c 629 | 35 | 66.0 | 46794 | 4 | US-09-949-016-12399 | Sequence 12399, A |
| C 557 | 35 | 66.0 | 2647 | 4 | US-09-774-528-377 | Sequence 377, App | c 630 | 35 | 66.0 | 47284 | 4 | US-09-949-016-17029 | Sequence 17029, A |
| C 558 | 35 | 66.0 | 2690 | 1 | US-08-524-757-11 | Sequence 11, Appl | c 631 | 35 | 66.0 | 51336 | 4 | US-09-949-016-16054 | Sequence 16054, A |
| 559 | 35 | 66.0 | 2722 | 4 | US-09-949-016-3115 | Sequence 3115, Ap | c 632 | 35 | 66.0 | 51928 | 4 | US-09-949-016-13184 | Sequence 13184, A |
| 560 | 35 | 66.0 | 2828 | 4 | US-09-461-912A-31 | Sequence 31, Appl | c 634 | 35 | 66.0 | 55216 | 4 | US-09-716-865-23 | Sequence 23, Appl |
| 561 | 35 | 66.0 | 2828 | 4 | US-09-949-016-293 | Sequence 293, App | c 635 | 35 | 66.0 | 55844 | 4 | US-09-949-016-13769 | Sequence 13769, A |
| 562 | 35 | 66.0 | 2828 | 4 | US-09-949-016-3911 | Sequence 3911, Ap | c 636 | 35 | 66.0 | 63804 | 4 | US-09-949-016-15200 | Sequence 15200, A |
| 563 | 35 | 66.0 | 3035 | 1 | US-08-726-725-2 | Sequence 2, Appli | c 637 | 35 | 66.0 | 63804 | 4 | US-09-949-016-13608 | Sequence 13608, A |
| C 564 | 35 | 66.0 | 3156 | 4 | US-09-799-451-870 | Sequence 870, App | c 638 | 35 | 66.0 | 65062 | 4 | US-09-949-016-13609 | Sequence 13609, A |
| 565 | 35 | 66.0 | 3588 | 1 | US-08-307-382-1 | Sequence 1, Appli | c 639 | 35 | 66.0 | 65062 | 4 | US-09-949-016-12890 | Sequence 12890, A |
| 566 | 35 | 66.0 | 3588 | 1 | US-08-366-779-1 | Sequence 1, Appli | c 640 | 35 | 66.0 | 65687 | 4 | US-09-949-016-12890 | Sequence 12890, A |
| 567 | 35 | 66.0 | 3588 | 1 | US-08-478-727-1 | Sequence 1, Appli | c 641 | 35 | 66.0 | 75176 | 4 | US-09-949-016-13300 | Sequence 13300, A |
| 568 | 35 | 66.0 | 3588 | 1 | US-08-473-508-1 | Sequence 1, Appli | c 642 | 35 | 66.0 | 81701 | 4 | US-09-949-016-14891 | Sequence 14891, A |
| 569 | 35 | 66.0 | 3588 | 1 | US-08-789-936-1 | Sequence 1, Appli | c 643 | 35 | 66.0 | 92681 | 4 | US-09-949-016-14772 | Sequence 14772, A |
| 570 | 35 | 66.0 | 3588 | 3 | US-08-934-254-1 | Sequence 1, Appli | c 644 | 35 | 66.0 | 94155 | 4 | US-09-949-016-12388 | Sequence 12388, A |
| 571 | 35 | 66.0 | 3588 | 4 | US-09-685-775-1 | Sequence 1, Appli | c 645 | 35 | 66.0 | 94855 | 4 | US-09-949-016-12264 | Sequence 12264, A |
| C 572 | 35 | 66.0 | 3615 | 3 | US-09-221-017B-971 | Sequence 971, App | c 646 | 35 | 66.0 | 97221 | 4 | US-09-949-016-12755 | Sequence 12755, A |
| C 573 | 35 | 66.0 | 3675 | 3 | US-09-930-872-3 | Sequence 3, Appli | c 647 | 35 | 66.0 | 97448 | 4 | US-09-949-016-11990 | Sequence 11990, A |
| C 574 | 35 | 66.0 | 3675 | 4 | US-10-217-774-3 | Sequence 3, Appli | c 648 | 35 | 66.0 | 99749 | 4 | US-09-949-016-16518 | Sequence 16518, A |
| 575 | 35 | 66.0 | 4031 | 1 | US-08-159-784-1 | Sequence 1, Appli | c 649 | 35 | 66.0 | 102406 | 4 | US-09-949-016-14673 | Sequence 14673, A |
| C 576 | 35 | 66.0 | 4042 | 3 | US-09-930-872-5 | Sequence 5, Appli | c 650 | 35 | 66.0 | 105038 | 4 | US-09-949-016-12199 | Sequence 12199, A |
| C 577 | 35 | 66.0 | 4042 | 4 | US-10-217-774-5 | Sequence 5, Appli | c 651 | 35 | 66.0 | 114842 | 4 | US-09-949-016-14993 | Sequence 14993, A |
| C 578 | 35 | 66.0 | 4050 | 4 | US-09-270-767-12166 | Sequence 12166, A | c 652 | 35 | 66.0 | 119032 | 4 | US-09-949-016-12160 | Sequence 12160, A |
| C 579 | 35 | 66.0 | 4528 | 4 | US-08-809-254A-6 | Sequence 6, Appli | c 653 | 35 | 66.0 | 119032 | 4 | US-09-949-016-17268 | Sequence 17268, A |
| C 580 | 35 | 66.0 | 4895 | 3 | US-09-053-866-1 | Sequence 1, Appli | c 654 | 35 | 66.0 | 120609 | 4 | US-09-949-016-13915 | Sequence 13915, A |
| C 581 | 35 | 66.0 | 4895 | 3 | US-09-479-130-1 | Sequence 1, Appli | c 655 | 35 | 66.0 | 127280 | 4 | US-09-949-016-14857 | Sequence 14857, A |
| C 582 | 35 | 66.0 | 4895 | 4 | US-09-472-130A-1 | Sequence 1, Appli | c 656 | 35 | 66.0 | 132266 | 4 | US-09-949-016-14860 | Sequence 14860, A |
| 583 | 35 | 66.0 | 5293 | 4 | US-09-949-016-17385 | Sequence 17385, A | c 657 | 35 | 66.0 | 145241 | 4 | US-09-949-016-17395 | Sequence 17395, A |
| 584 | 35 | 66.0 | 5304 | 4 | US-09-583-110-1314 | Sequence 1314, Ap | c 658 | 35 | 66.0 | 145241 | 4 | US-09-949-016-17395 | Sequence 17395, A |
| 585 | 35 | 66.0 | 5310 | 4 | US-09-107-433-1073 | Sequence 1073, Ap | c 659 | 35 | 66.0 | 150833 | 4 | US-09-949-016-14859 | Sequence 14859, A |
| C 586 | 35 | 66.0 | 6138 | 3 | US-09-067-800-4 | Sequence 4, Appli | c 660 | 35 | 66.0 | 152393 | 4 | US-09-949-016-14514 | Sequence 14514, A |
| C 587 | 35 | 66.0 | 6138 | 2 | US-09-349-677-4 | Sequence 4, Appli | c 661 | 35 | 66.0 | 152393 | 4 | US-09-949-016-14515 | Sequence 14515, A |
| C 588 | 35 | 66.0 | 6318 | 2 | US-08-808-793-1 | Sequence 1, Appli | c 662 | 35 | 66.0 | 156894 | 4 | US-09-949-016-12765 | Sequence 12765, A |
| C 589 | 35 | 66.0 | 6318 | 3 | US-08-772-512A-1 | Sequence 1, Appli | c 663 | 35 | 66.0 | 156894 | 4 | US-09-949-016-12766 | Sequence 12766, A |
| C 590 | 35 | 66.0 | 6318 | 4 | US-09-428-371-1 | Sequence 1, Appli | c 664 | 35 | 66.0 | 156895 | 4 | US-09-949-016-16957 | Sequence 16957, A |
| 591 | 35 | 66.0 | 6468 | 4 | US-09-902-540-895 | Sequence 895, App | c 665 | 35 | 66.0 | 156895 | 4 | US-09-949-016-16958 | Sequence 16958, A |
| C 592 | 35 | 66.0 | 6468 | 4 | US-09-902-540-853 | Sequence 853, App | c 666 | 35 | 66.0 | 159963 | 4 | US-09-949-016-14858 | Sequence 14858, A |
| 593 | 35 | 66.0 | 6828 | 4 | US-09-949-016-12035 | Sequence 12035, A | c 667 | 35 | 66.0 | 159963 | 4 | US-09-949-016-14861 | Sequence 14861, A |
| 594 | 35 | 66.0 | 6828 | 4 | US-09-949-016-15653 | Sequence 15653, A | c 668 | 35 | 66.0 | 171130 | 4 | US-09-949-016-15970 | Sequence 15970, A |
| 595 | 35 | 66.0 | 7594 | 4 | US-09-949-016-17582 | Sequence 17582, A | c 669 | 35 | 66.0 | 181251 | 4 | US-09-949-016-15970 | Sequence 15970, A |
| C 596 | 35 | 66.0 | 8657 | 3 | US-08-961-527-44 | Sequence 44, Appl | c 669 | 35 | 66.0 | 197336 | 4 | US-09-949-016-12881 | Sequence 12881, A |

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|-------|------|------|---------|---|----------------------|-------------------|-------|----|------|-----|---|----------------------|--------------------|
| c 670 | 35 | 66.0 | 197337 | 4 | US-09-949-016-14376 | Sequence 14376, A | 743 | 34 | 64.2 | 344 | 2 | US-09-032-684-16 | Sequence 16, Appl |
| c 671 | 35 | 66.0 | 199945 | 4 | US-09-949-016-15436 | Sequence 15436, A | 744 | 34 | 64.2 | 344 | 4 | US-09-644-460-16 | Sequence 16, Appl |
| c 672 | 35 | 66.0 | 212449 | 4 | US-09-949-016-15419 | Sequence 15419, A | 745 | 34 | 64.2 | 366 | 4 | US-09-902-540-2718 | Sequence 2718, Ap |
| c 673 | 35 | 66.0 | 234288 | 4 | US-09-949-016-17272 | Sequence 17272, A | 746 | 34 | 64.2 | 368 | 4 | US-09-513-999C-2349 | Sequence 2349, Ap |
| c 674 | 35 | 66.0 | 247781 | 4 | US-09-949-016-14193 | Sequence 14193, A | 747 | 34 | 64.2 | 382 | 4 | US-09-513-999C-34543 | Sequence 34543, A |
| c 675 | 35 | 66.0 | 251672 | 4 | US-09-949-016-17296 | Sequence 17296, A | 748 | 34 | 64.2 | 408 | 4 | US-09-134-000C-2905 | Sequence 2905, Ap |
| c 676 | 35 | 66.0 | 251682 | 4 | US-09-949-016-11973 | Sequence 11973, A | 749 | 34 | 64.2 | 411 | 3 | US-09-071-035-433 | Sequence 433, App |
| c 677 | 35 | 66.0 | 252682 | 4 | US-09-596-002-41 | Sequence 41, Appl | 750 | 34 | 64.2 | 432 | 3 | US-09-397-787-191 | Sequence 191, App |
| c 678 | 35 | 66.0 | 269223 | 4 | US-09-949-016-15371 | Sequence 15371, A | c 751 | 34 | 64.2 | 433 | 3 | US-09-615-192A-167 | Sequence 167, App |
| c 679 | 35 | 66.0 | 304533 | 4 | US-09-949-016-15372 | Sequence 15372, A | c 752 | 34 | 64.2 | 433 | 4 | US-09-169-789-167 | Sequence 167, App |
| c 680 | 35 | 66.0 | 312470 | 4 | US-09-949-016-14043 | Sequence 14043, A | 753 | 34 | 64.2 | 439 | 4 | US-09-270-767-835 | Sequence 835, App |
| c 681 | 35 | 66.0 | 319608 | 4 | US-09-539-333D-1 | Sequence 1, Appl | 754 | 34 | 64.2 | 439 | 4 | US-09-270-767-16117 | Sequence 16117, A |
| c 682 | 35 | 66.0 | 319608 | 4 | US-09-679-409-1 | Sequence 1, Appl | 755 | 34 | 64.2 | 441 | 4 | US-09-252-991A-9359 | Sequence 9359, Ap |
| c 683 | 35 | 66.0 | 325034 | 4 | US-09-949-016-14957 | Sequence 14957, A | c 756 | 34 | 64.2 | 459 | 4 | US-09-621-976-18663 | Sequence 18663, A |
| c 684 | 35 | 66.0 | 336024 | 4 | US-09-949-016-12373 | Sequence 12373, A | c 757 | 34 | 64.2 | 461 | 4 | US-09-513-999C-4024 | Sequence 4024, Ap |
| c 685 | 35 | 66.0 | 389504 | 4 | US-09-949-016-11774 | Sequence 11774, A | 758 | 34 | 64.2 | 479 | 4 | US-09-495-050A-278 | Sequence 278, App |
| c 686 | 35 | 66.0 | 421491 | 4 | US-09-949-016-12805 | Sequence 12805, A | 759 | 34 | 64.2 | 492 | 4 | US-09-252-991A-12040 | Sequence 12040, A |
| c 687 | 35 | 66.0 | 421494 | 4 | US-09-949-016-14060 | Sequence 14060, A | c 760 | 34 | 64.2 | 517 | 4 | US-09-621-976-2387 | Sequence 2387, Ap |
| c 688 | 35 | 66.0 | 455726 | 4 | US-09-949-016-14157 | Sequence 14157, A | c 761 | 34 | 64.2 | 537 | 4 | US-09-252-991A-15043 | Sequence 15043, A |
| c 689 | 35 | 66.0 | 481115 | 4 | US-09-949-016-11940 | Sequence 11940, A | c 762 | 34 | 64.2 | 591 | 4 | US-09-949-016-14508 | Sequence 14508, A |
| c 690 | 35 | 66.0 | 1230025 | 4 | US-09-198-452A-1 | Sequence 1, Appl | 763 | 34 | 64.2 | 601 | 4 | US-09-949-016-18456 | Sequence 18456, A |
| c 691 | 35 | 66.0 | 1230230 | 4 | US-09-438-185A-1 | Sequence 1, Appl | 764 | 34 | 64.2 | 601 | 4 | US-09-949-016-19999 | Sequence 19999, A |
| c 692 | 35 | 66.0 | 1830121 | 4 | US-09-557-884-1 | Sequence 1, Appl | c 765 | 34 | 64.2 | 601 | 4 | US-09-949-016-24098 | Sequence 24098, A |
| c 693 | 35 | 66.0 | 1830121 | 4 | US-09-643-990A-1 | Sequence 1, Appl | c 766 | 34 | 64.2 | 601 | 4 | US-09-949-016-27960 | Sequence 27960, A |
| c 694 | 34.5 | 65.1 | 601 | 4 | US-09-949-016-195920 | Sequence 195920, | c 767 | 34 | 64.2 | 601 | 4 | US-09-949-016-27960 | Sequence 27961, A |
| c 695 | 34.5 | 65.1 | 1128 | 3 | US-09-161-994A-1 | Sequence 1, Appl | 768 | 34 | 64.2 | 601 | 4 | US-09-949-016-31754 | Sequence 31754, A |
| c 696 | 34.5 | 65.1 | 1222 | 1 | US-08-314-596-43 | Sequence 43, Appl | 769 | 34 | 64.2 | 601 | 4 | US-09-949-016-32011 | Sequence 32011, A |
| c 697 | 34.5 | 65.1 | 1222 | 1 | US-08-320-982-43 | Sequence 43, Appl | 770 | 34 | 64.2 | 601 | 4 | US-09-949-016-32012 | Sequence 32012, A |
| c 698 | 34.5 | 65.1 | 1222 | 3 | US-08-819-037-43 | Sequence 43, Appl | c 771 | 34 | 64.2 | 601 | 4 | US-09-949-016-34020 | Sequence 34020, A |
| c 699 | 34.5 | 65.1 | 1222 | 3 | US-09-045-940-43 | Sequence 43, Appl | c 772 | 34 | 64.2 | 601 | 4 | US-09-949-016-34021 | Sequence 34021, A |
| c 700 | 34.5 | 65.1 | 1311 | 4 | US-09-638-937-3 | Sequence 3, Appl | c 773 | 34 | 64.2 | 601 | 4 | US-09-949-016-34032 | Sequence 34032, A |
| c 701 | 34.5 | 65.1 | 1312 | 3 | US-09-059-769-3 | Sequence 3, Appl | c 774 | 34 | 64.2 | 601 | 4 | US-09-949-016-34326 | Sequence 34326, A |
| c 702 | 34.5 | 65.1 | 1337 | 3 | US-09-638-937-12 | Sequence 12, Appl | c 775 | 34 | 64.2 | 601 | 4 | US-09-949-016-38964 | Sequence 38964, A |
| c 703 | 34.5 | 65.1 | 1358 | 3 | US-09-059-769-1 | Sequence 1, Appl | c 776 | 34 | 64.2 | 601 | 4 | US-09-949-016-46868 | Sequence 46868, A |
| c 704 | 34.5 | 65.1 | 1361 | 4 | US-09-638-937-10 | Sequence 10, Appl | c 777 | 34 | 64.2 | 601 | 4 | US-09-949-016-53273 | Sequence 53273, A |
| c 705 | 34.5 | 65.1 | 1369 | 2 | US-08-872-302-3 | Sequence 3, Appl | c 778 | 34 | 64.2 | 601 | 4 | US-09-949-016-53274 | Sequence 53274, A |
| c 706 | 34.5 | 65.1 | 1369 | 3 | US-09-133-962A-11 | Sequence 11, Appl | c 779 | 34 | 64.2 | 601 | 4 | US-09-949-016-53275 | Sequence 53275, A |
| c 707 | 34.5 | 65.1 | 1448 | 1 | US-08-314-596-39 | Sequence 39, Appl | 780 | 34 | 64.2 | 601 | 4 | US-09-949-016-55181 | Sequence 55181, A |
| c 708 | 34.5 | 65.1 | 1448 | 1 | US-08-320-982-39 | Sequence 39, Appl | 781 | 34 | 64.2 | 601 | 4 | US-09-949-016-59863 | Sequence 59863, A |
| c 709 | 34.5 | 65.1 | 1448 | 3 | US-08-819-037-39 | Sequence 39, Appl | 782 | 34 | 64.2 | 601 | 4 | US-09-949-016-59904 | Sequence 59904, A |
| c 710 | 34.5 | 65.1 | 1448 | 3 | US-09-045-940-39 | Sequence 39, Appl | c 783 | 34 | 64.2 | 601 | 4 | US-09-949-016-60298 | Sequence 60298, A |
| c 711 | 34.5 | 65.1 | 1457 | 4 | US-09-638-937-1 | Sequence 1, Appl | c 784 | 34 | 64.2 | 601 | 4 | US-09-949-016-64344 | Sequence 64344, A |
| c 712 | 34.5 | 65.1 | 1855 | 3 | US-08-530-862B-3 | Sequence 3, Appl | c 785 | 34 | 64.2 | 601 | 4 | US-09-949-016-64375 | Sequence 64375, A |
| c 713 | 34.5 | 65.1 | 1855 | 3 | US-08-597-313D-3 | Sequence 3, Appl | c 786 | 34 | 64.2 | 601 | 4 | US-09-949-016-64406 | Sequence 64406, A |
| c 714 | 34.5 | 65.1 | 3670 | 2 | US-08-898-038-1 | Sequence 1, Appl | c 787 | 34 | 64.2 | 601 | 4 | US-09-949-016-64437 | Sequence 64437, A |
| c 715 | 34.5 | 65.1 | 3670 | 3 | US-09-352-125-1 | Sequence 1, Appl | c 788 | 34 | 64.2 | 601 | 4 | US-09-949-016-64468 | Sequence 64468, A |
| c 716 | 34 | 64.2 | 18 | 2 | US-08-244-205-22 | Sequence 22, Appl | c 789 | 34 | 64.2 | 601 | 4 | US-09-949-016-64499 | Sequence 64499, A |
| c 717 | 34 | 64.2 | 18 | 2 | US-08-244-205-23 | Sequence 23, Appl | c 790 | 34 | 64.2 | 601 | 4 | US-09-949-016-64530 | Sequence 64530, A |
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ALIGNMENTS

RESULT 1
US-08-831-570-1
; Sequence 1, Application US/08831570
; Patent No. 5959175
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; APPLICANT: Nunberg, Andrew N.
; APPLICANT: Berenbaum, Phillip D.
; TITLE OF INVENTION: A SUNFLOWER ALBUMIN 5' REGULATORY REGION
; TITLE OF INVENTION: FOR THE MODIFICATION OF PLANT SEED LIPID
; TITLE OF INVENTION: COMPOSITION
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/831,570
; FILING DATE: 09-APR-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.

; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10545
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 743-4366
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1684 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 43..1387
US-08-831-570-1
Alignment Scores:
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Score: 53.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
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Qy 1 TrrileglyHisaspAlaGlyHis 8
Db 508 TGGATTGGACATGATGCTGGCAT 531
RESULT 2
US-08-831-575-1
; Sequence 1, Application US/08831575
; Patent No. 5977436
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; APPLICANT: Li, Zhongsen
; TITLE OF INVENTION: AN OLEOSIN 5' REGULATORY REGION FOR THE
; TITLE OF INVENTION: MODIFICATION OF PLANT SEED LIPID COMPOSITION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/831,575
; FILING DATE: 09-APR-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 10203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1684 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS

| | | | | | | | | | | | | | | | | | | | | |
|---|----------------------------------|--|--|--|--|--|--|--|--------------------|--------------------------|-----------------------|-------------------------|-----------------------------|------------------------|--------------------------------|------------------------|--------------------------|------------------------|--------------------|------------------------|
| | LOCATION: 43...1387 | | | | | | | | | | | | | | | | | | | |
| QY | US-08-831-575-1 | | | | | | | | | | | | | | | | | | | |
| DB | | | | | | | | | | | | | | | | | | | | |
| <p>Alignment Scores:</p> <table border="0"><tr><td>Pred. No.: 2</td><td>Length: 1684</td></tr><tr><td>Score: 53.00</td><td>Matches: 8</td></tr><tr><td>Percent Similarity: 100.00%</td><td>Conservative: 0</td></tr><tr><td>Best Local Similarity: 100.00%</td><td>Mismatches: 0</td></tr><tr><td>Query Match: 100.00%</td><td>Indels: 0</td></tr><tr><td>DB: 2</td><td>Gaps: 0</td></tr></table> | | | | | | | | | Pred. No.: 2 | Length: 1684 | Score: 53.00 | Matches: 8 | Percent Similarity: 100.00% | Conservative: 0 | Best Local Similarity: 100.00% | Mismatches: 0 | Query Match: 100.00% | Indels: 0 | DB: 2 | Gaps: 0 |
| Pred. No.: 2 | Length: 1684 | | | | | | | | | | | | | | | | | | | |
| Score: 53.00 | Matches: 8 | | | | | | | | | | | | | | | | | | | |
| Percent Similarity: 100.00% | Conservative: 0 | | | | | | | | | | | | | | | | | | | |
| Best Local Similarity: 100.00% | Mismatches: 0 | | | | | | | | | | | | | | | | | | | |
| Query Match: 100.00% | Indels: 0 | | | | | | | | | | | | | | | | | | | |
| DB: 2 | Gaps: 0 | | | | | | | | | | | | | | | | | | | |
| US-10-029-756-6 (1-8) x US-08-831-575-1 (1-1684) | | | | | | | | | | | | | | | | | | | | |
| QY | 1 TtpIleGlyHisAspAlaGlyHis 8 | | | | | | | | | | | | | | | | | | | |
| DB | 508 TGGATTGGACATGATCTGGGCAT 531 | | | | | | | | | | | | | | | | | | | |
| <p>RESULT 3</p> <p>US-08-366-779-4</p> <p>; Sequence 4, Application US/08366779</p> <p>; Patent No. 5614393</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: Thomas, Terry L.</p> <p>; APPLICANT: Reddy, Avutu S.</p> <p>; APPLICANT: Nuccio, Michael</p> <p>; APPLICANT: Freyassinnet, Georges L.</p> <p>; APPLICANT: Nunberg, Andrew N.</p> <p>; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A</p> <p>; TITLE OF INVENTION: DELTA 6-DESATURASE</p> <p>; NUMBER OF SEQUENCES: 25</p> <p>; CORRESPONDENCE ADDRESS:</p> <p>; ADDRESSEE: Scully, Scott, Murphy & Presser</p> <p>; STREET: 400 Garden City Plaza</p> <p>; CITY: Garden City</p> <p>; STATE: New York</p> <p>; COUNTRY: United States</p> <p>; ZIP: 11530</p> <p>; COMPUTER READABLE FORM:</p> <p>; MEDIUM TYPE: Floppy disk</p> <p>; OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>; SOFTWARE: PatentIn Release #1.0, Version #1.25</p> <p>; CURRENT APPLICATION DATA:</p> <p>; APPLICATION NUMBER: US/08/366,779</p> <p>; FILING DATE: 30-DEC-1994</p> <p>; CLASSIFICATION: 800</p> <p>; ATTORNEY/AGENT INFORMATION:</p> <p>; NAME: Presser, Leopold</p> <p>; REGISTRATION NUMBER: 19,827</p> <p>; REFERENCE/DOCKET NUMBER: 8383ZYXW</p> <p>; TELECOMMUNICATION INFORMATION:</p> <p>; TELEPHONE: (516) 742-4343</p> <p>; TELEX: 230 901 SANS UR</p> <p>; INFORMATION FOR SEQ ID NO: 4:</p> <p>; LENGTH: 1685 base pairs</p> <p>; TYPE: nucleic acid</p> <p>; STRANDEDNESS: both</p> <p>; TOPOLOGY: linear</p> <p>; MOLECULE TYPE: DNA (genomic)</p> <p>US-08-366-779-4</p> <p>Alignment Scores:</p> <table border="0"><tr><td>Pred. No.: 2</td><td>Length: 1685</td></tr><tr><td>Score: 53.00</td><td>Matches: 8</td></tr><tr><td>Percent Similarity: 100.00%</td><td>Conservative: 0</td></tr><tr><td>Best Local Similarity: 100.00%</td><td>Mismatches: 0</td></tr><tr><td>Query Match: 100.00%</td><td>Indels: 0</td></tr><tr><td>DB: 1</td><td>Gaps: 0</td></tr></table> | | | | | | | | | Pred. No.: 2 | Length: 1685 | Score: 53.00 | Matches: 8 | Percent Similarity: 100.00% | Conservative: 0 | Best Local Similarity: 100.00% | Mismatches: 0 | Query Match: 100.00% | Indels: 0 | DB: 1 | Gaps: 0 |
| Pred. No.: 2 | Length: 1685 | | | | | | | | | | | | | | | | | | | |
| Score: 53.00 | Matches: 8 | | | | | | | | | | | | | | | | | | | |
| Percent Similarity: 100.00% | Conservative: 0 | | | | | | | | | | | | | | | | | | | |
| Best Local Similarity: 100.00% | Mismatches: 0 | | | | | | | | | | | | | | | | | | | |
| Query Match: 100.00% | Indels: 0 | | | | | | | | | | | | | | | | | | | |
| DB: 1 | Gaps: 0 | | | | | | | | | | | | | | | | | | | |
| US-10-029-756-6 (1-8) x US-08-366-779-4 (1-1685) | | | | | | | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | | | | | | |
|---|----------------------------------|--|--|--|--|--|--|--|--------------------|--------------------------|-----------------------|-------------------------|-----------------------------|------------------------|--------------------------------|------------------------|--------------------------|------------------------|--------------------|------------------------|
| | LOCATION: 43...1387 | | | | | | | | | | | | | | | | | | | |
| QY | US-08-831-575-1 | | | | | | | | | | | | | | | | | | | |
| DB | | | | | | | | | | | | | | | | | | | | |
| <p>Alignment Scores:</p> <table border="0"><tr><td>Pred. No.: 2</td><td>Length: 1684</td></tr><tr><td>Score: 53.00</td><td>Matches: 8</td></tr><tr><td>Percent Similarity: 100.00%</td><td>Conservative: 0</td></tr><tr><td>Best Local Similarity: 100.00%</td><td>Mismatches: 0</td></tr><tr><td>Query Match: 100.00%</td><td>Indels: 0</td></tr><tr><td>DB: 2</td><td>Gaps: 0</td></tr></table> | | | | | | | | | Pred. No.: 2 | Length: 1684 | Score: 53.00 | Matches: 8 | Percent Similarity: 100.00% | Conservative: 0 | Best Local Similarity: 100.00% | Mismatches: 0 | Query Match: 100.00% | Indels: 0 | DB: 2 | Gaps: 0 |
| Pred. No.: 2 | Length: 1684 | | | | | | | | | | | | | | | | | | | |
| Score: 53.00 | Matches: 8 | | | | | | | | | | | | | | | | | | | |
| Percent Similarity: 100.00% | Conservative: 0 | | | | | | | | | | | | | | | | | | | |
| Best Local Similarity: 100.00% | Mismatches: 0 | | | | | | | | | | | | | | | | | | | |
| Query Match: 100.00% | Indels: 0 | | | | | | | | | | | | | | | | | | | |
| DB: 2 | Gaps: 0 | | | | | | | | | | | | | | | | | | | |
| US-10-029-756-6 (1-8) x US-08-831-575-1 (1-1684) | | | | | | | | | | | | | | | | | | | | |
| QY | 1 TtpIleGlyHisAspAlaGlyHis 8 | | | | | | | | | | | | | | | | | | | |
| DB | 508 TGGATTGGACATGATCTGGGCAT 531 | | | | | | | | | | | | | | | | | | | |
| <p>RESULT 3</p> <p>US-08-366-779-4</p> <p>; Sequence 4, Application US/08366779</p> <p>; Patent No. 5614393</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: Thomas, Terry L.</p> <p>; APPLICANT: Reddy, Avutu S.</p> <p>; APPLICANT: Nuccio, Michael</p> <p>; APPLICANT: Freyassinnet, Georges L.</p> <p>; APPLICANT: Nunberg, Andrew N.</p> <p>; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A</p> <p>; TITLE OF INVENTION: DELTA 6-DESATURASE</p> <p>; NUMBER OF SEQUENCES: 25</p> <p>; CORRESPONDENCE ADDRESS:</p> <p>; ADDRESSEE: Scully, Scott, Murphy & Presser</p> <p>; STREET: 400 Garden City Plaza</p> <p>; CITY: Garden City</p> <p>; STATE: New York</p> <p>; COUNTRY: United States</p> <p>; ZIP: 11530</p> <p>; COMPUTER READABLE FORM:</p> <p>; MEDIUM TYPE: Floppy disk</p> <p>; OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>; SOFTWARE: PatentIn Release #1.0, Version #1.25</p> <p>; CURRENT APPLICATION DATA:</p> <p>; APPLICATION NUMBER: US/08/366,779</p> <p>; FILING DATE: 30-DEC-1994</p> <p>; CLASSIFICATION: 800</p> <p>; ATTORNEY/AGENT INFORMATION:</p> <p>; NAME: Presser, Leopold</p> <p>; REGISTRATION NUMBER: 19,827</p> <p>; REFERENCE/DOCKET NUMBER: 8383ZYXW</p> <p>; TELECOMMUNICATION INFORMATION:</p> <p>; TELEPHONE: (516) 742-4343</p> <p>; TELEX: 230 901 SANS UR</p> <p>; INFORMATION FOR SEQ ID NO: 4:</p> <p>; LENGTH: 1685 base pairs</p> <p>; TYPE: nucleic acid</p> <p>; STRANDEDNESS: both</p> <p>; TOPOLOGY: linear</p> <p>; MOLECULE TYPE: DNA (genomic)</p> <p>US-08-366-779-4</p> <p>Alignment Scores:</p> <table border="0"><tr><td>Pred. No.: 2</td><td>Length: 1685</td></tr><tr><td>Score: 53.00</td><td>Matches: 8</td></tr><tr><td>Percent Similarity: 100.00%</td><td>Conservative: 0</td></tr><tr><td>Best Local Similarity: 100.00%</td><td>Mismatches: 0</td></tr><tr><td>Query Match: 100.00%</td><td>Indels: 0</td></tr><tr><td>DB: 1</td><td>Gaps: 0</td></tr></table> | | | | | | | | | Pred. No.: 2 | Length: 1685 | Score: 53.00 | Matches: 8 | Percent Similarity: 100.00% | Conservative: 0 | Best Local Similarity: 100.00% | Mismatches: 0 | Query Match: 100.00% | Indels: 0 | DB: 1 | Gaps: 0 |
| Pred. No.: 2 | Length: 1685 | | | | | | | | | | | | | | | | | | | |
| Score: 53.00 | Matches: 8 | | | | | | | | | | | | | | | | | | | |
| Percent Similarity: 100.00% | Conservative: 0 | | | | | | | | | | | | | | | | | | | |
| Best Local Similarity: 100.00% | Mismatches: 0 | | | | | | | | | | | | | | | | | | | |
| Query Match: 100.00% | Indels: 0 | | | | | | | | | | | | | | | | | | | |
| DB: 1 | Gaps: 0 | | | | | | | | | | | | | | | | | | | |
| US-10-029-756-6 (1-8) x US-08-366-779-4 (1-1685) | | | | | | | | | | | | | | | | | | | | |

;; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
;; TITLE OF INVENTION: DELTA 6-DESATURASE
;; NUMBER OF SEQUENCES: 27
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Scully, Scott, Murphy & Presser
;; STREET: 400 Garden City Plaza
;; CITY: Garden City
;; STATE: New York
;; COUNTRY: United States
;; ZIP: 11530
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/934,254
;; FILING DATE:
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Presser, Leopold
;; REGISTRATION NUMBER: 19,827
;; REFERENCE/DOCKET NUMBER: 8383ZYXWVU
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (516) 742-4343
;; TELEFAX: (516) 742-4366
;; TELEX: 230 901 SANS UR
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1685 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; US-08-934-254-4

Alignment Scores:
Pred. No.: 2 Length: 1685
Score: 53.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-6 (1-8) x US-08-934-254-4 (1-1685)

Qy 1 TtpileGlyHisaspAlaGlyHis 8
Db 509 TGGATTGGACATGATGCTGGGCAT 532

RESULT 6
US-08-934-254-4
; Sequence 4, Application US/09685775
; Patent No. 6683232
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/685,775

;; FILING DATE: 10-Oct-2000
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/934,254
;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Presser, Leopold
;; REGISTRATION NUMBER: 19,827
;; REFERENCE/DOCKET NUMBER: 8383ZYXWVU
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (516) 742-4343
;; TELEFAX: (516) 742-4366
;; TELEX: 230 901 SANS UR
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1685 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-685-775-4

Alignment Scores:
Pred. No.: 2 Length: 1685
Score: 53.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-685-775-4 (1-1685)

Qy 1 TtpileGlyHisaspAlaGlyHis 8
Db 509 TGGATTGGACATGATGCTGGGCAT 532

RESULT 7
US-09-270-767-29759/C
; Sequence 29759, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 29759
; LENGTH: 162
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-29759

Alignment Scores:
Pred. No.: 6.56 Length: 162
Score: 44.00 Matches: 6
Percent Similarity: 87.50% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 83.02% Indels: 0
DB: 4 -Gaps: 0

US-10-029-756-6 (1-8) x US-09-270-767-29759 (1-162)

Qy 1 TtpileGlyHisaspAlaGlyHis 8
Db 50 TGGATGGGCATTCAGCTGGGCAT 27

RESULT 8
US-09-270-767-13737/C
; Sequence 13737, Application US/09270767
; Patent No. 6703491

```
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13737
; LENGTH: 833
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13737

Alignment Scores:
Pred. No.: 38.6 Length: 833
Score: 44.00 Matches: 6
Percent Similarity: 87.50% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 83.02% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-270-767-13737 (1-833)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
||||:||||| |||||
Db 721 TGGATGGGGCATTCAGCTGGGCAT 698

RESULT 9
US-09-252-991A-5494
; Sequence 5494, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: ABRUINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5494
; LENGTH: 1152
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5494

Alignment Scores:
Pred. No.: 102 Length: 1152
Score: 42.50 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 0
Query Match: 80.19% Indels: 1
DB: 4 Gaps: 1

US-10-029-756-6 (1-8) x US-09-252-991A-5494 (1-1152)

Qy 1 Trp----IleGlyHisAspAlaGlyHis 8
||||| ||||| ||||| |||||
Db 1075 TGGAGCATTTGGCCATGACGACGGGCAC 1101

RESULT 10
US-09-949-016-21341
; Sequence 21341, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21341
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-21341

Alignment Scores:
Pred. No.: 62 Length: 601
Score: 42.00 Matches: 6
Percent Similarity: 87.50% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 79.25% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-21341 (1-601)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
||||:||||| |||||
Db 578 TGGCTAGGTCATTGTGCTGGTCAC 601

RESULT 11
US-09-949-016-36968
; Sequence 36968, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36968
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-36968

Alignment Scores:
Pred. No.: 62 Length: 601
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-36968 (1-601)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
||||:||||| |||||
Db 356 TGGATTGGGCACAGCATGGGCCAC 379

RESULT 12
US-09-949-016-46094
; Sequence 46094, Application US/09949016
; Patent No. 6812339
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; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46094
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-46094

Alignment Scores:
Pred. No.: 62 Length: 601
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-46094 (1-601)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 356 TGGATTGGGCACAGCATGGCCAC 379

RESULT 13
US-09-949-016-74333
; Sequence 74333, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74333
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-74333

Alignment Scores:
Pred. No.: 62 Length: 601
Score: 42.00 Matches: 6
Percent Similarity: 87.50% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 79.25% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-74333 (1-601)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 578 TGGCTAGGTCATTGTGCTGGTCAC 601

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 183604
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-183604

Alignment Scores:
Pred. No.: 62 Length: 601
Score: 42.00 Matches: 5
Percent Similarity: 87.50% Conservative: 2
Best Local Similarity: 62.50% Mismatches: 1
Query Match: 79.25% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-183604 (1-601)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 509 TGGTTAGGCCATGACTCTAATCAC 486

RESULT 15
US-09-669-751-180/c
; Sequence 180, Application US/09669751
; Patent No. 6551575
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Ralph J.
; TITLE OF INVENTION: Methods for Identifying Compounds for
; Motion Sickness, Vertigo and Other Disorders Related to
; Balance and the Perception of Gravity
; FILE REFERENCE: P-NI 3864
; CURRENT APPLICATION NUMBER: US/09/669,751
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 60/168,579
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 261
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 180
; LENGTH: 650
; TYPE: DNA
; ORGANISM: Drosophila
US-09-669-751-180

Alignment Scores:
Pred. No.: 67.5 Length: 650
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-669-751-180 (1-650)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
```

```

RESULT 14
US-09-949-016-183604/c
; Sequence 183604, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 183604
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-183604

Alignment Scores:
Pred. No.: 62 Length: 601
Score: 42.00 Matches: 5
Percent Similarity: 87.50% Conservative: 2
Best Local Similarity: 62.50% Mismatches: 1
Query Match: 79.25% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-183604 (1-601)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 509 TGGTTAGGCCATGACTCTAATCAC 486

RESULT 15
US-09-669-751-180/c
; Sequence 180, Application US/09669751
; Patent No. 6551575
; GENERAL INFORMATION:
; APPLICANT: Greenspan, Ralph J.
; TITLE OF INVENTION: Methods for Identifying Compounds for
; Motion Sickness, Vertigo and Other Disorders Related to
; Balance and the Perception of Gravity
; FILE REFERENCE: P-NI 3864
; CURRENT APPLICATION NUMBER: US/09/669,751
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 60/168,579
; PRIOR FILING DATE: 1999-12-02
; NUMBER OF SEQ ID NOS: 261
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 180
; LENGTH: 650
; TYPE: DNA
; ORGANISM: Drosophila
US-09-669-751-180

Alignment Scores:
Pred. No.: 67.5 Length: 650
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-669-751-180 (1-650)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
```

```
Db 415 TGGTGTGGGCATAGCGCAGGGCCAC 392
RESULT 16
; US-09-949-016-1322/c
; Sequence 1322, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1322
; LENGTH: 760
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1322
Alignment Scores:
Pred. No.: 79.9 Length: 760
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 4 Gaps: 0
US-10-029-756-6 (1-8) x US-09-949-016-1322 (1-760)
Qy 1 TrrpIleGlyHisAspAlaGlyHis 8
Db 582 TGGATTGGGCACAGCATGGCCAC 559
RESULT 17
; US-09-270-767-13129/c
; Sequence 13129, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13129
; LENGTH: 816
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13129
Alignment Scores:
Pred. No.: 86.3 Length: 816
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 4 Gaps: 0
US-10-029-756-6 (1-8) x US-09-270-767-13129 (1-816)
Qy 1 TrrpIleGlyHisAspAlaGlyHis 8
Db 415 TGGTGTGGGCATAGCGCAGGGCCAC 392
RESULT 18
; US-09-673-395A-136/c
; Sequence 136, Application US/09673395A
; Patent No. 6620923
; GENERAL INFORMATION:
; APPLICANT: SPECHT, THOMAS
; APPLICANT: HINZMANN, BERND
; APPLICANT: SCHMITT, ARMIN
; APPLICANT: PILARSKY, CHRISTIAN
; APPLICANT: DAHL, EDGAR
; APPLICANT: ROSENTHAL, ANDRE
; TITLE OF INVENTION: HUMAN NUCLEIC ACID SEQUENCES FROM UTERUS TUMOR TISSUE
; FILE REFERENCE: ALBRE-12
; CURRENT APPLICATION NUMBER: US/09/673.395A
; CURRENT FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 637
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 136
; LENGTH: 2238
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-673-395A-136
Alignment Scores:
Pred. No.: 257 Length: 2238
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 4 Gaps: 0
US-10-029-756-6 (1-8) x US-09-673-395A-136 (1-2238)
Qy 1 TrrpIleGlyHisAspAlaGlyHis 8
Db 331 TGGATAGGGCATTCATTGGCCAC 308
RESULT 19
; US-08-967-101-28/c
; Sequence 28, Application US/08967101
; Patent No. 5840540
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,101
; FILING DATE: 10-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/592,541
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
```

;; INFORMATION FOR SEQ ID NO: 28:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2307 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-08-967-101-28

Alignment Scores:
Pred. No.: 266 Length: 2307
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-6 (1-8) x US-08-967-101-28 (1-2307)

Qy 1 TtpileGlyHisaspalaGlyHis 8
Db 550 TGGATAGGCGCATTCCTGGCCAC 527

RESULT 20

US-08-592-541-28/c
; Sequence 28, Application US/08592541
; Patent No. 5986054
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,541
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2307 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-592-541-28

Alignment Scores:
Pred. No.: 266 Length: 2307
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 2 Gaps: 0
US-10-029-756-6 (1-8) x US-08-592-541-28 (1-2307)

Qy 1 TtpileGlyHisaspalaGlyHis 8
Db 550 TGGATAGGCGCATTCCTGGCCAC 527

RESULT 21

US-09-124-698-28/c
; Sequence 28, Application US/09124698
; Patent No. 6117978
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/124,698
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/592,541
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2307 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-124-698-28

Alignment Scores:
Pred. No.: 266 Length: 2307
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 3 Gaps: 0
US-10-029-756-6 (1-8) x US-09-124-698-28 (1-2307)

Qy 1 TtpileGlyHisaspalaGlyHis 8
Db 550 TGGATAGGCGCATTCCTGGCCAC 527

RESULT 22

US-09-127-480-28/c
; Sequence 28, Application US/09127480
; Patent No. 6194153
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; APPLICANT: ROMMENS, JOHANNA M
; APPLICANT: FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TO ALZHEIMER'S DISEASE

; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/127,480
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,541
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2307 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-127-480-28

Alignment Scores: 266 Length: 2307
Pred. No.: 42.00 Matches: 6
Score: 75.00% Conservative: 0
Percent Similarity: 75.00% Mismatches: 2
Best Local Similarity: 75.00% Indels: 0
Query Match: 79.25% Gaps: 0
DB: 3

US-10-029-756-6 (1-8) x US-09-127-480-28 (1-2307)

Oy 1 TptlleglyHisAspAlaGlyHis 8
|||||
Db 550 TGGATAGGCGCATTCATTGGCCAC 527

RESULT 23
US-08-496-841C-28/c
; Sequence 28, Application US/08496841C
; Patent No. 6210919
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; ROMMENS, JOHANNA M
; FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby, PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/496,841C

; FILING DATE: 28-Jun-1995
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul F. Fehlner, Ph.D.
; REGISTRATION NUMBER: 35,135
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2307 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-08-496-841C-28

Alignment Scores: 266 Length: 2307
Pred. No.: 42.00 Matches: 6
Score: 75.00% Conservative: 0
Percent Similarity: 75.00% Mismatches: 2
Best Local Similarity: 75.00% Indels: 0
Query Match: 79.25% Gaps: 0
DB: 3

US-10-029-756-6 (1-8) x US-08-496-841C-28 (1-2307)

Oy 1 TptlleglyHisAspAlaGlyHis 8
|||||
Db 550 TGGATAGGCGCATTCATTGGCCAC 527

RESULT 24
US-09-124-523-28/c
; Sequence 28, Application US/09124523
; Patent No. 6395960
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; ROMMENS, JOHANNA M
; FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/124,523
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,541
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2307 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)
US-09-124-523-28

Alignment Scores:
Pred. No.: 266 Length: 2307
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-6 (1-8) x US-09-124-523-28 (1-2307)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
|||||
Db 550 TGGATAGGCATTCCTGGCCAC 527

RESULT 25
US-09-636-796A-28/c
; Sequence 28, Application US/09636796A
; Patent No. 6485911
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; ROMMENS, JOHANNA M
; FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 183
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TESTA, HURWITZ & THIBEAULT
; STREET: High Street Tower - 125 High Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 11-Aug-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,541
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pitcher, Edmund R.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2307 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-636-796A-28

Alignment Scores:
Pred. No.: 266 Length: 2307
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-636-796A-28 (1-2307)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8

Db 550 TGGATAGGCATTCCTGGCCAC 527

RESULT 26
US-08-431-048F-28/c
; Sequence 28, Application US/08431048F
; Patent No. 6531586
; GENERAL INFORMATION:
; APPLICANT: ST. GEORGE-HYSLOP, PETER H
; ROMMENS, JOHANNA M
; FRASER, PAUL E
; TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
; TO ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 155
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DARBY & DARBY P.C.
; STREET: 805 THIRD AVENUE
; CITY: NEW YORK
; STATE: N.Y.
; COUNTRY: U.S.A.
; ZIP: 10022-7513
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,048F
; FILING DATE: 28-Apr-1995
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: FEHLNER, PAUL F.
; REGISTRATION NUMBER: 35135
; REFERENCE/DOCKET NUMBER: 1034/0F808
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-527-6237
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2307 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-08-431-048F-28

Alignment Scores:
Pred. No.: 266 Length: 2307
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-08-431-048F-28 (1-2307)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
|||||
Db 550 TGGATAGGCATTCCTGGCCAC 527

RESULT 27
US-09-949-016-973/c
; Sequence 973, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 973
; LENGTH: 3050
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-973

Alignment Scores:
Pred. No.: 360 Length: 3050
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-973 (1-3050)

Qy 1 TrrileGlyHisAspAlaGlyHis 8
Db 1606 TGGATTGGGCACAGCATGGGCCAC 1583

RESULT 28
US-09-620-312D-1097/c
; Sequence 1097, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yungqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 1097
; LENGTH: 3144
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (129)..(2027)
US-09-620-312D-1097

Alignment Scores:
Pred. No.: 372 Length: 3144
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0

; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 973
; LENGTH: 3050
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-973

Alignment Scores:
Pred. No.: 360 Length: 3050
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-973 (1-3050)

Qy 1 TrrileGlyHisAspAlaGlyHis 8
Db 1606 TGGATTGGGCACAGCATGGGCCAC 1583

RESULT 29
US-09-949-016-13064/c
; Sequence 13064, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13064
; LENGTH: 28556
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(28556)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13064

Alignment Scores:
Pred. No.: 4,05e+03 Length: 28556
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-13064 (1-28556)

Qy 1 TrrileGlyHisAspAlaGlyHis 8
Db 26266 TGGATTGGGCACAGCATGGGCCAC 26243

RESULT 30
US-09-949-016-12715/c
; Sequence 12715, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12715
```

```
; LENGTH: 40037
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(40037)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12715

Alignment Scores:
Pred. No.: 5.84e+03 Length: 40037
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-12715 (1-40037)

Qy 1 TrrileGlyHisAspAlaGlyHis 8
Db 34941 TGGATTGGGCACGATGGGTCAC 34918

RESULT 31
US-09-949-016-11919
; Sequence 11919, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11919
; LENGTH: 84761
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-11919

Alignment Scores:
Pred. No.: 1.32e+04 Length: 84761
Score: 42.00 Matches: 6
Percent Similarity: 87.50% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 79.25% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-11919 (1-84761)

Qy 1 TrrileGlyHisAspAlaGlyHis 8
Db 58464 TGGCTAGGTCATTGTGCTGGTCAC 58487

RESULT 32
US-09-949-016-13914
; Sequence 13914, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13914
; LENGTH: 84763
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13914

Alignment Scores:
Pred. No.: 1.32e+04 Length: 84763
Score: 42.00 Matches: 6
Percent Similarity: 87.50% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 79.25% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-13914 (1-84763)

Qy 1 TrrileGlyHisAspAlaGlyHis 8
Db 58464 TGGCTAGGTCATTGTGCTGGTCAC 58487

RESULT 33
US-09-949-016-17009/c
; Sequence 17009, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17009
; LENGTH: 205163
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17009

Alignment Scores:
Pred. No.: 3.4e+04 Length: 205163
Score: 42.00 Matches: 5
Percent Similarity: 87.50% Conservative: 2
Best Local Similarity: 62.50% Mismatches: 1
Query Match: 79.25% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-17009 (1-205163)

Qy 1 TrrileGlyHisAspAlaGlyHis 8
Db 179865 TGGTTAGGCCATGACTCTAATCAC 179842

RESULT 34
US-09-583-110-1558
; Sequence 1558, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
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; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: Pneumoniae for Diagnostics and Therapeutics
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 1558
; LENGTH: 2463
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-1558

Alignment Scores:
Pred. No.: 432 Length: 2463
Score: 41.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 77.36% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-583-110-1558 (1-2463)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 2023 TGGATTGGCGATGATGATAATCAT 2046

RESULT 35
US-09-377-465A-1
; Sequence 1, Application US/09377465A
; Patent No. H002021
; GENERAL INFORMATION:
; APPLICANT: Hoskins, JoAnn
; APPLICANT: Jaskunas, Stanley R
; APPLICANT: Zhao, Genshi
; APPLICANT: Rockety, Pamela K
; TITLE OF INVENTION: NOVEL PENICILLIN BINDING PROTEIN FROM STREPTOCOCCUS
; FILE REFERENCE: X12498 Sequence List
; Patent No. H002021
; CURRENT APPLICATION NUMBER: US/09/377,465A
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: 60/100,887
; PRIOR FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2466
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
; NAME/KEY: CDS
; LOCATION: (1)..(2466)
US-09-377-465A-1

Alignment Scores:
Pred. No.: 432 Length: 2466
Score: 41.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 77.36% Indels: 0
DB: 1 Gaps: 0

US-10-029-756-6 (1-8) x US-09-377-465A-1 (1-2466)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 2023 TGGATTGGCGATGATGATAATCAT 2046

RESULT 36
US-09-377-465A-3
; Sequence 3, Application US/09377465A
; Patent No. H002021
; GENERAL INFORMATION:
; APPLICANT: Hoskins, JoAnn
; APPLICANT: Jaskunas, Stanley R
; APPLICANT: Zhao, Genshi
; APPLICANT: Rockety, Pamela K
; TITLE OF INVENTION: NOVEL PENICILLIN BINDING PROTEIN FROM STREPTOCOCCUS
; FILE REFERENCE: X12498 Sequence List
; Patent No. H002021
; CURRENT APPLICATION NUMBER: US/09/377,465A
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: 60/100,887
; PRIOR FILING DATE: 1998-09-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2466
; TYPE: RNA
; ORGANISM: Streptococcus pneumoniae
US-09-377-465A-3

Alignment Scores:
Pred. No.: 432 Length: 2466
Score: 41.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 77.36% Indels: 0
DB: 1 Gaps: 0

US-10-029-756-6 (1-8) x US-09-377-465A-3 (1-2466)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 2023 UGGAUUGGCGAUGAUAUACAU 2046

RESULT 37
US-09-107-433-2157
; Sequence 2157, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESS: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; 
```

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; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 2157:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2505 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...2505
; SEQUENCE DESCRIPTION: SEQ ID NO: 2157:
US-09-107-433-2157
Alignment Scores:
Pred. No.: 440 Length: 2505
Score: 41.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 77.36% Indels: 0
DB: 4 Gaps: 0
US-10-029-756-6 (1-8) x US-09-107-433-2157 (1-2505)
Qy 1 TrrlleglyHisaspAlaGlyHis 8
Db 2065 TGGATTGGCGCATGATGATCAT 2088
RESULT 38
; Sequence 143 Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/961.527
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 143:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4965 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 14..2593
; NAME/KEY: mat_peptide
; LOCATION: 77..2593
US-08-092-817-3
Alignment Scores:
Pred. No.: 922 Length: 4965
Score: 41.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 77.36% Indels: 0
DB: 3 Gaps: 0
US-10-029-756-6 (1-8) x US-08-961-527-143 (1-4965)
Qy 1 TrrlleglyHisaspAlaGlyHis 8
Db 485 TGGATTGGCGCATGATGATCAT 462
RESULT 39
; Sequence 3, Application US/08092817
; Patent No. 5496926
; GENERAL INFORMATION:
; APPLICANT: RUBINSTEIN, Menachem
; APPLICANT: NOVICK, Daniela
; APPLICANT: TAL, Nathan
; TITLE OF INVENTION: SOLUBLE LDL RECEPTOR, ITS PRODUCTION AND
; TITLE OF INVENTION: USE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/092.817
; FILING DATE: 19-JUL-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 100696
; FILING DATE: 19-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 102915
; FILING DATE: 23-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: TOWNSEND, G. Kevin
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: RUBINSTEIN=5A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5095 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 14..2593
; NAME/KEY: mat_peptide
; LOCATION: 77..2593
US-08-092-817-3
```

Alignment Scores: 948 Length: 5095
Pred. No.: 41.00 Matches: 5
Score: 100.00% Conservative: 2
Percent Similarity: 100.00%
Best Local Similarity: 71.43% Mismatches: 0
Query Match: 77.36% Indels: 0
DB: 1 Gaps: 0

US-10-029-756-6 (1-8) x US-08-092-817-3 (1-5095)

QY 1 TtpileGlyHisAspAlaGly 7
||||:|||||:||||:|||||

Db 3115 TGGGTGGTCATGATTCGGG 3095

RESULT 40

US-08-485-128-3/c
; Sequence 3, Application US/08485128
; Patent No. 6365713
; GENERAL INFORMATION:
; APPLICANT: RUBINSTEIN, Menachem
; APPLICANT: NOVICK, Daniela
; APPLICANT: TAL, Nathan
; APPLICANT: Fischer, Dina
; TITLE OF INVENTION: SOLUBLE LDL RECEPTOR, ITS PRODUCTION AND USE
; FILE REFERENCE: RUBINSTEIN=5D
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,128
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/092,817
; FILING DATE: 19-JUL-1993
; APPLICATION NUMBER: IL 100696
; FILING DATE: 19-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 102915
; FILING DATE: 23-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: TOWNSEND, G. Kevin
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: RUBINSTEIN=5A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5095 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 14..2593
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 77..2593
US-08-485-128-3

Alignment Scores: 948 Length: 5095
Pred. No.: 41.00 Matches: 5
Score: 100.00% Conservative: 2
Percent Similarity: 100.00%
Best Local Similarity: 71.43% Mismatches: 0
Query Match: 77.36% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-6 (1-8) x US-08-485-128-3 (1-5095)

QY 1 TtpileGlyHisAspAlaGly 7
||||:|||||:||||:|||||

Db 3115 TGGGTGGTCATGATTCGGG 3095

RESULT 41

US-09-824-637-3/c
; Sequence 3, Application US/09824637
; Patent No. 6703222
; GENERAL INFORMATION:
; APPLICANT: RUBINSTEIN, Menachem
; APPLICANT: NOVICK, Daniela
; APPLICANT: TAL, Nathan
; APPLICANT: Fischer, Dina
; TITLE OF INVENTION: SOLUBLE LDL RECEPTOR, ITS PRODUCTION AND USE
; FILE REFERENCE: RUBINSTEIN=5D
; CURRENT APPLICATION NUMBER: US/09/824,637
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: US 08/485,128
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/092,817
; PRIOR FILING DATE: 1993-07-19
; PRIOR APPLICATION NUMBER: IL 100696
; PRIOR FILING DATE: 1992-01-19
; PRIOR APPLICATION NUMBER: IL 102915
; PRIOR FILING DATE: 1992-08-23
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 5095
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (14)..(2593)
US-09-824-637-3

Alignment Scores: 948 Length: 5095
Pred. No.: 41.00 Matches: 5
Score: 100.00% Conservative: 2
Percent Similarity: 100.00%
Best Local Similarity: 71.43% Mismatches: 0
Query Match: 77.36% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-824-637-3 (1-5095)

QY 1 TtpileGlyHisAspAlaGly 7
||||:|||||:||||:|||||

Db 3115 TGGGTGGTCATGATTCGGG 3095

RESULT 42

US-09-949-016-14032
; Sequence 14032, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20

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; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14032
; LENGTH: 46499
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(46499)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14032

Alignment Scores:
Pred. No.: 1.04e+04 Length: 46499
Score: 41.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 77.36% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-14032 (1-46499)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 15201 TGGGCTGGACATCCAGCTGGCCAC 15224

RESULT 43
US-09-949-016-12677/c
; Sequence 12677, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12677
; LENGTH: 119930
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12677

Alignment Scores:
Pred. No.: 2.88e+04 Length: 119930
Score: 41.00 Matches: 6
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 77.36% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-12677 (1-119930)

Qy 1 TrpIleGlyHisAspAlaGly 7
Db 111718 TGGATAGTCATGAGGCTGGG 111698

RESULT 44
US-09-949-016-16319/c
; Sequence 16319, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16319
; LENGTH: 119931
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16319

Alignment Scores:
Pred. No.: 2.88e+04 Length: 119931
Score: 41.00 Matches: 6
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 77.36% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-16319 (1-119931)

Qy 1 TrpIleGlyHisAspAlaGly 7
Db 111718 TGGATAGTCATGAGGCTGGG 111698

RESULT 45
US-09-949-016-14186/c
; Sequence 14186, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14186
; LENGTH: 125536
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14186

Alignment Scores:
Pred. No.: 3.02e+04 Length: 125536
Score: 41.00 Matches: 6
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 77.36% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-14186 (1-125536)

Qy 1 TrpIleGlyHisAspAlaGly 7
Db 111718 TGGATAGTCATGAGGCTGGG 111698
```


RESULT 46
US-09-107-433-2018/c
; Sequence 2018, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTICS
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneka
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 2018:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 828 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8) LOCATION 1...828
; SEQUENCE DESCRIPTION: SEQ ID NO: 2018:
US-09-107-433-2018
Alignment Scores:
Pred. No.: 201 Length: 828
Score: 201 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 75.47% Indels: 0
DB: 4 Gaps: 0
US-10-029-756-6 (1-8) x US-09-107-433-2018 (1-828)
Qy 1 TptlGlyHisAspAlaGlyHis 8
Db 678 TGGGATGGACATGACGATGGTCAC 655
RESULT 47
US-09-583-110-2134/c
; Sequence 2134, Application US/09583110
; Patent No. 6699703

; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 2134
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-2134
Alignment Scores:
Pred. No.: 231 Length: 945
Score: 231 Matches: 6
Percent Similarity: 40.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 75.47% Indels: 0
DB: 4 Gaps: 0
US-10-029-756-6 (1-8) x US-09-583-110-2134 (1-945)
Qy 1 TptlGlyHisAspAlaGlyHis 8
Db 795 TGGGATGGACATGACGATGGTCAC 772
RESULT 48
US-09-569-771B-20
; Sequence 20, Application US/09569771B
; Patent No. 6815580
; GENERAL INFORMATION:
; APPLICANT: Miller, Philip W
; APPLICANT: Staub, Robin L
; TITLE OF INVENTION: Expression of Sedoheptulose 1, 7 Bisphosphatase in Transgenic
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15408)B
; CURRENT APPLICATION NUMBER: US/09/569,771B
; CURRENT FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: 60/133,964
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 20
; TYPE: DNA
; ORGANISM: Chlorella sorokiniana
US-09-569-771B-20
Alignment Scores:
Pred. No.: 371 Length: 1460
Score: 371 Matches: 1460
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 75.47% Indels: 0
DB: 4 Gaps: 0
US-10-029-756-6 (1-8) x US-09-569-771B-20 (1-1460)
Qy 2 lIeGlyHisAspAlaGlyHis 8
Db 28 CTCGGCAGCATGACGATGGTCAC 48
RESULT 49
US-09-569-771B-22
; Sequence 22, Application US/09569771B

Alignment Scores:
Pred. No.: 438 Length: 1702
Score: 40.00 Matches: 5
Percent Similarity: 100.00% Conservative: 3
Best Local Similarity: 62.50% Mismatches: 0
Query Match: 75.47% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-685-775-26 (1-1702)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 516 TATGTGGGCCATGACTCCGGCCAT 539
:::|||||:|||||

RESULT 52
US-09-902-540-767/c
; Sequence 767, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 767
; LENGTH: 5641
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-767

Alignment Scores:
Pred. No.: 1,6e+03 Length: 5641
Score: 40.00 Matches: 5
Percent Similarity: 75.00% Conservative: 1
Best Local Similarity: 62.50% Mismatches: 2
Query Match: 75.47% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-902-540-767 (1-5641)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 344 TGGTGGGTGACGGCCTTGGTCAC 321
|||||:|||||

RESULT 53
US-08-961-527-60/c
; Sequence 60, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
; APPLICANT: Charles Kunesh
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESS: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527

FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 6827 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-961-527-60

Alignment Scores:
Pred. No.: 1,97e+03 Length: 6827
Score: 40.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 75.47% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-6 (1-8) x US-08-961-527-60 (1-6827)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 5606 TGGGATGGACATGACGATGGTCAC 5583
|||||:|||||

RESULT 54
US-09-902-540-904
; Sequence 904, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 904
; LENGTH: 11382
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-904

Alignment Scores:
Pred. No.: 3,42e+03 Length: 11382
Score: 40.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 75.47% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-902-540-904 (1-11382)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 7271 TGGTCCGGCAGCGGTGGGTGTCAT 7294
|||||:|||||

RESULT 55
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A

```
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2 4403765
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Alignment Scores:
Pred. No.: 1.43e+06 Length: 4403765
Score: 40.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 75.47% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-6 (1-8) x US-09-103-840A-2 (1-4403765)
Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 1104932 TGGCAAGGCCATCAAGCGGGCCAT 1104909

RESULT 56
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Alignment Scores:
Pred. No.: 1.43e+06 Length: 4411529
Score: 40.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 75.47% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-6 (1-8) x US-09-103-840A-1 (1-4411529)
Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 1104909 TGGCAAGGCCATCAAGCGGGCCAT 1104886
```

```
RESULT 57
US-09-949-016-12800/c
; Sequence 12800, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12800
; LENGTH: 8521
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12800

Alignment Scores:
Pred. No.: 3.08e+03 Length: 8521
Score: 39.50 Matches: 8
Percent Similarity: 53.33% Conservative: 0
Best Local Similarity: 53.33% Mismatches: 0
Query Match: 74.53% Indels: 7
DB: 4 Gaps: 1

US-10-029-756-6 (1-8) x US-09-949-016-12800 (1-8521)
Qy 1 TrpIle-----GlyHisAspAlaGlyHis 8
Db 7835 TGGATCCAGATGCCCTCTCTGCCCCAGGTCATGACGCTGGGCAC 7791

RESULT 58
US-09-949-016-15804/c
; Sequence 15804, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15804
; LENGTH: 13117
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(13117)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15804

Alignment Scores:
Pred. No.: 4.91e+03 Length: 13117
Score: 39.50 Matches: 8
Percent Similarity: 53.33% Conservative: 0
```

Best Local Similarity: 53.33% Mismatches: 0
 Query Match: 74.53% Indels: 7
 DB: 4 Gaps: 1

US-10-029-756-6 (1-8) x US-09-949-016-15804 (1-13117)

Qy 1 TrrileGlyHisAspAlaGlyHis 8
 |||||-----GlyHisAspAlaGlyHis 8
 |||||

Db 13046 TGGATCCAGATGCTCTCTGCCCCCAGGGTCTAGCTGGGCAC 13002

RESULT 59

US-09-513-999C-8520
 ; Sequence 8520, Application US/09513999C
 ; Patent No. 6783961
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, J.B.
 ; APPLICANT: Duclert, A.
 ; APPLICANT: Giordano, J.Y.
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
 ; Patent No. 6783961
 ; FILE REFERENCE: 59.US2.REG
 ; CURRENT APPLICATION NUMBER: US/09/513,999C
 ; CURRENT FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/122,487
 ; PRIOR FILING DATE: 1999-02-26
 ; NUMBER OF SEQ ID NOS: 36681
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 8520
 ; LENGTH: 415
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 88
 ; OTHER INFORMATION: m-a or c
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 108
 ; OTHER INFORMATION: r-a or g
 ; OTHER INFORMATION: r-a or g

US-09-513-999C-8520

Alignment Scores:

Pred. No.: 144 Length: 415
 Score: 39.00 Matches: 5
 Percent Similarity: 75.00% Conservatives: 1
 Best Local Similarity: 62.50% Mismatches: 2
 Query Match: 73.58% Indels: 0
 DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-513-999C-8520 (1-415)

Qy 1 TrrileGlyHisAspAlaGlyHis 8
 |||||-----GlyHisAspAlaGlyHis 8
 |||||

Db 45 TGGCTTGACATGATGTTCCGCAT 68

RESULT 60

US-09-513-999C-8520
 ; Sequence 8520, Application US/09513999C
 ; Patent No. 6783961
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, J.B.
 ; APPLICANT: Duclert, A.
 ; APPLICANT: Giordano, J.Y.
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
 ; Patent No. 6783961
 ; FILE REFERENCE: 59.US2.REG
 ; CURRENT APPLICATION NUMBER: US/09/513,999C
 ; CURRENT FILING DATE: 2000-02-24
 ; PRIOR APPLICATION NUMBER: US 60/122,487
 ; PRIOR FILING DATE: 1999-02-26
 ; NUMBER OF SEQ ID NOS: 36681
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 8520
 ; LENGTH: 415
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 88
 ; OTHER INFORMATION: m-a or c
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 108
 ; OTHER INFORMATION: r-a or g
 ; OTHER INFORMATION: r-a or g

US-09-513-999C-8520

TYPE: DNA
 ORGANISM: Myxococcus xanthus
 US-09-902-540-6391

Alignment Scores:

Pred. No.: 214 Length: 600
 Score: 39.00 Matches: 6
 Percent Similarity: 75.00% Conservatives: 0
 Best Local Similarity: 73.58% Mismatches: 2
 Query Match: 73.58% Indels: 0
 DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-902-540-6391 (1-600)

Qy 1 TrrileGlyHisAspAlaGlyHis 8
 |||||-----GlyHisAspAlaGlyHis 8
 |||||

Db 417 TGGCGGGCCATGAGCGGCACAT 440

RESULT 61

US-09-949-016-1172/c
 ; Sequence 1172, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; FILE REFERENCE: CLO01307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1172
 ; LENGTH: 1644
 ; TYPE: DNA
 ; ORGANISM: Human
 ; OTHER INFORMATION: r-a or g

US-09-949-016-1172

Alignment Scores:

Pred. No.: 637 Length: 1644
 Score: 39.00 Matches: 6
 Percent Similarity: 75.00% Conservatives: 0
 Best Local Similarity: 73.58% Mismatches: 2
 Query Match: 73.58% Indels: 0
 DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-1172 (1-1644)

Qy 1 TrrileGlyHisAspAlaGlyHis 8
 |||||-----GlyHisAspAlaGlyHis 8
 |||||

Db 169 TGGCAGGGCCACCCGCGAGGCAC 146

RESULT 62

US-09-902-540-8493
 ; Sequence 8493, Application US/09902540
 ; Patent No. 6833447
 ; GENERAL INFORMATION:
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Wiegand, Roger C.
 ; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
 ; FILE REFERENCE: 38-10(15849)B
 ; CURRENT APPLICATION NUMBER: US/09/902,540
 ; CURRENT FILING DATE: 2001-07-10
 ; PRIOR APPLICATION NUMBER: 60/217,883
 ; PRIOR FILING DATE: 2000-07-10
 ; NUMBER OF SEQ ID NOS: 16825
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 8493
 ; LENGTH: 600
 ; TYPE: DNA
 ; ORGANISM: Myxococcus xanthus
 ; OTHER INFORMATION: r-a or g

US-09-902-540-8493

```
; SEQ ID NO 8493
; LENGTH: 1788
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-8493

Alignment Scores:
Pred. No.: 698          Length: 1788
Score: 39.00           Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 73.58%     Indels: 0
DB: 4                  Gaps: 0

US-10-029-756-6 (1-8) x US-09-902-540-8493 (1-1788)
Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 1749 TGGCGGGACATGCGCTGGTGCAC 1772

RESULT 63
US-09-614-891-2/c
; Sequence 2, Application US/09614891
; Patent No. 6680379
; GENERAL INFORMATION:
; APPLICANT: SUN, WILLIAM
; TITLE OF INVENTION: ORGANIC ANION TRANSPORTER GENES AND PROTEINS
; FILE REFERENCE: 030727.0022.CIP.1
; CURRENT APPLICATION NUMBER: US/09/614,891
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,771
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1950
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-614-891-2

Alignment Scores:
Pred. No.: 767          Length: 1950
Score: 39.00           Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 73.58%     Indels: 0
DB: 4                  Gaps: 0

US-10-029-756-6 (1-8) x US-09-614-891-2 (1-1950)
Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 200 TGGCAGGGGCACCCGCGCAGGCAC 177

RESULT 64
US-08-635-130A-3
; Sequence 3, Application US/08635130A
; Patent No. 6696557
; GENERAL INFORMATION:
; APPLICANT: Caras, Ingrid W
; TITLE OF INVENTION: A2-1 Neurotrophic Factor
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

```
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/635,130A
; FILING DATE: 19-Mar-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, PhD., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2380 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-635-130A-3

Alignment Scores:
Pred. No.: 951          Length: 2380
Score: 39.00           Matches: 5
Percent Similarity: 87.50% Conservative: 2
Best Local Similarity: 62.50% Mismatches: 1
Query Match: 73.58%     Indels: 0
DB: 4                  Gaps: 0

US-10-029-756-6 (1-8) x US-08-635-130A-3 (1-2380)
Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 1976 TGGTTGGGTGCATGCACGTACCAT 1999

RESULT 65
US-09-614-891-3/c
; Sequence 3, Application US/09614891
; Patent No. 6680379
; GENERAL INFORMATION:
; APPLICANT: SUN, WILLIAM
; TITLE OF INVENTION: ORGANIC ANION TRANSPORTER GENES AND PROTEINS
; FILE REFERENCE: 030727.0022.CIP.1
; CURRENT APPLICATION NUMBER: US/09/614,891
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,771
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2501
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-614-891-3

Alignment Scores:
Pred. No.: 1e+03        Length: 2501
Score: 39.00           Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 73.58%     Indels: 0
DB: 4                  Gaps: 0

US-10-029-756-6 (1-8) x US-09-614-891-3 (1-2501)
Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 200 TGGCAGGGGCACCCGCGCAGGCAC 177

RESULT 66
US-09-949-016-5096
; Sequence 5096, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
```

```
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5096
; LENGTH: 2993
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5096

Alignment Scores:
Pred. No.: 1.22e+03 Length: 2993
Score: 39.00 Matches: 5
Percent Similarity: 87.50% Conservative: 2
Best Local Similarity: 62.50% Mismatches: 1
Query Match: 73.58% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-5096 (1-2993)

Qy 1 TrrpGlyHisAspAlaGlyHis 8
|||:::|||||:::|
Db 1948 TGGTGGGTGTCAGACAGTACCAT 1971

RESULT 67
US-09-949-016-205
; Sequence 205, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 205
; LENGTH: 3394
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-205

Alignment Scores:
Pred. No.: 1.4e+03 Length: 3394
Score: 39.00 Matches: 5
Percent Similarity: 87.50% Conservative: 2
Best Local Similarity: 62.50% Mismatches: 1
Query Match: 73.58% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-205 (1-3394)

Qy 1 TrrpGlyHisAspAlaGlyHis 8
|||:::|||||:::|
Db 2346 TGGTGGGTGTCAGACAGTACCAT 2369
```

```
RESULT 68
US-09-902-540-894
; Sequence 894, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 894
; LENGTH: 7538
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-894

Alignment Scores:
Pred. No.: 3.31e+03 Length: 7538
Score: 39.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 73.58% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-902-540-894 (1-7538)

Qy 1 TrrpGlyHisAspAlaGlyHis 8
|||:::|||||:::|
Db 3597 TGGCGCGACATGCGCTGGTCCAC 3620

RESULT 69
US-09-949-016-16838
; Sequence 16838, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16838
; LENGTH: 9948
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16838

Alignment Scores:
Pred. No.: 4.47e+03 Length: 9948
Score: 39.00 Matches: 5
Percent Similarity: 87.50% Conservative: 2
Best Local Similarity: 62.50% Mismatches: 1
Query Match: 73.58% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-16838 (1-9948)

Qy 1 TrrpGlyHisAspAlaGlyHis 8
|||:::|||||:::|
```


Pred. No.: 1.47e+04 Length: 29905
Score: 39.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 73.58% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-16788 (1-29905)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 17368 TGGAGTGGCCGGAGTCAGGGCAC 17391

RESULT 74

US-09-949-016-12818/c

; Sequence 12818, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12818

; LENGTH: 30678

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(30678)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-12818

Alignment Scores:

Pred. No.: 1.51e+04 Length: 30678

Score: 39.00 Matches: 6

Percent Similarity: 85.71% Conservative: 0

Best Local Similarity: 85.71% Mismatches: 1

Query Match: 73.58% Indels: 0

DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-12818 (1-30678)

Qy 1 TrpIleGlyHisAspAlaGly 7

Db 21624 TGGATAGGCCACTCAGCTGGA 21604

RESULT 75

US-09-949-016-13610

; Sequence 13610, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

US-09-949-016-13610

Alignment Scores:

Pred. No.: 1.51e+04 Length: 30678

Score: 39.00 Matches: 6

Percent Similarity: 85.71% Conservative: 0

Best Local Similarity: 85.71% Mismatches: 1

Query Match: 73.58% Indels: 0

DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-12818 (1-30678)

Qy 1 TrpIleGlyHisAspAlaGly 7

Db 21624 TGGATAGGCCACTCAGCTGGA 21604

RESULT 76

US-09-949-016-17513/c

; Sequence 17513, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

US-09-949-016-17513/c

Alignment Scores:

Pred. No.: 1.51e+04 Length: 30678

Score: 39.00 Matches: 6

Percent Similarity: 85.71% Conservative: 0

Best Local Similarity: 85.71% Mismatches: 1

Query Match: 73.58% Indels: 0

DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-12818 (1-30678)

Qy 1 TrpIleGlyHisAspAlaGly 7

Db 21624 TGGATAGGCCACTCAGCTGGA 21604

RESULT 77

US-09-949-016-13610

; Sequence 13610, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

US-09-949-016-13610

Alignment Scores:

Pred. No.: 1.51e+04 Length: 30678

Score: 39.00 Matches: 6

Percent Similarity: 85.71% Conservative: 0

Best Local Similarity: 85.71% Mismatches: 1

Query Match: 73.58% Indels: 0

DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-12818 (1-30678)

Qy 1 TrpIleGlyHisAspAlaGly 7

Db 21624 TGGATAGGCCACTCAGCTGGA 21604

RESULT 78

US-09-949-016-13610

; Sequence 13610, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

US-09-949-016-13610

Alignment Scores:

Pred. No.: 1.51e+04 Length: 30678

Score: 39.00 Matches: 6

Percent Similarity: 85.71% Conservative: 0

Best Local Similarity: 85.71% Mismatches: 1

Query Match: 73.58% Indels: 0

DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-12818 (1-30678)

Qy 1 TrpIleGlyHisAspAlaGly 7

Db 21624 TGGATAGGCCACTCAGCTGGA 21604

RESULT 79

US-09-949-016-13610

; Sequence 13610, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

US-09-949-016-13610

Alignment Scores:

Pred. No.: 1.51e+04 Length: 30678

Score: 39.00 Matches: 6

Percent Similarity: 85.71% Conservative: 0

Best Local Similarity: 85.71% Mismatches: 1

Query Match: 73.58% Indels: 0

DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-12818 (1-30678)

Qy 1 TrpIleGlyHisAspAlaGly 7

Db 21624 TGGATAGGCCACTCAGCTGGA 21604

RESULT 80

US-09-949-016-13610

; Sequence 13610, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

US-09-949-016-13610

Alignment Scores:

Pred. No.: 1.51e+04 Length: 30678

Score: 39.00 Matches: 6

Percent Similarity: 85.71% Conservative: 0

Best Local Similarity: 85.71% Mismatches: 1

Query Match: 73.58% Indels: 0

DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-12818 (1-30678)

Qy 1 TrpIleGlyHisAspAlaGly 7

Db 21624 TGGATAGGCCACTCAGCTGGA 21604

RESULT 81

US-09-949-016-13610

; Sequence 13610, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

US-09-949-016-13610

Alignment Scores:

Pred. No.: 1.51e+04 Length: 30678

Score: 39.00 Matches: 6

Percent Similarity: 85.71% Conservative: 0

Best Local Similarity: 85.71% Mismatches: 1

Query Match: 73.58% Indels: 0

DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-12818 (1-30678)

Qy 1 TrpIleGlyHisAspAlaGly 7

Db 21624 TGGATAGGCCACTCAGCTGGA 21604

RESULT 82

US-09-949-016-13610

; Sequence 13610, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

US-09-949-016-13610

Alignment Scores:

Pred. No.: 1.51e+04 Length: 30678

Score: 39.00 Matches: 6</


```
; NAME/KEY: misc_feature
; LOCATION: 281
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-15096

Alignment Scores:
Pred. No.: 192 Length: 371
Score: 38.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 71.70% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-621-976-15096 (1-371)
Oy 1 TptleGlyHisAspAlaGlyHis 8
Db 49 TGGACCTTTCATGACGCTGGTCAT 72

RESULT 81
US-09-854-133-354
; Sequence 354, Application US/09854133
; Patent No. 6759508
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
; APPLICANT: Secretist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 354
; LENGTH: 379
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(379)
; OTHER INFORMATION: n = A,T,C or G
US-09-854-133-354

Alignment Scores:
Pred. No.: 197 Length: 379
Score: 38.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 71.70% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-854-133-354 (1-379)
Oy 3 GlyHisAspAlaGlyHis 8
Db 40 GGCCATGATGCTGGACAC 57

RESULT 82
US-08-125-462-4/c
; Sequence 4, Application US/08125462
; Patent No. 5940840
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Youle, Richard J.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Nicholls, Peter J.
; TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
```

```
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/125,462
; FILING DATE: 22-SEP-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-110-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 405 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..405
; OTHER INFORMATION: /standard_name= "Synthetic EDN"
; OTHER INFORMATION: Gene"
; OTHER INFORMATION: /note= "Expression of the synthetic gene generates
; OTHER INFORMATION: a protein identical to the natural product, with
; OTHER INFORMATION: the exception that an additional methionine
US-08-125-462-4

Alignment Scores:
Pred. No.: 211 Length: 405
Score: 38.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 71.70% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-6 (1-8) x US-08-125-462-4 (1-405)
Oy 3 GlyHisAspAlaGlyHis 8
Db 361 GGTCAAGACGCTGGTCAC 344

RESULT 83
US-08-891-848-4/c
; Sequence 4, Application US/08891848
; Patent No. 5955073
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Youle, Richard J.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Nicholls, Peter J.
; TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

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;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,848
; FILING DATE: No. 5955073 yet assigned
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/125,462
; FILING DATE: 22-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/014,082
; FILING DATE: 04-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/779,195
; FILING DATE: 22-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/510,696
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-110310US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 405 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..405
; OTHER INFORMATION: /note= "synthetic eosinophil derived
; neurotoxin (EDN) gene sequence"
;
; US-08-891-848-4
;
Alignment Scores:
Pred. No.: 211 Length: 405
Score: 38.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 71.70% Indels: 0
DB: 2 Gaps: 0
;
US-10-029-756-6 (1-8) x US-08-891-848-4 (1-405)
;
Qy 3 GlyHisaspalaGlyHis 8
Db 361 GGCACGACGCTGGCTCAC 344
;
RESULT 84
US-09-621-976-19010
; Sequence 19010, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 19010
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Homo sapiens
;
US-09-621-976-19010
```

```
Alignment Scores:
Pred. No.: 229 Length: 436
Score: 38.00 Matches: 5
Percent Similarity: 62.50% Conservative: 0
Best Local Similarity: 62.50% Mismatches: 3
Query Match: 71.70% Indels: 0
DB: 4 Gaps: 0
;
US-10-029-756-6 (1-8) x US-09-621-976-19010 (1-436)
;
Qy 1 TrpIleGlyHisaspalaGlyHis 8
Db 133 TGGGCTGGGCATGATGGCTCACAC 156
;
RESULT 85
US-09-513-999C-12630
; Sequence 12630, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 12630
; LENGTH: 459
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 18
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 52
; OTHER INFORMATION: n=a, g, c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 53
; OTHER INFORMATION: y=c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 97
; OTHER INFORMATION: y=c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 391
; OTHER INFORMATION: k=g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 393
; OTHER INFORMATION: n=a, g, c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 396
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 401
; OTHER INFORMATION: y=c or t
;
US-09-513-999C-12630
;
Alignment Scores:
Pred. No.: 242 Length: 459
Score: 38.00 Matches: 6
```

Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 71.70% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-513-999C-12630 (1-459)

Oy 3 GlyHisAspAlaGlyHis 8
Db 105 GGACACGATGCAGGCCAT 122

RESULT 86

US-09-513-999C-1880
; Sequence 1880, Application US/09513999C
; Patent No. 6783961

GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Duclert, A.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

; FILE REFERENCE: 59.US2.REG

; CURRENT APPLICATION NUMBER: US/09/513,999C

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/122,487

; PRIOR FILING DATE: 1999-02-26

; NUMBER OF SEQ ID NOS: 36681

; SOFTWARE: Patent.pm

; SEQ ID NO 1880

; LENGTH: 486

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 112...486

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 18

; OTHER INFORMATION: r=a or g

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 52

; OTHER INFORMATION: n=a, g, c or t

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 53

; OTHER INFORMATION: y=c or t

US-09-513-999C-1880

Alignment Scores:

Pred. No.: 258 Length: 486
Score: 38.00 Matches: 6
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 71.70% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-513-999C-1880 (1-486)

Oy 3 GlyHisAspAlaGlyHis 8
Db 105 GGACACGATGCAGGCCAT 122

RESULT 87

US-09-949-016-143643

; Sequence 143643, Application US/09949016

; Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: CLO01307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 143643

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-143643

Alignment Scores:

Pred. No.: 324 Length: 601
Score: 38.00 Matches: 5
Percent Similarity: 75.00% Conservatives: 1
Best Local Similarity: 62.50% Mismatches: 2
Query Match: 71.70% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-143643 (1-601)

Oy 1 TrpIleGlyHisAspAlaGlyHis 8

Db 505 TGGGTGGTCACAGTGCCTGGCAT 528

RESULT 88

US-09-949-016-143644

; Sequence 143644, Application US/09949016

; Patent No. 6812339

GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: CLO01307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 143644

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-143644

Alignment Scores:

Pred. No.: 324 Length: 601
Score: 38.00 Matches: 5
Percent Similarity: 75.00% Conservatives: 1
Best Local Similarity: 62.50% Mismatches: 2
Query Match: 71.70% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-143644 (1-601)

Oy 1 TrpIleGlyHisAspAlaGlyHis 8

Db 231 TGGGTGGTCACAGTGCCTGGCAT 254

RESULT 89

US-09-949-016-171125/c

; Sequence 171125, Application US/09949016

; Patent No. 6812339

GENERAL INFORMATION:

```

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 171125
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-171125

Alignment Scores:
Pred. No.: 324 Length: 601
Score: 38.00 Matches: 5
Percent Similarity: 62.50% Conservative: 0
Best Local Similarity: 62.50% Mismatches: 3
Query Match: 71.70% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-171125 (1-601)
Qy 1 TrrpIcGlyHisAspAlaGlyHis 8
Db 44 TGGGCTGGGCATGATGGCTCACAC 21

RESULT 90
US-09-949-016-171126/c
; Sequence 171126, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 171126
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-171126

Alignment Scores:
Pred. No.: 324 Length: 601
Score: 38.00 Matches: 5
Percent Similarity: 62.50% Conservative: 0
Best Local Similarity: 62.50% Mismatches: 3
Query Match: 71.70% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-171126 (1-601)
Qy 1 TrrpIcGlyHisAspAlaGlyHis 8
Db 210 TGGGCTGGGCATGATGGCTCACAC 187

```

```

RESULT 91
US-09-949-016-171255/c
; Sequence 171255, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 171255
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-171255

Alignment Scores:
Pred. No.: 324 Length: 601
Score: 38.00 Matches: 5
Percent Similarity: 62.50% Conservative: 0
Best Local Similarity: 71.70% Mismatches: 3
Query Match: 4 Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-171255 (1-601)
Qy 1 TrrpIcGlyHisAspAlaGlyHis 8
Db 44 TGGGCTGGGCATGATGGCTCACAC 21

RESULT 92
US-09-949-016-171256/c
; Sequence 171256, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 171256
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-171256

Alignment Scores:
Pred. No.: 324 Length: 601
Score: 38.00 Matches: 5
Percent Similarity: 62.50% Conservative: 0
Best Local Similarity: 71.70% Mismatches: 3
Query Match: 4 Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-949-016-171256 (1-601)

```

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 210 TGGGCTGGGCATGATGGCTCACAC 187

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RESULT 93
US-09-949-016-179881/c
; Sequence 179881, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 179881
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-179881

```

| | | | | | |
|------------------------|---------|---------------|-----|--|--|
| Alignment Scores: | | | | | |
| Pred. No.: | 324 | Length: | 601 | | |
| Score: | 38.00 | Matches: | 5 | | |
| Percent Similarity: | 100.00% | Conservative: | | | |
| Best Local Similarity: | 83.33% | Mismatches: | 0 | | |
| Query Match: | 71.70% | Indels: | 0 | | |
| DB: | 4 | Gaps: | 0 | | |

US-10-029-756-6 (1-8) x US-09-949-016-179881 (1-601)

Qy 1 TrpIleGlyHisAspAla 6
|||::|||
Db 322 TGGGTTGGGCACCATGCC 305

```

RESULT 94
US-09-949-016-200124
; Sequence 200124, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASES, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 200124
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-200124

```

| | |
|---------------------|--------|
| Alignment Scores: | |
| Pred. No.: | 324 |
| Score: | 38.00 |
| Percent Similarity: | 62.50% |
| Length: | 601 |
| Matches: | 5 |
| Conservative: | 0 |

| | | | |
|------------------------|--------|-------------|---|
| Best Local Similarity: | 62.50% | Mismatches: | 3 |
| Query Match: | 71.70% | Indels: | 0 |
| DB: | 4 | Gaps: | 0 |

US-10-029-756-6 (1-8) X US-09-949-016-200124 (1-601)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
||| ||| ||| ||| ||| ||| ||| |||
pB 61 TGGGCGGGGCACGATGGTCCAC 84

RESULT 95
US-09-949-016-205533
; Sequence 205533, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 205533
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-205533

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| Prod. No.: | 324 | Length: 601 |
| Score: | 38.00 | Matches: 6 |
| Percent Similarity: | 75.00% | Conservative: 0 |
| Best Local Similarity: | 75.00% | Mismatches: 2 |
| Query Match: | 71.70% | Indels: 0 |
| DB: | 4 | Gaps: 0 |

US-10-029-756-6 (1-8) x US-09-949-016-205533 (1-601)

QY 1 TrpIleGlyHisAspAlaGlyHis 8
pb 378 TGGGCTGGAGCAGACGCTGGACAT 401

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RESULT 96 .
US-09-543-681A-1128
; Sequence 1128, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID S
; FILE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 1128
; LENGTH: 603
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-1128

Alignment Scores:
Pred. No.: 325
Score: 38.00
Percent Similarity: 100.00%
Conservative:

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| Alignment Scores: | |
| Pred. No.: | 325 |
| Score: | 38.00 |
| Percent Similarity: | 100.00% |
| Conservative: | 0 |
| Matches: | 6 |
| Length: | 603 |

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 71.70% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-543-681A-1128 (1-603)

Qy 3 GlyHisaspAlaGlyHis 8
Db 474 GCCATGATGCGGTCCAC 491

RESULT 97
US-09-252-991A-4810/c
; Sequence 4810, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4810
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4810

Alignment Scores:
Pred. No.: 338 Length: 624
Score: 38.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 71.70% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-252-991A-4810 (1-624)

Qy 3 GlyHisaspAlaGlyHis 8
Db 142 GCCACGACGCTGGCCAT 125

RESULT 98
US-09-252-991A-7908
; Sequence 7908, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7908
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7908

Alignment Scores:
Pred. No.: 382 Length: 699
Score: 38.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 71.70% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-252-991A-7908 (1-699)

Qy 3 GlyHisaspAlaGlyHis 8
Db 654 GCCATGATGCTGGCCAT 671

RESULT 99
US-09-270-767-11527/c
; Sequence 11527, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11527
; LENGTH: 737
; TYPE: DNA
; ORGANISM: *Drosophila melanogaster*
US-09-270-767-11527

Alignment Scores:
Pred. No.: 404 Length: 737
Score: 38.00 Matches: 5
Percent Similarity: 75.00% Conservative: 1
Best Local Similarity: 62.50% Mismatches: 2
Query Match: 71.70% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-270-767-11527 (1-737)

Qy 1 TtpIleGlyHisaspAlaGlyHis 8
Db 191 TGGCTTGGCCATGCCAGGCCAC 168

RESULT 100
US-09-902-540-5908
; Sequence 5908, Application US/09902540
; Patent No. 8833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: *Myxococcus xanthus* Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR FILING DATE: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 5908
; LENGTH: 753
; TYPE: DNA
; ORGANISM: *Myxococcus xanthus*
US-09-902-540-5908

Alignment Scores:
Pred. No.: 414 Length: 753
Score: 38.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 71.70% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x US-09-902-540-5908 (1-753)

Qy 3 GlyHisSepAlaGlyHis 8
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Db 588 GCCCATGACGCTGCCAC 605

Search completed: June 8, 2005, 15:28:08
Job time : 1074.11 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 8, 2005, 09:39:06 ; Search time 1648.42 Seconds

(without alignments)
235.159 Million cell updates/sec

Title: US-10-029-756-6

Perfect score: 53

Sequence: 1 WIGHDAGH 8

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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-DB=GenEmbl -QWIT=fastap -SUPPIX=p2n.rge -MINMATCH=0.1 -LOPCL=0 -LOPEXT=0
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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SUMMARIES

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| 2 | 53 | 100.0 | 1478 | 8 | AY055117 Echium ge |
| 3 | 53 | 100.0 | 1684 | 6 | AR076814 Sequence |
| 4 | 53 | 100.0 | 1684 | 6 | AR084177 Sequence |

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| 6 | 53 | 100.0 | 1684 | 6 | BD070919 | An oleos1 |
| 7 | 53 | 100.0 | 1685 | 6 | AR020904 | Sequence |
| 8 | 53 | 100.0 | 1685 | 6 | I38430 | Sequence 4 |
| 9 | 53 | 100.0 | 1685 | 6 | AR200408 | Sequence |
| 10 | 53 | 100.0 | 1685 | 6 | AR455421 | Sequence |
| 11 | 53 | 100.0 | 1685 | 6 | AF007561 | Borago of |
| 12 | 53 | 100.0 | 1687 | 6 | AX951561 | Sequence |
| 13 | 53 | 100.0 | 1687 | 6 | BOU79010 | U79010 Borago offi |
| 14 | 50 | 94.3 | 1362 | 6 | AX824969 | Sequence |
| 15 | 50 | 94.3 | 1362 | 6 | AX824971 | Sequence |
| 16 | 50 | 94.3 | 1410 | 8 | AY234125 | Primula f |
| 17 | 50 | 94.3 | 1618 | 8 | AY234127 | Primula v |
| 18 | 50 | 94.3 | 1788 | 8 | AF031194 | Triticum |
| 19 | 50 | 94.3 | 1856 | 8 | AF005096 | AF005096 Ricinus c |
| 20 | 50 | 94.3 | 1972 | 8 | BT009556 | BT009556 Triticum |
| 21 | 49 | 92.5 | 140990 | 10 | AC142257 | AC142257 Mus muscu |
| 22 | 49 | 92.5 | 174714 | 2 | AC107366 | AC107366 Mus muscu |
| 23 | 49 | 92.5 | 183187 | 10 | AC104328 | AC104328 Mus muscu |
| 24 | 48 | 90.6 | 1347 | 8 | AY131238 | Argania s |
| 25 | 48 | 90.6 | 1385 | 8 | AY234126 | Primula v |
| 26 | 48 | 90.6 | 1681 | 8 | AY234124 | Primula f |
| 27 | 47 | 88.7 | 1798 | 8 | AK058543 | Oryza sat |
| 28 | 47 | 88.7 | 83296 | 2 | AC022588 | Homo sapi |
| 29 | 47 | 88.7 | 95161 | 8 | AF005554 | Oryza sat |
| 30 | 47 | 88.7 | 139537 | 9 | AC021039 | Homo sapi |
| 31 | 47 | 88.7 | 158262 | 2 | AC013757 | Homo sapi |
| 32 | 46 | 86.8 | 649 | 6 | AX320439 | Sequence |
| 33 | 46 | 86.8 | 1570 | 3 | AB127388 | Haemaphys |
| 34 | 46 | 86.8 | 42208 | 9 | AL589989 | Human DNA |
| 35 | 46 | 86.8 | 42601 | 9 | AC004210 | Homo sapi |
| 36 | 46 | 86.8 | 43003 | 9 | AL845556 | Human DNA |
| 37 | 46 | 86.8 | 100000 | 9 | AF000508 | Homo sapi |
| 38 | 46 | 86.8 | 102821 | 2 | CR759828 | Homo sapi |
| 39 | 46 | 86.8 | 138102 | 9 | AC004866 | Homo sapi |
| 40 | 46 | 86.8 | 160147 | 9 | AC146233 | Homo sapi |
| 41 | 46 | 86.8 | 166079 | 9 | AC090151 | Pan trogl |
| 42 | 46 | 86.8 | 166335 | 2 | AC012461 | Homo sapi |
| 43 | 46 | 86.8 | 178168 | 2 | AC012350 | Homo sapi |
| 44 | 46 | 86.8 | 181727 | 2 | AC036232 | Homo sapi |
| 45 | 46 | 86.8 | 182152 | 2 | AC067929 | Homo sapi |
| 46 | 46 | 86.8 | 184852 | 2 | AC026032 | Homo sapi |
| 47 | 46 | 86.8 | 209452 | 2 | AC108778 | Mus muscu |
| 48 | 46 | 86.8 | 211237 | 10 | AC126280 | Mus muscu |
| 49 | 46 | 86.8 | 236822 | 9 | D84394 | Homo sapien |
| 50 | 46 | 86.8 | 244928 | 2 | AC097177 | Rattus no |
| 51 | 46 | 86.8 | 245125 | 2 | AC133759 | Rattus no |
| 52 | 46 | 86.8 | 256373 | 2 | AC128269 | Rattus no |
| 53 | 46 | 86.8 | 333800 | 1 | SME591792 | Sinorhizo |
| 54 | 46 | 86.8 | 338579 | 1 | AP003004 | Mesorhizo |
| 55 | 45 | 84.9 | 1258 | 10 | BC008166 | Mus muscu |
| 56 | 45 | 84.9 | 1623 | 10 | AB069965 | Mus muscu |
| 57 | 45 | 84.9 | 1910 | 10 | BC024119 | Mus muscu |
| 58 | 45 | 84.9 | 1927 | 10 | BC013474 | Mus muscu |
| 59 | 45 | 84.9 | 1951 | 10 | BC026598 | Mus muscu |
| 60 | 45 | 84.9 | 1976 | 10 | BC026597 | Mus muscu |
| 61 | 45 | 84.9 | 99059 | 10 | AL929383 | Mouse DNA |
| 62 | 45 | 84.9 | 101937 | 9 | AC010221 | Homo sapi |
| 63 | 45 | 84.9 | 127121 | 2 | AC008874 | Homo sapi |
| 64 | 45 | 84.9 | 165176 | 2 | AC022199 | Homo sapi |
| 65 | 45 | 84.9 | 167322 | 2 | AC016788 | Homo sapi |
| 66 | 45 | 84.9 | 190032 | 9 | AP003462 | Homo sapi |
| 67 | 45 | 84.9 | 193415 | 2 | AC074180 | Homo sapi |
| 68 | 45 | 84.9 | 197591 | 9 | AC113404 | Homo sapi |
| 69 | 45 | 84.9 | 197997 | 6 | AX663810 | Sequence |
| 70 | 45 | 84.9 | 200232 | 9 | AC026783 | Homo sapi |
| 71 | 45 | 84.9 | 208710 | 10 | AC126262 | Mus muscu |
| 72 | 45 | 84.9 | 218575 | 2 | AL844841 | Mus muscu |
| 73 | 45 | 84.9 | 220283 | 2 | AC103391 | Mus muscu |
| 74 | 45 | 84.9 | 224037 | 10 | AL670399 | Mouse DNA |
| 75 | 45 | 84.9 | 231770 | 2 | AC109171 | Mus muscu |
| 76 | 45 | 84.9 | 235505 | 2 | AC133422 | Rattus no |
| 77 | 45 | 84.9 | 238637 | 2 | AC092254 | Mus muscu |

| | | | | | | | | | | | | | |
|-----|----|------|--------|----|----------|---------------------|-------|----|------|--------|----|------------|--------------------|
| 78 | 45 | 84.9 | 245515 | 2 | AC151275 | AC151275 Mus muscu | 151 | 43 | 81.1 | 266766 | 2 | AC094770 | AC094770 Rattus no |
| 79 | 45 | 84.9 | 245515 | 2 | AC151275 | AC151275 Mus muscu | 152 | 43 | 81.1 | 275555 | 2 | AC097204 | AC097204 Rattus no |
| 80 | 45 | 84.9 | 251564 | 2 | AC125698 | AC125698 Rattus no | c 153 | 43 | 81.1 | 299750 | 1 | AP005964 | AP005964 Bradyrhiz |
| 81 | 44 | 83.0 | 162 | 6 | AR524799 | AR524799 Sequence | c 154 | 43 | 81.1 | 300400 | 1 | AP005943 | AP005943 Bradyrhiz |
| 82 | 83 | 83.0 | 833 | 6 | AR508777 | AR508777 Sequence | c 155 | 43 | 81.1 | 301675 | 1 | AP005027 | AP005027 Streptomy |
| 83 | 44 | 83.0 | 2734 | 6 | CQ590748 | CQ590748 Sequence | c 156 | 43 | 81.1 | 309050 | 1 | SC093917 | AL939117 Streptomy |
| 84 | 44 | 83.0 | 5679 | 6 | CQ590747 | CQ590747 Sequence | c 157 | 43 | 81.1 | 311050 | 1 | BX294133 | BX294133 Pirellula |
| 85 | 44 | 83.0 | 33443 | 2 | AC014332 | AC014332 Sequence | c 158 | 42 | 79.2 | 385 | 10 | S66658 | S66658 alpha-globi |
| 86 | 44 | 83.0 | 160817 | 3 | AC008316 | AC008316 Drosophil | c 159 | 42 | 79.2 | 393 | 10 | RATAGLO28X | M94075 Rat alpha-g |
| 87 | 44 | 83.0 | 167230 | 8 | AP003275 | AP003275 Oryza sat | c 160 | 42 | 79.2 | 424 | 10 | S5233753 | S52345 OSF-1-pleio |
| 88 | 44 | 83.0 | 172704 | 10 | AC121531 | AC121531 Mus muscu | c 161 | 42 | 79.2 | 517 | 10 | BC048363 | BC048363 Mus muscu |
| 89 | 44 | 83.0 | 177028 | 3 | AC008315 | AC008315 Drosophil | c 162 | 42 | 79.2 | 522 | 6 | AX577903 | AX577903 Sequence |
| 90 | 44 | 83.0 | 211153 | 2 | AC136636 | AC136636 Mus muscu | c 163 | 42 | 79.2 | 533 | 11 | GX00099 | G90099 S208P6678FC |
| 91 | 44 | 83.0 | 214124 | 2 | AC098578 | AC098578 Rattus no | c 164 | 42 | 79.2 | 650 | 6 | AR307081 | AR307081 Sequence |
| 92 | 44 | 83.0 | 227182 | 2 | AC111765 | AC111765 Rattus no | c 165 | 42 | 79.2 | 650 | 6 | AX154831 | AX154831 Sequence |
| 93 | 44 | 83.0 | 236198 | 2 | AC108547 | AC108547 Rattus no | c 166 | 42 | 79.2 | 672 | 6 | CQ718202 | CQ718202 Sequence |
| 94 | 44 | 83.0 | 238323 | 3 | AE003684 | AE003684 Drosophil | c 167 | 42 | 79.2 | 734 | 6 | BD147575 | BD147575 Primer fo |
| 95 | 44 | 83.0 | 239808 | 2 | AC126585 | AC126585 Rattus no | c 168 | 42 | 79.2 | 734 | 6 | AX867513 | AX867513 Sequence |
| 96 | 44 | 83.0 | 246850 | 1 | AP005346 | AP005346 Vibrio vu | c 169 | 42 | 79.2 | 816 | 6 | AR508169 | AR508169 Sequence |
| 97 | 44 | 83.0 | 301936 | 1 | AE015808 | AE015808 Vibrio vu | c 170 | 42 | 79.2 | 1167 | 8 | AK109032 | AK109032 Oryza sat |
| 98 | 44 | 83.0 | 344321 | 1 | EX640429 | EX640429 Bordetell | c 171 | 42 | 79.2 | 1249 | 10 | RNU622315 | U62315 Rattus norv |
| 99 | 44 | 83.0 | 346274 | 1 | EX640443 | EX640443 Bordetell | c 172 | 42 | 79.2 | 1331 | 10 | BC002064 | BC002064 Mus muscu |
| 100 | 44 | 83.0 | 349354 | 1 | EX640416 | EX640416 Bordetell | c 173 | 42 | 79.2 | 1452 | 6 | CQ733333 | CQ733333 Sequence |
| 101 | 43 | 81.1 | 24453 | 9 | HS404P13 | AL035069 Human DNA | c 174 | 42 | 79.2 | 1514 | 6 | AX305712 | AX305712 Sequence |
| 102 | 43 | 81.1 | 33765 | 2 | AC103836 | AC103836 Homo sapi | c 175 | 42 | 79.2 | 1514 | 10 | MUSOSF1 | D90225 Mus musculu |
| 103 | 43 | 81.1 | 39338 | 9 | AC004644 | AC004644 Homo sapi | c 176 | 42 | 79.2 | 1542 | 6 | E03564 | E03564 cDNA encodi |
| 104 | 43 | 81.1 | 51240 | 2 | AC104999 | AC104999 Homo sapi | c 177 | 42 | 79.2 | 1591 | 8 | HACVYBERN | H87143 Helianthus |
| 105 | 43 | 81.1 | 59271 | 10 | AL929456 | AL929456 Mouse DNA | c 178 | 42 | 79.2 | 1603 | 10 | BC061695 | BC061695 Mus muscu |
| 106 | 43 | 81.1 | 66917 | 2 | AC104368 | AC104368 Homo sapi | c 179 | 42 | 79.2 | 1606 | 6 | AC007273 | AC007273 Sequence |
| 107 | 43 | 81.1 | 87099 | 2 | AC151336 | AC151336 Xenopus t | c 180 | 42 | 79.2 | 1638 | 10 | BC078828 | BC078828 Rattus no |
| 108 | 43 | 81.1 | 110000 | 2 | AC140815 | Continuation (2 of | c 181 | 42 | 79.2 | 1866 | 6 | BD157966 | BD157966 Primer fo |
| 109 | 43 | 81.1 | 114521 | 9 | AL159985 | AL159985 Human DNA | c 182 | 42 | 79.2 | 1866 | 6 | AX879681 | AX879681 Sequence |
| 110 | 43 | 81.1 | 123153 | 2 | AC149083 | AC149083 Pan trogl | c 183 | 42 | 79.2 | 1866 | 9 | AC022726 | AC022726 Homo sapi |
| 111 | 43 | 81.1 | 133786 | 9 | AC091839 | AC091839 Homo sapi | c 184 | 42 | 79.2 | 1917 | 9 | BC033824 | BC033824 Homo sapi |
| 112 | 43 | 81.1 | 135407 | 2 | AC124114 | AC124114 Mus muscu | c 185 | 42 | 79.2 | 1974 | 3 | BT001527 | BT001527 Drosophil |
| 113 | 43 | 81.1 | 136155 | 8 | GNS08C80 | AL7131751 Oryza sat | c 186 | 42 | 79.2 | 1978 | 9 | CR533565 | CR533565 Homo sapi |
| 114 | 43 | 81.1 | 140531 | 2 | AC105341 | AC105341 Homo sapi | c 187 | 42 | 79.2 | 2077 | 8 | SCYNR012W | Z71627 S.cerevisia |
| 115 | 43 | 81.1 | 150649 | 2 | AC142157 | AC142157 Rattus no | c 188 | 42 | 79.2 | 2188 | 5 | CR760964 | CR760964 Xenopus t |
| 116 | 43 | 81.1 | 155937 | 2 | AC016341 | AC016341 Homo sapi | c 189 | 42 | 79.2 | 2238 | 6 | BD206377 | BD206377 Human nuc |
| 117 | 43 | 81.1 | 160378 | 2 | AC090076 | AC090076 Homo sapi | c 190 | 42 | 79.2 | 2238 | 6 | AR400692 | AR400692 Sequence |
| 118 | 43 | 81.1 | 165344 | 2 | AL162577 | AL162577 Homo sapi | c 191 | 42 | 79.2 | 2238 | 6 | AX013196 | AX013196 Sequence |
| 119 | 43 | 81.1 | 167789 | 2 | AC084260 | AC084260 Homo sapi | c 192 | 42 | 79.2 | 2305 | 6 | CQ718453 | CQ718453 Sequence |
| 120 | 43 | 81.1 | 167794 | 9 | AC092472 | AC092472 Homo sapi | c 193 | 42 | 79.2 | 2307 | 6 | AR060049 | AR060049 Sequence |
| 121 | 43 | 81.1 | 170973 | 9 | AC090097 | AC090097 Homo sapi | c 194 | 42 | 79.2 | 2307 | 6 | AR087204 | AR087204 Sequence |
| 122 | 43 | 81.1 | 172551 | 9 | AC008518 | AC008518 Homo sapi | c 195 | 42 | 79.2 | 2307 | 6 | AR134391 | AR134391 Sequence |
| 123 | 43 | 81.1 | 172927 | 2 | AC119701 | AC119701 Rattus no | c 196 | 42 | 79.2 | 2307 | 6 | AR144492 | AR144492 Sequence |
| 124 | 43 | 81.1 | 173888 | 9 | AC105091 | AC105091 Homo sapi | c 197 | 42 | 79.2 | 2307 | 6 | AR256663 | AR256663 Sequence |
| 125 | 43 | 81.1 | 174741 | 2 | AC024280 | AC024280 Homo sapi | c 198 | 42 | 79.2 | 2307 | 6 | AR372547 | AR372547 Sequence |
| 126 | 43 | 81.1 | 175838 | 9 | AC026427 | AC026427 Homo sapi | c 199 | 42 | 79.2 | 2307 | 9 | HUMORFC | L40393 Homo sapien |
| 127 | 43 | 81.1 | 176116 | 2 | AC138590 | AC138590 Mus muscu | c 200 | 42 | 79.2 | 2307 | 11 | G27111 | G27111 human STS S |
| 128 | 43 | 81.1 | 176889 | 9 | AC090274 | AC090274 Homo sapi | c 201 | 42 | 79.2 | 2395 | 8 | AB126085 | AB126085 Oryza sat |
| 129 | 43 | 81.1 | 176902 | 9 | AF280813 | AF280813 Homo sapi | c 202 | 42 | 79.2 | 2395 | 8 | AK068159 | AK068159 Oryza sat |
| 130 | 43 | 81.1 | 185010 | 2 | AC022514 | AC022514 Mus muscu | c 203 | 42 | 79.2 | 2486 | 6 | AX747833 | AX747833 Sequence |
| 131 | 43 | 81.1 | 186340 | 2 | AC016684 | AC016684 Homo sapi | c 204 | 42 | 79.2 | 2486 | 9 | AK092975 | AK092975 Homo sapi |
| 132 | 43 | 81.1 | 190814 | 9 | AC006111 | AC006111 Homo sapi | c 205 | 42 | 79.2 | 2702 | 6 | CQ493997 | CQ493997 Sequence |
| 133 | 43 | 81.1 | 198475 | 2 | AC150880 | AC150880 Bos tauru | c 206 | 42 | 79.2 | 2707 | 8 | SCURK1 | X51998 S.cerevisia |
| 134 | 43 | 81.1 | 203083 | 2 | AC069459 | AC069459 Mus muscu | c 207 | 42 | 79.2 | 2741 | 6 | CQ603213 | CQ603213 Sequence |
| 135 | 43 | 81.1 | 204430 | 2 | AC118027 | AC118027 Mus muscu | c 208 | 42 | 79.2 | 2818 | 9 | AB040911 | AB040911 Homo sapi |
| 136 | 43 | 81.1 | 207364 | 2 | AC120564 | AC120564 Rattus no | c 209 | 42 | 79.2 | 2846 | 6 | AX321399 | AX321399 Sequence |
| 137 | 43 | 81.1 | 210643 | 9 | AC137723 | AC137723 Homo sapi | c 210 | 42 | 79.2 | 2995 | 6 | A84104 | A84104 Sequence 8 |
| 138 | 43 | 81.1 | 214382 | 10 | AC098733 | AC098733 Mus muscu | c 211 | 42 | 79.2 | 2995 | 9 | AF015040 | AF015040 Homo sapi |
| 139 | 43 | 81.1 | 217584 | 2 | AC113299 | AC113299 Mus muscu | c 212 | 42 | 79.2 | 3045 | 9 | BC024144 | BC024144 Homo sapi |
| 140 | 43 | 81.1 | 220737 | 2 | AC128459 | AC128459 Rattus no | c 213 | 42 | 79.2 | 3050 | 6 | AX342026 | AX342026 Sequence |
| 141 | 43 | 81.1 | 223877 | 2 | AC098923 | AC098923 Rattus no | c 214 | 42 | 79.2 | 3050 | 6 | AX342529 | AX342529 Sequence |
| 142 | 43 | 81.1 | 228998 | 2 | AC112472 | AC112472 Rattus no | c 215 | 42 | 79.2 | 3050 | 6 | AX590316 | AX590316 Sequence |
| 143 | 43 | 81.1 | 232535 | 2 | AC110702 | AC110702 Rattus no | c 216 | 42 | 79.2 | 3050 | 9 | AB030251 | AB030251 Homo sapi |
| 144 | 43 | 81.1 | 233882 | 2 | AC112119 | AC112119 Rattus no | c 217 | 42 | 79.2 | 3079 | 6 | AX321395 | AX321395 Sequence |
| 145 | 43 | 81.1 | 234182 | 10 | AL603707 | AL603707 Mouse DNA | c 218 | 42 | 79.2 | 3079 | 9 | AK000733 | AK000733 Homo sapi |
| 146 | 43 | 81.1 | 235276 | 10 | AC110234 | AC110234 Mus muscu | c 219 | 42 | 79.2 | 3079 | 9 | BC032754 | BC032754 Homo sapi |
| 147 | 43 | 81.1 | 239030 | 2 | AC135695 | AC135695 Rattus no | c 220 | 42 | 79.2 | 3144 | 6 | AR339606 | AR339606 Sequence |
| 148 | 43 | 81.1 | 251002 | 3 | CNS07EGI | AL590451 chromosom | c 221 | 42 | 79.2 | 3155 | 6 | CQ590060 | CQ590060 Sequence |
| 149 | 43 | 81.1 | 261587 | 2 | AC126139 | AC126139 Rattus no | c 222 | 42 | 79.2 | 3237 | 6 | AX086632 | AX086632 Sequence |
| 150 | 43 | 81.1 | 261968 | 2 | AC120289 | AC120289 Rattus no | c 223 | 42 | 79.2 | 3270 | 9 | AF108092 | AF108092 Homo sapi |

| | | | | | | | | | | | | | | | |
|-------|----|------|--------|----|-------------|---------------------|---------------------|--------------------|-------|------|--------|--------|----------|-----------|--------------------|
| C 224 | 42 | 79.2 | 3336 | 6 | C0586230 | Sequence | C0586230 | Sequence | 297 | 42 | 79.2 | 188774 | 2 | AC116853 | Mus muscu |
| C 225 | 42 | 79.2 | 3370 | 6 | AX281755 | Sequence | AX281755 | Sequence | c 298 | 42 | 79.2 | 190630 | 9 | AC145773 | Pan trogl |
| C 226 | 42 | 79.2 | 3429 | 9 | AF171941 | Homo sapi | AF171941 | Homo sapi | 299 | 42 | 79.2 | 191606 | 10 | AC126272 | Mus muscu |
| C 227 | 42 | 79.2 | 3462 | 9 | AF171939 | Homo sapi | AF171939 | Homo sapi | c 300 | 42 | 79.2 | 191655 | 2 | AC139828 | Homo sapi |
| C 228 | 42 | 79.2 | 3479 | 9 | HSM807281 | Homo sapi | BX647137 | Homo sapi | c 301 | 42 | 79.2 | 193700 | 2 | AC139472 | Homo sapi |
| C 229 | 42 | 79.2 | 3509 | 9 | BC068476 | Homo sapi | BC068476 | Homo sapi | 302 | 42 | 79.2 | 194454 | 2 | AC140176 | Homo sapi |
| C 230 | 42 | 79.2 | 3573 | 9 | AF171940 | Homo sapi | AF171940 | Homo sapi | 303 | 42 | 79.2 | 194866 | 2 | AC142140 | Rattus no |
| C 231 | 42 | 79.2 | 3606 | 9 | AF171938 | Homo sapi | AF171938 | Homo sapi | 304 | 42 | 79.2 | 194897 | 3 | AC007697 | Drosophill |
| C 232 | 42 | 79.2 | 4741 | 6 | C0603212 | Sequence | C0603212 | Sequence | 305 | 42 | 79.2 | 195768 | 9 | AC022034 | Homo sapi |
| C 233 | 42 | 79.2 | 6005 | 6 | C0586229 | Sequence | C0586229 | Sequence | c 306 | 42 | 79.2 | 198141 | 2 | AC138893 | Homo sapi |
| C 234 | 42 | 79.2 | 12869 | 1 | AE015268 | Shigella | AE015268 | Shigella | c 307 | 42 | 79.2 | 199016 | 9 | HS48G12 | Human DNA |
| C 235 | 42 | 79.2 | 23901 | 8 | SCN201952 | X77395 S. cerevisia | X77395 S. cerevisia | 308 | 42 | 79.2 | 203046 | 2 | AC006342 | Homo sapi | |
| C 236 | 42 | 79.2 | 39835 | 2 | AC014355 | AC014355 Drosophi | AC014355 | Drosophi | 309 | 42 | 79.2 | 203256 | 2 | AC117787 | Mus muscu |
| C 237 | 42 | 79.2 | 41839 | 9 | AC104815 | AC104815 Homo sapi | AC104815 | Homo sapi | 310 | 42 | 79.2 | 203980 | 2 | AC134058 | Rattus no |
| C 238 | 42 | 79.2 | 62327 | 9 | AL365226 | AL365226 Human DNA | AL365226 | Human DNA | 311 | 42 | 79.2 | 209284 | 2 | AC107589 | Rattus no |
| C 239 | 42 | 79.2 | 66091 | 2 | AC124273 | AC124273 Homo sapi | AC124273 | Homo sapi | c 312 | 42 | 79.2 | 209539 | 2 | AC139802 | Homo sapi |
| C 240 | 42 | 79.2 | 74994 | 9 | AP000651 | AP000651 Homo sapi | AP000651 | Homo sapi | c 313 | 42 | 79.2 | 210000 | 2 | AC110556 | Mus muscu |
| C 241 | 42 | 79.2 | 84102 | 9 | AY498860 | AY498860 Homo sapi | AY498860 | Homo sapi | c 314 | 42 | 79.2 | 211927 | 2 | AC150462 | Callithri |
| C 242 | 42 | 79.2 | 103606 | 9 | AC005004 | AC005004 Homo sapi | AC005004 | Homo sapi | c 315 | 42 | 79.2 | 213232 | 5 | BX294395 | Zebrafish |
| C 243 | 42 | 79.2 | 110000 | 1 | AE017354_08 | Continuation (9 of | Continuation (9 of | Continuation (9 of | c 316 | 42 | 79.2 | 214895 | 10 | AL845313 | Mouse DNA |
| C 244 | 42 | 79.2 | 110000 | 1 | AE017354_09 | Continuation (10 o | Continuation (10 o | Continuation (10 o | c 317 | 42 | 79.2 | 216194 | 10 | AC096051 | Rattus no |
| C 245 | 42 | 79.2 | 110000 | 1 | CR628336_09 | Continuation (10 o | Continuation (10 o | Continuation (10 o | c 318 | 42 | 79.2 | 216387 | 9 | DJ534K4 | Homo sapi |
| C 246 | 42 | 79.2 | 110000 | 1 | CR628336_10 | Continuation (11 o | Continuation (11 o | Continuation (11 o | c 319 | 42 | 79.2 | 222386 | 2 | AC138852 | Homo sapi |
| C 247 | 42 | 79.2 | 110000 | 1 | CR628337_09 | Continuation (10 o | Continuation (10 o | Continuation (10 o | c 320 | 42 | 79.2 | 223363 | 2 | AC120700 | Rattus no |
| C 248 | 42 | 79.2 | 110000 | 2 | AC115960_0 | AC115960 Mus muscu | AC115960 | Mus muscu | 321 | 42 | 79.2 | 228657 | 2 | AC123333 | Rattus no |
| C 249 | 42 | 79.2 | 110000 | 2 | AC138524_1 | Continuation (2 of | Continuation (2 of | Continuation (2 of | c 322 | 42 | 79.2 | 229923 | 2 | AC125666 | Rattus no |
| C 250 | 42 | 79.2 | 110000 | 2 | AC139486_3 | Continuation (4 of | Continuation (4 of | Continuation (4 of | c 323 | 42 | 79.2 | 230800 | 10 | AL831742 | Mouse DNA |
| C 251 | 42 | 79.2 | 110000 | 2 | AC139487_2 | Continuation (3 of | Continuation (3 of | Continuation (3 of | c 324 | 42 | 79.2 | 233076 | 2 | AC130090 | Rattus no |
| C 252 | 42 | 79.2 | 110000 | 2 | AC139489_3 | Continuation (4 of | Continuation (4 of | Continuation (4 of | c 325 | 42 | 79.2 | 238134 | 2 | AC115520 | Rattus no |
| C 253 | 42 | 79.2 | 11655 | 2 | AC010239 | AC010239 Homo sapi | AC010239 | Homo sapi | c 326 | 42 | 79.2 | 240645 | 2 | AC131537 | Rattus no |
| C 254 | 42 | 79.2 | 119393 | 9 | AC003658 | AC003658 Homo sapi | AC003658 | Homo sapi | 327 | 42 | 79.2 | 241912 | 2 | AC106197 | Rattus no |
| C 255 | 42 | 79.2 | 122105 | 2 | AL355998 | AL355998 Homo sapi | AL355998 | Homo sapi | 328 | 42 | 79.2 | 243648 | 2 | AC128576 | Rattus no |
| C 256 | 42 | 79.2 | 122912 | 2 | AC151251 | AC151251 Bos tauru | AC151251 | Bos tauru | 329 | 42 | 79.2 | 246095 | 3 | AE003802 | Drosophill |
| C 257 | 42 | 79.2 | 124441 | 2 | AC027098 | AC027098 Homo sapi | AC027098 | Homo sapi | 330 | 42 | 79.2 | 248109 | 2 | AC127914 | Rattus no |
| C 258 | 42 | 79.2 | 132077 | 9 | AC005589 | AC005589 Homo sapi | AC005589 | Homo sapi | 331 | 42 | 79.2 | 249245 | 2 | AC110695 | Rattus no |
| C 259 | 42 | 79.2 | 135978 | 10 | AL645582 | AL645582 Mouse DNA | AL645582 | Mouse DNA | c 332 | 42 | 79.2 | 249565 | 2 | AC097125 | Rattus no |
| C 260 | 42 | 79.2 | 140096 | 9 | AC092617 | AC092617 Homo sapi | AC092617 | Homo sapi | 333 | 42 | 79.2 | 250064 | 2 | AC103494 | Rattus no |
| C 261 | 42 | 79.2 | 140626 | 9 | AC008127 | AC008127 Homo sapi | AC008127 | Homo sapi | c 334 | 42 | 79.2 | 251769 | 2 | AC117913 | Rattus no |
| C 262 | 42 | 79.2 | 148232 | 2 | AC121068 | AC121068 Pan trogl | AC121068 | Pan trogl | c 335 | 42 | 79.2 | 251947 | 2 | AC138849 | Homo sapi |
| C 263 | 42 | 79.2 | 151262 | 9 | AC093824 | AC093824 Homo sapi | AC093824 | Homo sapi | 336 | 42 | 79.2 | 252968 | 2 | AC112300 | Rattus no |
| C 264 | 42 | 79.2 | 151498 | 9 | AL357835 | AL357835 Human DNA | AL357835 | Human DNA | c 337 | 42 | 79.2 | 262198 | 2 | AC106703 | Rattus no |
| C 265 | 42 | 79.2 | 153863 | 2 | AC025361 | AC025361 Homo sapi | AC025361 | Homo sapi | 338 | 42 | 79.2 | 268850 | 2 | AC110949 | Rattus no |
| C 266 | 42 | 79.2 | 154616 | 9 | AC004846 | AC004846 Homo sapi | AC004846 | Homo sapi | 339 | 42 | 79.2 | 276008 | 2 | AC112310 | Rattus no |
| C 267 | 42 | 79.2 | 157734 | 8 | OSJN000058 | AL606624 Oryza sat | AL606624 | Oryza sat | 340 | 42 | 79.2 | 287344 | 3 | AE003816 | Drosophill |
| C 268 | 42 | 79.2 | 160438 | 2 | AC024971 | AC024971 Homo sapi | AC024971 | Homo sapi | c 341 | 42 | 79.2 | 289103 | 2 | AC136288 | Rattus no |
| C 269 | 42 | 79.2 | 160869 | 2 | AC026378 | AC026378 Mus muscu | AC026378 | Mus muscu | 342 | 42 | 79.2 | 292088 | 1 | AE016986 | Shigella |
| C 270 | 42 | 79.2 | 161500 | 9 | AC103778 | AC103778 Homo sapi | AC103778 | Homo sapi | c 343 | 42 | 79.2 | 309677 | 2 | AC128863 | Rattus no |
| C 271 | 42 | 79.2 | 161540 | 2 | AC024229 | AC024229 Homo sapi | AC024229 | Homo sapi | 344 | 42 | 79.2 | 313518 | 1 | AE016856 | Pseudomon |
| C 272 | 42 | 79.2 | 162361 | 2 | AC023779 | AC023779 Homo sapi | AC023779 | Homo sapi | 345 | 42 | 79.2 | 335598 | 2 | AC133302 | Rattus no |
| C 273 | 42 | 79.2 | 162493 | 2 | AC138967 | AC138967 Homo sapi | AC138967 | Homo sapi | c 346 | 42 | 79.2 | 340750 | 1 | BX294135 | Drosophill |
| C 274 | 42 | 79.2 | 164813 | 9 | AC025154 | AC025154 Homo sapi | AC025154 | Homo sapi | 347 | 42 | 79.2 | 341944 | 2 | AC079158 | Homo sapi |
| C 275 | 42 | 79.2 | 165350 | 2 | AC134958 | AC134958 Rattus no | AC134958 | Rattus no | 348 | 41.5 | 78.3 | 231285 | 2 | AC097867 | Rattus no |
| C 276 | 42 | 79.2 | 165848 | 2 | AC138813 | AC138813 Homo sapi | AC138813 | Homo sapi | c 349 | 41 | 77.4 | 339 | 6 | CQ744270 | Sequence |
| C 277 | 42 | 79.2 | 166347 | 9 | AC098810 | AC098810 Papio anu | AC098810 | Papio anu | c 350 | 41 | 77.4 | 342 | 1 | XM342 | X88371 X.maltophi |
| C 278 | 42 | 79.2 | 167408 | 2 | AC025526 | AC025526 Homo sapi | AC025526 | Homo sapi | c 351 | 41 | 77.4 | 380 | 8 | AF358778 | Oryza sat |
| C 279 | 42 | 79.2 | 168683 | 2 | AC102348 | AC102348 Mus muscu | AC102348 | Mus muscu | c 352 | 41 | 77.4 | 532 | 3 | AF526232 | Argopecte |
| C 280 | 42 | 79.2 | 172617 | 2 | AC138816 | AC138816 Homo sapi | AC138816 | Homo sapi | 353 | 41 | 77.4 | 544 | 6 | CQ775970 | Sequence |
| C 281 | 42 | 79.2 | 173607 | 9 | AC139493 | AC139493 Homo sapi | AC139493 | Homo sapi | 354 | 41 | 77.4 | 544 | 6 | CQ790567 | Sequence |
| C 282 | 42 | 79.2 | 173856 | 8 | AP003203 | AP003203 Oryza sat | AP003203 | Oryza sat | c 355 | 41 | 77.4 | 742 | 8 | AF466103 | Theobroma |
| C 283 | 42 | 79.2 | 175222 | 2 | AC130641 | AC130641 Rattus no | AC130641 | Rattus no | 356 | 41 | 77.4 | 816 | 1 | AE003685 | Bacillus |
| C 284 | 42 | 79.2 | 175272 | 2 | AC140809 | AC140809 Homo sapi | AC140809 | Homo sapi | 357 | 41 | 77.4 | 816 | 6 | E50428 | ES0428 Process for |
| C 285 | 42 | 79.2 | 175357 | 9 | AC138956 | AC138956 Homo sapi | AC138956 | Homo sapi | c 358 | 41 | 77.4 | 955 | 6 | AX065567 | Sequence |
| C 286 | 42 | 79.2 | 176199 | 9 | AC093307 | AC093307 Homo sapi | AC093307 | Homo sapi | c 359 | 41 | 77.4 | 1058 | 4 | ECIL12P40 | Y11129 Equus cabal |
| C 287 | 42 | 79.2 | 176421 | 9 | AC095888 | AC095888 Homo sapi | AC095888 | Homo sapi | c 360 | 41 | 77.4 | 1069 | 8 | SP1ASCPEP | L20864 Spinacia ol |
| C 288 | 42 | 79.2 | 176740 | 2 | AC102471 | AC102471 Mus muscu | AC102471 | Mus muscu | 361 | 41 | 77.4 | 1077 | 1 | AB127053 | AB127053 Bacillus |
| C 289 | 42 | 79.2 | 177816 | 2 | AC017643 | AC017643 Drosophi | AC017643 | Drosophi | 362 | 41 | 77.4 | 1083 | 8 | SP1CAP | D85864 Spinacia ol |
| C 290 | 42 | 79.2 | 177819 | 9 | AC100771 | AC100771 Homo sapi | AC100771 | Homo sapi | c 363 | 41 | 77.4 | 1143 | 6 | AX653423 | AX653423 Sequence |
| C 291 | 42 | 79.2 | 178051 | 2 | AC141333 | AC141333 Rattus no | AC141333 | Rattus no | c 364 | 41 | 77.4 | 1312 | 5 | BC064281 | BC064281 Danio rer |
| C 292 | 42 | 79.2 | 182295 | 2 | AP001501 | AP001501 Homo sapi | AP001501 | Homo sapi | 365 | 41 | 77.4 | 1329 | 1 | AJ842019 | AJ842019 Streptoco |
| C 293 | 42 | 79.2 | 183161 | 3 | AC007851 | AC007851 Drosophi | AC007851 | Drosophi | 366 | 41 | 77.4 | 1329 | 1 | AJ842020 | AJ842020 Streptoco |
| C 294 | 42 | 79.2 | 183641 | 2 | AC118666 | AC118666 Rattus no | AC118666 | Rattus no | 367 | 41 | 77.4 | 1329 | 1 | AJ842021 | AJ842021 Stre |

| | | | | | | | | | | | | | |
|-------|----|------|------|----|-----------|--------------------|-------|----|------|--------|----|--------------------|---------------------|
| c 370 | 41 | 77.4 | 1461 | 6 | BD016516 | BD016516 Genes and | c 443 | 41 | 77.4 | 4694 | 9 | HSM807133 | BSX40976 Homo sapi |
| 371 | 41 | 77.4 | 1491 | 8 | BT003379 | BT003379 Arabidops | 444 | 41 | 77.4 | 4750 | 6 | CQ873929 | CQ873929 Sequence |
| 372 | 41 | 77.4 | 1534 | 8 | AB031546 | AB031546 Chlamydom | 445 | 41 | 77.4 | 4750 | 6 | AF220263 | AF220263 Homo sapi |
| c 373 | 41 | 77.4 | 1626 | 12 | AF401989 | AF401989 Synthetic | c 446 | 41 | 77.4 | 4965 | 6 | CQ789052 | CQ789052 Sequence |
| 374 | 41 | 77.4 | 1633 | 8 | AF001394 | AF001394 Arabidops | c 447 | 41 | 77.4 | 4965 | 6 | AR218911 | AR218911 Sequence |
| 375 | 41 | 77.4 | 1652 | 8 | AY087345 | AY087345 Arabidops | c 448 | 41 | 77.4 | 4965 | 6 | BD003823 | BD003823 Polynucle |
| 376 | 41 | 77.4 | 1678 | 6 | AK007241 | AK007241 Sequence | c 449 | 41 | 77.4 | 5095 | 6 | I18513 | I18513 Sequence 3 |
| 377 | 41 | 77.4 | 1704 | 8 | AF428420 | AF428420 Arabidops | c 450 | 41 | 77.4 | 5095 | 6 | AR204074 | AR204074 Sequence |
| 378 | 41 | 77.4 | 1705 | 8 | ATAJ4161 | ATAJ4161 Arabidops | c 451 | 41 | 77.4 | 5095 | 6 | AR482544 | AR482544 Sequence |
| c 379 | 41 | 77.4 | 1736 | 8 | AK069299 | AK069299 Oryza sat | c 452 | 41 | 77.4 | 5095 | 6 | BD094050 | BD094050 Shear str |
| 380 | 41 | 77.4 | 1743 | 8 | BT000442 | BT000442 Arabidops | c 453 | 41 | 77.4 | 5175 | 6 | CQ882057 | CQ882057 Sequence |
| c 381 | 41 | 77.4 | 1815 | 10 | AF170709 | AF170709 Mus muscu | c 454 | 41 | 77.4 | 5356 | 9 | BSX48281 Homo sapi | BSX48281 Homo sapi |
| c 382 | 41 | 77.4 | 1929 | 10 | AF169191 | AF169191 Mus muscu | c 455 | 41 | 77.4 | 5382 | 6 | BD141296 | BD141296 Method of |
| c 383 | 41 | 77.4 | 1962 | 10 | AF169192 | AF169192 Mus muscu | c 456 | 41 | 77.4 | 5591 | 1 | AY032955 | AY032955 Methyloco |
| c 384 | 41 | 77.4 | 2000 | 6 | AK656740 | AK656740 Sequence | c 457 | 41 | 77.4 | 5851 | 6 | BD171148 | BD171148 Novel gen |
| c 385 | 41 | 77.4 | 2258 | 9 | AK054685 | AK054685 Homo sapi | c 458 | 41 | 77.4 | 5851 | 6 | BD183308 | BD183308 Novel gen |
| 386 | 41 | 77.4 | 2338 | 5 | BC066589 | BC066589 Danio rer | c 459 | 41 | 77.4 | 5851 | 9 | AB051435 | AB051435 Homo sapi |
| 387 | 41 | 77.4 | 2463 | 1 | AB119810 | AB119810 Streptoco | c 460 | 41 | 77.4 | 10029 | 1 | AE008555 | AE008555 Streptoco |
| 388 | 41 | 77.4 | 2463 | 1 | AB119812 | AB119812 Streptoco | c 461 | 41 | 77.4 | 10595 | 1 | AB031319 | AB031319 Nocardioid |
| 389 | 41 | 77.4 | 2463 | 1 | AB119814 | AB119814 Streptoco | c 462 | 41 | 77.4 | 10826 | 1 | AE005947 | AE005947 Caulobact |
| 390 | 41 | 77.4 | 2463 | 1 | AB119824 | AB119824 Streptoco | c 463 | 41 | 77.4 | 11216 | 1 | AE007498 | AE007498 Streptoco |
| 391 | 41 | 77.4 | 2463 | 6 | AK480654 | AK480654 Sequence | c 464 | 41 | 77.4 | 11216 | 1 | AY165002 | AY165002 Pigmentip |
| 392 | 41 | 77.4 | 2466 | 1 | AB119793 | AB119793 Streptoco | c 465 | 41 | 77.4 | 19824 | 1 | RHMOTB | L49337 Sinothiob |
| 393 | 41 | 77.4 | 2466 | 1 | AB119794 | AB119794 Streptoco | c 466 | 41 | 77.4 | 29112 | 6 | CQ363821 | CQ363821 Sequence |
| 394 | 41 | 77.4 | 2466 | 1 | AB119795 | AB119795 Streptoco | c 467 | 41 | 77.4 | 29180 | 2 | AC019819 | AC019819 Drosophil |
| 395 | 41 | 77.4 | 2466 | 1 | AB119796 | AB119796 Streptoco | c 468 | 41 | 77.4 | 37719 | 10 | BSX294108 | BSX294108 Mouse DNA |
| 396 | 41 | 77.4 | 2466 | 1 | AB119797 | AB119797 Streptoco | c 469 | 41 | 77.4 | 42805 | 9 | AC004221 | AC004221 Homo sapi |
| 397 | 41 | 77.4 | 2466 | 1 | AB119798 | AB119798 Streptoco | c 470 | 41 | 77.4 | 44685 | 9 | HSB107C2 | AL008724 Human DNA |
| 398 | 41 | 77.4 | 2466 | 1 | AB119799 | AB119799 Streptoco | c 471 | 41 | 77.4 | 48600 | 9 | AY324609 | AY324609 Homo sapi |
| 399 | 41 | 77.4 | 2466 | 1 | AB119800 | AB119800 Streptoco | c 472 | 41 | 77.4 | 49736 | 1 | AF319998 | AF319998 Stigmatel |
| 400 | 41 | 77.4 | 2466 | 1 | AB119801 | AB119801 Streptoco | c 473 | 41 | 77.4 | 52777 | 9 | AP000268 | AP000268 Homo sapi |
| 401 | 41 | 77.4 | 2466 | 1 | AB119802 | AB119802 Streptoco | c 474 | 41 | 77.4 | 52993 | 2 | AC101518 | AC101518 Mus muscu |
| 402 | 41 | 77.4 | 2466 | 1 | AB119803 | AB119803 Streptoco | c 475 | 41 | 77.4 | 60733 | 2 | AC131946 | AC131946 Homo sapi |
| 403 | 41 | 77.4 | 2466 | 1 | AB119804 | AB119804 Streptoco | c 476 | 41 | 77.4 | 64347 | 2 | AC151337 | AC151337 Xenopus t |
| 404 | 41 | 77.4 | 2466 | 1 | AB119805 | AB119805 Streptoco | c 477 | 41 | 77.4 | 68662 | 9 | AL133293 | AL133293 Human DNA |
| 405 | 41 | 77.4 | 2466 | 1 | AB119806 | AB119806 Streptoco | c 478 | 41 | 77.4 | 74165 | 8 | BSX97678 | BSX97678 Neurospor |
| 406 | 41 | 77.4 | 2466 | 1 | AB119807 | AB119807 Streptoco | c 479 | 41 | 77.4 | 77207 | 2 | AC074067 | AC074067 Homo sapi |
| 407 | 41 | 77.4 | 2466 | 1 | AB119808 | AB119808 Streptoco | c 480 | 41 | 77.4 | 87840 | 2 | AC149900 | AC149900 Xenopus t |
| 408 | 41 | 77.4 | 2466 | 1 | AB119809 | AB119809 Streptoco | c 481 | 41 | 77.4 | 88892 | 9 | AC096758 | AC096758 Homo sapi |
| 409 | 41 | 77.4 | 2466 | 1 | AB119811 | AB119811 Streptoco | c 482 | 41 | 77.4 | 89003 | 1 | BSZ75208 | Z75208 B.subtilis |
| 410 | 41 | 77.4 | 2466 | 1 | AB119813 | AB119813 Streptoco | c 483 | 41 | 77.4 | 95993 | 8 | ATF2A19 | AL132962 Arabidops |
| 411 | 41 | 77.4 | 2466 | 1 | AB119815 | AB119815 Streptoco | c 484 | 41 | 77.4 | 100000 | 9 | AP000033 | AP000033 Homo sapi |
| 412 | 41 | 77.4 | 2466 | 1 | AB119816 | AB119816 Streptoco | c 485 | 41 | 77.4 | 100000 | 9 | AP000102 | AP000102 Homo sapi |
| 413 | 41 | 77.4 | 2466 | 1 | AB119817 | AB119817 Streptoco | c 486 | 41 | 77.4 | 100000 | 9 | AP000178 | AP000178 Homo sapi |
| 414 | 41 | 77.4 | 2466 | 1 | AB119818 | AB119818 Streptoco | c 487 | 41 | 77.4 | 103804 | 9 | AP003472 | AP003472 Homo sapi |
| 415 | 41 | 77.4 | 2466 | 1 | AB119819 | AB119819 Streptoco | c 488 | 41 | 77.4 | 103973 | 8 | AP004028 | AP004028 Oryza sat |
| 416 | 41 | 77.4 | 2466 | 1 | AB119820 | AB119820 Streptoco | c 489 | 41 | 77.4 | 108930 | 9 | AL513122 | AL513122 Human DNA |
| 417 | 41 | 77.4 | 2466 | 1 | AB119821 | AB119821 Streptoco | c 490 | 41 | 77.4 | 109022 | 8 | AP004926 | AP004926 Lotus cor |
| 418 | 41 | 77.4 | 2466 | 1 | AB119822 | AB119822 Streptoco | c 491 | 41 | 77.4 | 110000 | 1 | AE017282 | Continuation (2 of |
| 419 | 41 | 77.4 | 2466 | 1 | AB119823 | AB119823 Streptoco | c 492 | 41 | 77.4 | 110000 | 2 | AE017283 | Continuation (9 of |
| 420 | 41 | 77.4 | 2466 | 1 | AB119825 | AB119825 Streptoco | c 493 | 41 | 77.4 | 110000 | 2 | AE017283 | Continuation (3 of |
| 421 | 41 | 77.4 | 2466 | 1 | AB119826 | AB119826 Streptoco | c 494 | 41 | 77.4 | 110000 | 2 | BSZ5276 | Continuation (9 of |
| 422 | 41 | 77.4 | 2466 | 1 | AB119827 | AB119827 Streptoco | c 495 | 41 | 77.4 | 110000 | 2 | BSZ5276 | Continuation (28 o |
| 423 | 41 | 77.4 | 2466 | 1 | AB119828 | AB119828 Streptoco | c 496 | 41 | 77.4 | 110000 | 8 | CR382132 | Continuation (28 o |
| 424 | 41 | 77.4 | 2466 | 1 | AB119829 | AB119829 Streptoco | c 497 | 41 | 77.4 | 114600 | 9 | HS477H23 | Continuation (27 |
| 425 | 41 | 77.4 | 2466 | 1 | AB119830 | AB119830 Streptoco | c 498 | 41 | 77.4 | 116704 | 10 | AL591921 | AL591921 Mouse DNA |
| 426 | 41 | 77.4 | 2466 | 1 | AB119831 | AB119831 Streptoco | c 499 | 41 | 77.4 | 128618 | 9 | AC011485 | AC011485 Homo sapi |
| 427 | 41 | 77.4 | 2466 | 1 | AB119832 | AB119832 Streptoco | c 500 | 41 | 77.4 | 129921 | 8 | AC146568 | AC146568 Medicago |
| 428 | 41 | 77.4 | 2466 | 1 | AF101781 | AF101781 Streptoco | c 501 | 41 | 77.4 | 132049 | 9 | AL954207 | AL954207 Pan trogl |
| 429 | 41 | 77.4 | 2466 | 6 | BD223944 | BD223944 Nucleic a | c 502 | 41 | 77.4 | 132981 | 8 | AC147802 | AC147802 Oryza sat |
| 430 | 41 | 77.4 | 2475 | 6 | AX571171 | AX571171 Sequence | c 503 | 41 | 77.4 | 135527 | 2 | CR391995 | CR391995 Danio rer |
| 431 | 41 | 77.4 | 2511 | 1 | SPAJ7291 | AJ002291 Streptoco | c 504 | 41 | 77.4 | 137952 | 2 | SPNEU1909 | AL449931 Streptoco |
| c 432 | 41 | 77.4 | 2550 | 6 | AK658183 | AK658183 Sequence | c 505 | 41 | 77.4 | 139111 | 9 | AC008768 | AC008768 Homo sapi |
| c 433 | 41 | 77.4 | 2550 | 9 | HUMLDLR18 | L00352 Human low d | c 506 | 41 | 77.4 | 142294 | 2 | AP002352 | AP002352 Homo sapi |
| 434 | 41 | 77.4 | 3057 | 6 | BD165200 | BD165200 Novel pol | c 507 | 41 | 77.4 | 145014 | 8 | AP004048 | AP004048 Oryza sat |
| 435 | 41 | 77.4 | 3057 | 6 | AX123083 | AX123083 Sequence | c 508 | 41 | 77.4 | 148567 | 10 | AC128738 | AC128738 Mus muscu |
| c 436 | 41 | 77.4 | 3070 | 10 | BC013893 | BC013893 Mus muscu | c 509 | 41 | 77.4 | 148811 | 9 | AC073857 | AC073857 Homo sapi |
| 437 | 41 | 77.4 | 3187 | 6 | AX813957 | AX813957 Sequence | c 510 | 41 | 77.4 | 150900 | 9 | AC068075 | AC068075 Homo sapi |
| c 438 | 41 | 77.4 | 3331 | 10 | MMU70674 | U70674 Mus musculu | c 511 | 41 | 77.4 | 152426 | 9 | AC145724 | AC145724 Pan trogl |
| c 439 | 41 | 77.4 | 3495 | 10 | BC033459 | BC033459 Mus muscu | c 512 | 41 | 77.4 | 153753 | 9 | AL954206 | AL954206 Pan trogl |
| c 440 | 41 | 77.4 | 3522 | 9 | BC014514 | BC014514 Homo sapi | c 513 | 41 | 77.4 | 156539 | 9 | AC091736 | AC091736 Homo sapi |
| 441 | 41 | 77.4 | 3549 | 6 | AX411489 | AX411489 Sequence | c 514 | 41 | 77.4 | 156603 | 2 | BSX27116 | BSX27116 Danio rer |
| c 442 | 41 | 77.4 | 4131 | 5 | AY070261 | AY070261 Danio rer | c 515 | 41 | 77.4 | 158134 | 5 | BSX548006 | BSX548006 Zebrafish |

| | | | | | | | | | | | | | |
|-------|----|------|--------|----|-------------|---------------------|-------|----|------|--------|----|--------------|---------------------|
| c 662 | 40 | 75.5 | 2843 | 8 | MESBRNNA | X77012 M. esculenta | 735 | 40 | 75.5 | 110000 | 1 | AE017180_34 | Continuation (35 o |
| c 663 | 40 | 75.5 | 2927 | 5 | BC077822 | BC077822 Xenopus l | 736 | 40 | 75.5 | 110000 | 1 | AE017283_21 | Continuation (22 o |
| c 664 | 40 | 75.5 | 3248 | 6 | BD156510 | BD156510 Primer fo | c 737 | 40 | 75.5 | 110000 | 2 | AC119568_3 | Continuation (4 of |
| c 665 | 40 | 75.5 | 3248 | 6 | CQ721025 | CQ721025 Sequence | c 738 | 40 | 75.5 | 110000 | 2 | AC138332_3 | Continuation (4 of |
| c 666 | 40 | 75.5 | 3248 | 6 | AX8077148 | AX8077148 Sequence | c 739 | 40 | 75.5 | 110000 | 2 | LMF1CHR31_00 | AL499621 Leishmani |
| c 667 | 40 | 75.5 | 3248 | 6 | AK001629 | AK001629 Homo sapi | c 740 | 40 | 75.5 | 110000 | 8 | CR382125_17 | Continuation (18 o |
| c 668 | 40 | 75.5 | 3296 | 6 | CO411989 | CO411989 Sequence | c 741 | 40 | 75.5 | 110000 | 8 | CR382129_12 | Continuation (13 o |
| c 669 | 40 | 75.5 | 3344 | 3 | DMU18307 | U18307 Drosophila | c 742 | 40 | 75.5 | 110000 | 8 | CR382129_13 | Continuation (14 o |
| c 670 | 40 | 75.5 | 3491 | 9 | BC006085 | BC006085 Homo sapi | c 743 | 40 | 75.5 | 110000 | 8 | CR382132_35 | Continuation (36 o |
| c 671 | 40 | 75.5 | 3499 | 9 | BC011876 | BC011876 Homo sapi | c 744 | 40 | 75.5 | 110149 | 8 | AC005397_35 | AC005397 Arabidops |
| c 672 | 40 | 75.5 | 3500 | 9 | BC000786 | BC000786 Homo sapi | c 745 | 40 | 75.5 | 111170 | 9 | AL354766 | AL354766 Human DNA |
| c 673 | 40 | 75.5 | 4269 | 8 | NCCPC2 | X81875 N. crassa cp | c 746 | 40 | 75.5 | 114491 | 9 | AC010331 | AC010331 Homo sapi |
| c 674 | 40 | 75.5 | 4540 | 6 | AX472454 | AX472454 Sequence | c 747 | 40 | 75.5 | 116351 | 8 | AP005574 | AP005574 Oryza sat |
| c 675 | 40 | 75.5 | 4559 | 1 | TFEN1FHDK | M15238 T. ferrooxid | c 748 | 40 | 75.5 | 117333 | 8 | AC113394 | AC113394 Homo sapi |
| c 676 | 40 | 75.5 | 5057 | 6 | CO611588 | CO611588 Sequence | c 749 | 40 | 75.5 | 121337 | 8 | OSJN00104 | AL606653 Oryza sat |
| c 677 | 40 | 75.5 | 5353 | 1 | AF204275 | AF204275 Desulfito | c 750 | 40 | 75.5 | 121852 | 9 | AP003965 | AP003965 Homo sapi |
| c 678 | 40 | 75.5 | 6070 | 5 | AB066588 | AB066588 Xenopus l | c 751 | 40 | 75.5 | 127917 | 6 | CQ861449 | CQ861449 Sequence |
| c 679 | 40 | 75.5 | 6827 | 6 | CQ788969 | CQ788969 Sequence | c 752 | 40 | 75.5 | 127917 | 9 | HS25747 | AL008729 Human DNA |
| c 680 | 40 | 75.5 | 6827 | 6 | AR2118828 | AR2118828 Sequence | c 753 | 40 | 75.5 | 128748 | 10 | AL671732 | AL671732 Mouse DNA |
| c 681 | 40 | 75.5 | 6827 | 6 | BD003740 | BD003740 Polynucle | c 754 | 40 | 75.5 | 130328 | 2 | AC079622 | AC079622 Homo sapi |
| c 682 | 40 | 75.5 | 7437 | 14 | RHDVGNs | Z49271 Rabbit hemo | c 755 | 40 | 75.5 | 132644 | 9 | AC104801 | AC104801 Homo sapi |
| c 683 | 40 | 75.5 | 7655 | 8 | UM040753 | U40753 Ustilago ma | c 756 | 40 | 75.5 | 136625 | 2 | AC120597 | AC120597 Homo sapi |
| c 684 | 40 | 75.5 | 8600 | 1 | AY129009 | AY129009 Streptomy | c 757 | 40 | 75.5 | 139418 | 8 | OSJN00149 | AL6663017 Oryza sat |
| c 685 | 40 | 75.5 | 9612 | 1 | AE012312 | AE012312 Xanthomon | c 758 | 40 | 75.5 | 141313 | 9 | AC004943 | AC004943 Homo sapi |
| c 686 | 40 | 75.5 | 10170 | 1 | AE008122 | AE008122 Agrobacte | c 759 | 40 | 75.5 | 141912 | 6 | AX646791 | AX646791 Sequence |
| c 687 | 40 | 75.5 | 10486 | 1 | AE008400 | AE008400 Streptoco | c 760 | 40 | 75.5 | 143411 | 8 | AP004346 | AP004346 Oryza sat |
| c 688 | 40 | 75.5 | 10542 | 1 | AE010881 | AE010881 Methanosa | c 761 | 40 | 75.5 | 144092 | 5 | AC092081 | AC092081 Gallus ga |
| c 689 | 40 | 75.5 | 10886 | 1 | AE011955 | AE011955 Xanthomon | c 762 | 40 | 75.5 | 144233 | 8 | AP003240 | AP003240 Oryza sat |
| c 690 | 40 | 75.5 | 11116 | 1 | AE012408 | AE012408 Xanthomon | c 763 | 40 | 75.5 | 144252 | 8 | AP005399 | AP005399 Oryza sat |
| c 691 | 40 | 75.5 | 11249 | 1 | AE006095 | AE006095 Pasteurel | c 764 | 40 | 75.5 | 146346 | 2 | AC111120 | AC111120 Mus muscu |
| c 692 | 40 | 75.5 | 11348 | 1 | AE007333 | AE007333 Streptoco | c 765 | 40 | 75.5 | 146408 | 8 | AC130610 | AC130610 Oryza sat |
| c 693 | 40 | 75.5 | 11428 | 1 | AE005465 | AE005465 Escherich | c 766 | 40 | 75.5 | 146570 | 3 | AC117076 | AC117076 Dictyoste |
| c 694 | 40 | 75.5 | 11936 | 1 | AE009156 | AE009156 Agrobacte | c 767 | 40 | 75.5 | 146898 | 8 | AP005258 | AP005258 Oryza sat |
| c 695 | 40 | 75.5 | 12008 | 1 | AE009784 | AE009784 Pyrobacul | c 768 | 40 | 75.5 | 147201 | 2 | AC053459 | AC053459 Homo sapi |
| c 696 | 40 | 75.5 | 12575 | 1 | AE015257 | AE015257 Shigella | c 769 | 40 | 75.5 | 148046 | 9 | AC034226 | AC034226 Homo sapi |
| c 697 | 40 | 75.5 | 14000 | 10 | AY029613 | AY029613 Mus muscu | c 770 | 40 | 75.5 | 148498 | 8 | AC125780 | AC125780 Oryza sat |
| c 698 | 40 | 75.5 | 14462 | 10 | AF348402 | AF348402 Mus muscu | c 771 | 40 | 75.5 | 148862 | 2 | AC116881 | AC116881 Mus muscu |
| c 699 | 40 | 75.5 | 14668 | 1 | D90864 | D90864 E.coli geno | c 772 | 40 | 75.5 | 149697 | 9 | AC091162 | AC091162 Homo sapi |
| c 700 | 40 | 75.5 | 15182 | 2 | AC011219 | AC011219 Drosophil | c 773 | 40 | 75.5 | 150494 | 10 | AC091617 | AC091617 Rattus no |
| c 701 | 40 | 75.5 | 16748 | 1 | D90865 | D90865 E.coli geno | c 774 | 40 | 75.5 | 150803 | 2 | AC073490 | AC073490 Homo sapi |
| c 702 | 40 | 75.5 | 20167 | 1 | AE008807 | AE008807 Salmonell | c 775 | 40 | 75.5 | 151227 | 2 | AC011267 | AC011267 Homo sapi |
| c 703 | 40 | 75.5 | 26309 | 6 | CQ363747 | CQ363747 Sequence | c 776 | 40 | 75.5 | 151284 | 9 | CR626880 | CR626880 Human DNA |
| c 704 | 40 | 75.5 | 31595 | 9 | AC142399 | AC142399 Homo sapi | c 777 | 40 | 75.5 | 151600 | 2 | AC010278 | AC010278 Homo sapi |
| c 705 | 40 | 75.5 | 31705 | 9 | HS4A00626 | AJ400626 Homo sapi | c 778 | 40 | 75.5 | 151894 | 2 | AL389926 | AL389926 Homo sapi |
| c 706 | 40 | 75.5 | 36628 | 9 | AC145059 | AC145059 Homo sapi | c 779 | 40 | 75.5 | 152048 | 2 | AC115343 | AC115343 Rattus no |
| c 707 | 40 | 75.5 | 37881 | 1 | AJ586889 | AJ586889 Escherich | c 780 | 40 | 75.5 | 152232 | 9 | AC008445 | AC008445 Homo sapi |
| c 708 | 40 | 75.5 | 38334 | 2 | AC142530 | AC142530 Homo sapi | c 781 | 40 | 75.5 | 152232 | 2 | AC126438 | AC126438 Mus muscu |
| c 709 | 40 | 75.5 | 38514 | 3 | CRC27A7 | Z81041 Caenorhabdi | c 782 | 40 | 75.5 | 152802 | 10 | AC140377 | AC140377 Mus muscu |
| c 710 | 40 | 75.5 | 45045 | 9 | AL359954 | AL359954 Human DNA | c 783 | 40 | 75.5 | 153227 | 2 | AC068899 | AC068899 Mus muscu |
| c 711 | 40 | 75.5 | 48558 | 9 | AC110001 | AC110001 Homo sapi | c 784 | 40 | 75.5 | 153483 | 2 | AL513191 | AL513191 Human DNA |
| c 712 | 40 | 75.5 | 50149 | 2 | AC132494 | AC132494 Oryza sat | c 785 | 40 | 75.5 | 153830 | 9 | AL513191 | AL513191 Human DNA |
| c 713 | 40 | 75.5 | 62954 | 2 | AC102036 | AC102036 Mus muscu | c 786 | 40 | 75.5 | 154278 | 2 | AC025531 | AC025531 Homo sapi |
| c 714 | 40 | 75.5 | 65871 | 10 | AY016022 | AY016022 Mus muscu | c 787 | 40 | 75.5 | 155172 | 2 | AC021110 | AC021110 Homo sapi |
| c 715 | 40 | 75.5 | 68840 | 2 | AC087282 | AC087282 Homo sapi | c 788 | 40 | 75.5 | 155174 | 5 | BX649628 | BX649628 Zebrafish |
| c 716 | 40 | 75.5 | 69294 | 2 | AC100360 | AC100360 Mus muscu | c 789 | 40 | 75.5 | 157200 | 9 | AP005233 | AP005233 Homo sapi |
| c 717 | 40 | 75.5 | 71255 | 1 | RSU0928_3 | Continuation (4 of | c 790 | 40 | 75.5 | 157216 | 9 | AC087491 | AC087491 Homo sapi |
| c 718 | 40 | 75.5 | 72007 | 2 | AC103336 | AC103336 Mus muscu | c 791 | 40 | 75.5 | 157250 | 5 | AC087305 | AC087305 Homo sapi |
| c 719 | 40 | 75.5 | 74549 | 9 | HSJ890015 | AL049540 Human DNA | c 792 | 40 | 75.5 | 157502 | 5 | AC14486 | AC14486 Gasterost |
| c 720 | 40 | 75.5 | 74732 | 2 | AP006485_4 | Continuation (5 of | c 793 | 40 | 75.5 | 158608 | 9 | AC051635 | AC051635 Homo sapi |
| c 721 | 40 | 75.5 | 78491 | 2 | AC016211 | AC016211 Homo sapi | c 794 | 40 | 75.5 | 159175 | 9 | BX322234 | BX322234 Human DNA |
| c 722 | 40 | 75.5 | 79039 | 2 | CR626867 | CR626867 Homo sapi | c 795 | 40 | 75.5 | 159274 | 9 | AC112651 | AC112651 Homo sapi |
| c 723 | 40 | 75.5 | 81476 | 10 | BX004788 | BX004788 Mouse DNA | c 796 | 40 | 75.5 | 159639 | 5 | AL953875 | AL953875 Zebrafish |
| c 724 | 40 | 75.5 | 83149 | 2 | AC128511_3 | Continuation (4 of | c 797 | 40 | 75.5 | 160423 | 5 | AL953875 | AL953875 Zebrafish |
| c 725 | 40 | 75.5 | 86784 | 2 | AC138362 | AC138362 Mus muscu | c 798 | 40 | 75.5 | 160737 | 2 | AC024486 | AC024486 Homo sapi |
| c 726 | 40 | 75.5 | 87613 | 8 | AP004857 | AP004857 Oryza sat | c 799 | 40 | 75.5 | 161099 | 10 | AC132624 | AC132624 Homo sapi |
| c 727 | 40 | 75.5 | 88624 | 2 | AC020676 | AC020676 Homo sapi | c 800 | 40 | 75.5 | 161127 | 9 | AC073592 | AC073592 Homo sapi |
| c 728 | 40 | 75.5 | 89808 | 10 | AL591703 | AL591703 Mouse DNA | c 801 | 40 | 75.5 | 161278 | 3 | AC009749 | AC009749 Drosophil |
| c 729 | 40 | 75.5 | 98221 | 9 | AL161940 | AL161940 Human DNA | c 802 | 40 | 75.5 | 161815 | 9 | AC079199 | AC079199 Homo sapi |
| c 730 | 40 | 75.5 | 106093 | 9 | AC007561 | AC007561 Homo sapi | c 803 | 40 | 75.5 | 162639 | 9 | AC079142 | AC079142 Homo sapi |
| c 731 | 40 | 75.5 | 110000 | 1 | AE000516_10 | Continuation (11 o | c 804 | 40 | 75.5 | 162933 | 9 | AC108105 | AC108105 Homo sapi |
| c 732 | 40 | 75.5 | 110000 | 1 | AE000516_11 | Continuation (12 o | c 805 | 40 | 75.5 | 163800 | 10 | AC122510 | AC122510 Mus muscu |
| c 733 | 40 | 75.5 | 110000 | 1 | RSU0928_2 | Continuation (3 of | c 806 | 40 | 75.5 | 164846 | 4 | AC104482 | AC104482 Sub scro |
| c 734 | 40 | 75.5 | 110000 | 1 | U00096_24 | Continuation (25 o | c 807 | 40 | 75.5 | 164878 | 2 | AC148648 | AC148648 Dasydyp n |

| | | | | | | | | | | | | | |
|-------|----|------|--------|----|-----------|---------------------|-------|----|------|--------|----|-----------|--------------------|
| C 808 | 40 | 75.5 | 165103 | 10 | AC116596 | AC116596 Mus muscu | 881 | 40 | 75.5 | 213153 | 2 | AC129348 | AC129348 Rattus no |
| 809 | 40 | 75.5 | 165261 | 2 | AC012659 | AC012659 Homo sapi | C 882 | 40 | 75.5 | 213362 | 2 | AC146884 | AC146884 Callithri |
| C 810 | 40 | 75.5 | 166680 | 9 | AC010132 | AC010132 Homo sapi | C 883 | 40 | 75.5 | 214250 | 2 | AC103314 | AC103314 Rattus no |
| 811 | 40 | 75.5 | 167810 | 9 | AC007051 | AC007051 Homo sapi | C 884 | 40 | 75.5 | 214922 | 2 | AC150991 | AC150991 Bos tauru |
| C 812 | 40 | 75.5 | 168585 | 9 | AC040933 | AC040933 Homo sapi | C 885 | 40 | 75.5 | 215685 | 10 | AC036121 | AC036121 Mus muscu |
| C 813 | 40 | 75.5 | 169662 | 2 | AC022241 | AC022241 Homo sapi | C 886 | 40 | 75.5 | 216943 | 2 | AC134134 | AC134134 Rattus no |
| C 814 | 40 | 75.5 | 169969 | 2 | AL390727 | AL390727 Homo sapi | C 887 | 40 | 75.5 | 220285 | 10 | AC130818 | AC130818 Mus muscu |
| C 815 | 40 | 75.5 | 170227 | 9 | AC093816 | AC093816 Homo sapi | C 888 | 40 | 75.5 | 221157 | 2 | AC091540 | AC091540 Canis fam |
| C 816 | 40 | 75.5 | 170749 | 10 | AL133159 | AL133159 Mouse DNA | C 889 | 40 | 75.5 | 222860 | 2 | AC113065 | AC113065 Mus muscu |
| C 817 | 40 | 75.5 | 171260 | 2 | AC084351 | AC084351 Homo sapi | C 890 | 40 | 75.5 | 224034 | 10 | AL672049 | AL672049 Mouse DNA |
| C 818 | 40 | 75.5 | 172090 | 2 | AC051661 | AC051661 Homo sapi | C 891 | 40 | 75.5 | 224566 | 2 | AC095793 | AC095793 Rattus no |
| C 819 | 40 | 75.5 | 173277 | 2 | AC014817 | AC014817 Mus muscu | C 892 | 40 | 75.5 | 225046 | 2 | AC112674 | AC112674 Mus muscu |
| C 820 | 40 | 75.5 | 173304 | 9 | AC023818 | AC023818 Homo sapi | C 893 | 40 | 75.5 | 225274 | 2 | AC130251 | AC130251 Rattus no |
| C 821 | 40 | 75.5 | 174780 | 8 | AC135242 | AC135242 Oryza sat | C 894 | 40 | 75.5 | 228489 | 10 | AC127433 | AC127433 Mus muscu |
| C 822 | 40 | 75.5 | 174861 | 10 | AC122022 | AC122022 Mus muscu | C 895 | 40 | 75.5 | 229494 | 10 | AL627328 | AL627328 Mouse DNA |
| C 823 | 40 | 75.5 | 175022 | 2 | AC134481 | AC134481 Rattus no | C 896 | 40 | 75.5 | 230700 | 2 | AC073777 | AC073777 Mus muscu |
| C 824 | 40 | 75.5 | 175061 | 8 | AC097446 | AC097446 Oryza sat | C 897 | 40 | 75.5 | 230926 | 2 | AC114457 | AC114457 Rattus no |
| C 825 | 40 | 75.5 | 175552 | 10 | AC101691 | AC101691 Mus muscu | C 898 | 40 | 75.5 | 231959 | 2 | AC126907 | AC126907 Rattus no |
| C 826 | 40 | 75.5 | 175936 | 2 | SNBU1908 | SNBU1908 Streptoco | C 899 | 40 | 75.5 | 232049 | 10 | AC121296 | AC121296 Mus muscu |
| C 827 | 40 | 75.5 | 176178 | 2 | AC151037 | AC151037 Callithri | C 900 | 40 | 75.5 | 236442 | 2 | AC128089 | AC128089 Rattus no |
| C 828 | 40 | 75.5 | 176767 | 9 | AF196779 | AF196779 Homo sapi | C 901 | 40 | 75.5 | 236702 | 2 | AC125661 | AC125661 Rattus no |
| C 829 | 40 | 75.5 | 177403 | 2 | AC138278 | AC138278 Mus muscu | C 902 | 40 | 75.5 | 236702 | 2 | AC147047 | AC147047 Mus muscu |
| C 830 | 40 | 75.5 | 177680 | 9 | AC091589 | AC091589 Homo sapi | C 903 | 40 | 75.5 | 241795 | 2 | AC123410 | AC123410 Rattus no |
| C 831 | 40 | 75.5 | 178049 | 5 | EX571886 | EX571886 Zebrafish | C 904 | 40 | 75.5 | 242885 | 2 | AC097836 | AC097836 Rattus no |
| C 832 | 40 | 75.5 | 178120 | 2 | AC135870 | AC135870 Rattus no | C 905 | 40 | 75.5 | 243996 | 2 | AC103098 | AC103098 Rattus no |
| C 833 | 40 | 75.5 | 178444 | 2 | AC127008 | AC127008 Rattus no | C 906 | 40 | 75.5 | 244135 | 2 | AC117143 | AC117143 Rattus no |
| C 834 | 40 | 75.5 | 179327 | 9 | AC149133 | AC149133 Pan trogl | C 907 | 40 | 75.5 | 244291 | 2 | AC107416 | AC107416 Rattus no |
| C 835 | 40 | 75.5 | 179539 | 2 | AC016369 | AC016369 Homo sapi | C 908 | 40 | 75.5 | 244696 | 2 | AC103554 | AC103554 Rattus no |
| C 836 | 40 | 75.5 | 180736 | 2 | AC023925 | AC023925 Homo sapi | C 909 | 40 | 75.5 | 245139 | 2 | AC126156 | AC126156 Rattus no |
| C 837 | 40 | 75.5 | 180748 | 2 | AC118958 | AC118958 Rattus no | C 910 | 40 | 75.5 | 245880 | 2 | AC106245 | AC106245 Rattus no |
| C 838 | 40 | 75.5 | 183936 | 10 | AC123921 | AC123921 Mus muscu | C 911 | 40 | 75.5 | 245993 | 2 | AC130970 | AC130970 Rattus no |
| C 839 | 40 | 75.5 | 184815 | 2 | AC025685 | AC025685 Homo sapi | C 912 | 40 | 75.5 | 246387 | 2 | AC119756 | AC119756 Rattus no |
| C 840 | 40 | 75.5 | 184989 | 9 | AC007919 | AC007919 Homo sapi | C 913 | 40 | 75.5 | 248528 | 2 | AC096420 | AC096420 Rattus no |
| C 841 | 40 | 75.5 | 185276 | 2 | AC136050 | AC136050 Rattus no | C 914 | 40 | 75.5 | 248675 | 10 | AC123072 | AC123072 Mus muscu |
| C 842 | 40 | 75.5 | 185517 | 10 | AC140231 | AC140231 Mus muscu | C 915 | 40 | 75.5 | 248951 | 2 | AC106428 | AC106428 Rattus no |
| C 843 | 40 | 75.5 | 185768 | 10 | AC102173 | AC102173 Mus muscu | C 916 | 40 | 75.5 | 249235 | 2 | AC094741 | AC094741 Rattus no |
| C 844 | 40 | 75.5 | 186246 | 9 | AL138749 | AL138749 Human DNA | C 917 | 40 | 75.5 | 252394 | 2 | AC096112 | AC096112 Rattus no |
| C 845 | 40 | 75.5 | 186325 | 8 | OSJN00188 | OSJN00188 Oryza sat | C 918 | 40 | 75.5 | 252904 | 2 | AC094307 | AC094307 Rattus no |
| C 846 | 40 | 75.5 | 186486 | 10 | AC132459 | AC132459 Mus muscu | C 919 | 40 | 75.5 | 253556 | 2 | AC112832 | AC112832 Rattus no |
| C 847 | 40 | 75.5 | 186608 | 10 | AL844178 | AL844178 Mouse DNA | C 920 | 40 | 75.5 | 253895 | 2 | AL772142 | AL772142 Mus muscu |
| C 848 | 40 | 75.5 | 186758 | 2 | AC073678 | AC073678 Mus muscu | C 921 | 40 | 75.5 | 254420 | 2 | AC107545 | AC107545 Rattus no |
| C 849 | 40 | 75.5 | 187017 | 2 | AC010101 | AC010101 Homo sapi | C 922 | 40 | 75.5 | 255349 | 2 | AC128233 | AC128233 Rattus no |
| C 850 | 40 | 75.5 | 187332 | 2 | EX270664 | EX270664 Danio rer | C 923 | 40 | 75.5 | 255773 | 2 | AC127416 | AC127416 Mus muscu |
| C 851 | 40 | 75.5 | 187415 | 10 | AC133896 | AC133896 Mus muscu | C 924 | 40 | 75.5 | 256050 | 1 | AL627274 | AL627274 Salmonell |
| C 852 | 40 | 75.5 | 187557 | 2 | AC069032 | AC069032 Homo sapi | C 925 | 40 | 75.5 | 261821 | 2 | AC140500 | AC140500 Mus muscu |
| C 853 | 40 | 75.5 | 187614 | 2 | AC115839 | AC115839 Mus muscu | C 926 | 40 | 75.5 | 262673 | 2 | AC098093 | AC098093 Rattus no |
| C 854 | 40 | 75.5 | 188281 | 9 | AL450108 | AL450108 Human DNA | C 927 | 40 | 75.5 | 263687 | 2 | AC125247 | AC125247 Rattus no |
| C 855 | 40 | 75.5 | 189616 | 10 | AC124480 | AC124480 Mus muscu | C 928 | 40 | 75.5 | 266098 | 2 | AC099280 | AC099280 Rattus no |
| C 856 | 40 | 75.5 | 190619 | 9 | AC108172 | AC108172 Homo sapi | C 929 | 40 | 75.5 | 269708 | 2 | AC097787 | AC097787 Rattus no |
| C 857 | 40 | 75.5 | 193390 | 2 | AC112168 | AC112168 Homo sapi | C 930 | 40 | 75.5 | 269956 | 2 | AC094994 | AC094994 Rattus no |
| C 858 | 40 | 75.5 | 193946 | 2 | AC121339 | AC121339 Homo sapi | C 931 | 40 | 75.5 | 270216 | 2 | AC112038 | AC112038 Rattus no |
| C 859 | 40 | 75.5 | 194241 | 2 | AC093324 | AC093324 Homo sapi | C 932 | 40 | 75.5 | 271726 | 2 | AC129344 | AC129344 Rattus no |
| C 860 | 40 | 75.5 | 197288 | 10 | AC123215 | AC123215 Mus muscu | C 933 | 40 | 75.5 | 288313 | 2 | AC121685 | AC121685 Rattus no |
| C 861 | 40 | 75.5 | 197652 | 2 | AC133472 | AC133472 Rattus no | C 934 | 40 | 75.5 | 289209 | 2 | AC127408 | AC127408 Rattus no |
| C 862 | 40 | 75.5 | 198825 | 10 | AC124095 | AC124095 Mus muscu | C 935 | 40 | 75.5 | 292088 | 1 | AE016986 | AE016986 Shigella |
| C 863 | 40 | 75.5 | 199818 | 10 | AL732563 | AL732563 Mouse DNA | C 936 | 40 | 75.5 | 293695 | 10 | AC137749 | AC137749 Mus muscu |
| C 864 | 40 | 75.5 | 200050 | 1 | AL646068 | AL646068 Ralstonia | C 937 | 40 | 75.5 | 296827 | 1 | AP002561 | AP002561 Escherich |
| C 865 | 40 | 75.5 | 200933 | 10 | AL805910 | AL805910 Mouse DNA | C 938 | 40 | 75.5 | 298550 | 1 | AP005047 | AP005047 Streptomy |
| C 866 | 40 | 75.5 | 201289 | 2 | AC118571 | AC118571 Lemur cat | C 939 | 40 | 75.5 | 300029 | 8 | AE017058 | AE017058 Oryza sat |
| C 867 | 40 | 75.5 | 202272 | 2 | AC128030 | AC128030 Rattus no | C 940 | 40 | 75.5 | 300052 | 1 | AE017232 | AE017232 Mycobacte |
| C 868 | 40 | 75.5 | 202415 | 10 | AC123647 | AC123647 Mus muscu | C 941 | 40 | 75.5 | 300099 | 1 | AE016764 | AE016764 Escherich |
| C 869 | 40 | 75.5 | 202810 | 2 | AC113128 | AC113128 Mus muscu | C 942 | 40 | 75.5 | 300431 | 1 | AE016835 | AE016835 Salmonell |
| C 870 | 40 | 75.5 | 204050 | 1 | AL646070 | AL646070 Ralstonia | C 943 | 40 | 75.5 | 301877 | 2 | AC096091 | AC096091 Rattus no |
| C 871 | 40 | 75.5 | 204237 | 2 | AC145179 | AC145179 Gallus ga | C 944 | 40 | 75.5 | 301995 | 1 | AE016779 | AE016779 Pseudomon |
| C 872 | 40 | 75.5 | 204692 | 2 | CR847987 | CR847987 Danio rer | C 945 | 40 | 75.5 | 308015 | 1 | AE016783 | AE016783 Pseudomon |
| C 873 | 40 | 75.5 | 206288 | 10 | AC131758 | AC131758 Mus muscu | C 946 | 40 | 75.5 | 308354 | 2 | AC093482 | AC093482 Mus muscu |
| C 874 | 40 | 75.5 | 206806 | 2 | AC149802 | AC149802 Otlemur | C 947 | 40 | 75.5 | 310613 | 1 | AE016875 | AE016875 Pseudomon |
| C 875 | 40 | 75.5 | 206894 | 10 | AC109152 | AC109152 Mus muscu | C 948 | 40 | 75.5 | 313050 | 3 | PFA929352 | PFA929352 Plasmodi |
| C 876 | 40 | 75.5 | 208332 | 10 | AC122227 | AC122227 Mus muscu | C 949 | 40 | 75.5 | 316119 | 2 | AC119083 | AC119083 Rattus no |
| C 877 | 40 | 75.5 | 211178 | 10 | AC139209 | AC139209 Mus muscu | C 950 | 40 | 75.5 | 327650 | 1 | EX248337 | EX248337 Mycobacte |
| C 878 | 40 | 75.5 | 211400 | 2 | AC024452 | AC024452 Mus muscu | C 951 | 40 | 75.5 | 330401 | 3 | AE003575 | AE003575 Drosophil |
| C 879 | 40 | 75.5 | 212140 | 2 | AC148220 | AC148220 Colobus g | C 952 | 40 | 75.5 | 331955 | 2 | AC117292 | AC117292 Rattus no |
| C 880 | 40 | 75.5 | 212659 | 2 | AL390737 | AL390737 Homo sapi | C 953 | 40 | 75.5 | 346301 | 1 | EX640432 | EX640432 Bordetell |

| | | | | | | |
|------------|---|-------------|--------|--------|-----------------|---------------------|
| c 954 | 40 | 75.5 | 348642 | 1 | BX640446 | BX640446 Bordetell |
| c 955 | 40 | 75.5 | 349306 | 1 | BX842575 | BX842575 Mycobacte |
| c 956 | 40 | 75.5 | 349354 | 1 | BX640416 | BX640416 Bordetell |
| c 957 | 40 | 75.5 | 349980 | 6 | AX571760 | AX571760 Sequence |
| c 958 | 39.5 | 74.5 | 11589 | 1 | AE004778 | AE004778 Pseudomon |
| c 959 | 39.5 | 74.5 | 12749 | 1 | AB012285 | AB012285 Xanthomon |
| c 960 | 39.5 | 74.5 | 35828 | 9 | AC005347 | AC005347 Homo sapi |
| c 961 | 39.5 | 74.5 | 65674 | 9 | AF158748 | AF158748 Homo sapi |
| c 962 | 39.5 | 74.5 | 160111 | 9 | AC124862 | AC124862 Homo sapi |
| c 963 | 39.5 | 74.5 | 169391 | 2 | AC111190 | AC111190 Homo sapi |
| c 964 | 39.5 | 74.5 | 176733 | 2 | AC068001 | AC068001 Homo sapi |
| c 965 | 39.5 | 74.5 | 194718 | 9 | AC011474 | AC011474 Homo sapi |
| c 966 | 39 | 73.6 | 181 | 11 | CR384422 | CR384422 Arabidops |
| c 967 | 39 | 73.6 | 224 | 12 | AY202642 | AY202642 Arabidops |
| c 968 | 39 | 73.6 | 248 | 8 | BT011814 | BT011814 Arabidops |
| c 969 | 39 | 73.6 | 287 | 8 | AF451192 | AF451192 Brassica |
| c 970 | 39 | 73.6 | 299 | 11 | G47756 | G47756 Z26025_1 Ze |
| c 971 | 39 | 73.6 | 301 | 11 | CR377779 | CR377779 Arabidops |
| c 972 | 39 | 73.6 | 348 | 9 | AY358103 | AY358103 Homo sapi |
| c 973 | 39 | 73.6 | 378 | 8 | BT011715 | BT011715 Arabidops |
| c 974 | 39 | 73.6 | 415 | 6 | AX892657 | AX892657 Sequence |
| c 975 | 39 | 73.6 | 415 | 6 | BD028190 | BD028190 Sequence |
| c 976 | 39 | 73.6 | 437 | 6 | AX775445 | AX775445 Sequence |
| c 977 | 39 | 73.6 | 491 | 9 | HSA334904 | HSA334904 Homo sapi |
| c 978 | 39 | 73.6 | 496 | 6 | AX401097 | AX401097 Sequence |
| c 979 | 39 | 73.6 | 567 | 6 | C0647266 | C0647266 Sequence |
| c 980 | 39 | 73.6 | 577 | 8 | AF145259 | AF145259 Nicotiana |
| c 981 | 39 | 73.6 | 645 | 10 | MMDH4 | X07298 M.musculus |
| c 982 | 39 | 73.6 | 681 | 8 | ATH532241 | AJ532241 Arabidops |
| c 983 | 39 | 73.6 | 749 | 5 | CR405758 | CR405758 Gallus ga |
| c 984 | 39 | 73.6 | 855 | 6 | C0743578 | C0743578 Sequence |
| c 985 | 39 | 73.6 | 857 | 5 | BX931651 | BX931651 Gallus ga |
| c 986 | 39 | 73.6 | 883 | 9 | AB023808 | AB023808 Homo sapi |
| c 987 | 39 | 73.6 | 902 | 6 | BD018039 | BD018039 Novel gen |
| c 988 | 39 | 73.6 | 902 | 6 | BD097977 | BD097977 Novel gen |
| c 989 | 39 | 73.6 | 906 | 6 | AX647315 | AX647315 Sequence |
| c 990 | 39 | 73.6 | 1027 | 10 | RN018565 | Y18565 Rattus Norv |
| c 991 | 39 | 73.6 | 1031 | 5 | CF523357 | CR523357 Gallus ga |
| c 992 | 39 | 73.6 | 1112 | 10 | RN018571 | Y18571 Rattus Norv |
| c 993 | 39 | 73.6 | 1192 | 10 | RNMDHR | X04240 Rat mRNA fo |
| c 994 | 39 | 73.6 | 1244 | 6 | BD131673 | BD131673 Variable |
| c 995 | 39 | 73.6 | 1244 | 10 | MUSMDH | M16229 Mouse mitoc |
| c 996 | 39 | 73.6 | 1283 | 9 | BC017963 | BC017963 Homo sapi |
| c 997 | 39 | 73.6 | 1297 | 10 | BC023482 | BC023482 Mus muscu |
| c 998 | 39 | 73.6 | 1324 | 10 | BC063165 | BC063165 Rattus no |
| c 999 | 39 | 73.6 | 1341 | 8 | AF406816 | AF406816 Aquilegia |
| 1000 | 39 | 73.6 | 1341 | 8 | AF536526 | AF536526 Anemone 1 |
| ALIGNMENTS | | | | | | |
| RESULT 1 | AY055118 | 1450 bp | DNA | linear | PLN 01-DEC-2001 | |
| LOCUS | Echium pitardii var. pitardii | | | | | |
| DEFINITION | Echium pitardii var. pitardii complete cds. | | | | | |
| ACCESSION | AY055118 | | | | | |
| VERSION | AY055118.1 | GI:17223796 | | | | |
| KEYWORDS | Echium pitardii var. pitardii | | | | | |
| SOURCE | Echium pitardii var. pitardii | | | | | |
| ORGANISM | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Boraginaceae; Echium. | | | | | |
| REFERENCE | 1 (bases 1 to 1450) | | | | | |
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| AUTHORS | Maroto,F.G., Alonso,D.L., Garrido,J.-A.S., Ferron,M.V. and Ruiz,J.R. | | | | | |
| TITLE | Direct Submission | | | | | |
| JOURNAL | Submitted (10-SEP-2001) Biochemistry, Universidad de Almeria, | | | | | |
| REFERENCE | 2 (bases 1 to 1450) | | | | | |
| AUTHORS | Maroto,F.G., Alonso,D.L., Garrido,J.-A.S., Ferron,M.V. and Ruiz,J.R. | | | | | |
| TITLE | Direct Submission | | | | | |
| JOURNAL | Submitted (10-SEP-2001) Biochemistry, Universidad de Almeria, | | | | | |
| REFERENCE | 2 (bases 1 to 1450) | | | | | |
| AUTHORS | Maroto,F.G., Alonso,D.L., Garrido,J.-A.S., Ferron,M.V. and Ruiz,J.R. | | | | | |
| TITLE | Direct Submission | | | | | |
| JOURNAL | Submitted (10-SEP-2001) Biochemistry, Universidad de Almeria, | | | | | |
| REFERENCE | 2 (bases 1 to 1450) | | | | | |
| AUTHORS | Maroto,F.G., Alonso,D.L., Garrido,J.-A.S., Ferron,M.V. and Ruiz,J.R. | | | | | |
| TITLE | Direct Submission | | | | | |
| JOURNAL | Submitted (10-SEP-2001) Biochemistry, Universidad de Almeria, | | | | | |
| REFERENCE | 2 (bases 1 to 1450) | | | | | |
| AUTHORS | Maroto,F.G., Alonso,D.L., Garrido,J.-A.S., Ferron,M.V. and Ruiz,J.R. | | | | | |
| TITLE | Direct Submission | | | | | |
| JOURNAL | Submitted (10-SEP-2001) Biochemistry, Universidad de Almeria, | | | | | |
| REFERENCE | 2 (bases 1 to 1450) | | | | | |
| AUTHORS | Maroto,F.G., Alonso,D.L., Garrido,J.-A.S., Ferron,M.V. and Ruiz,J.R. | | | | | |
| TITLE | Direct Submission | | | | | |
| JOURNAL | Submitted (10-SEP-2001) Biochemistry, Universidad de Almeria, | | | | | |
| REFERENCE | 2 (bases 1 to 1450) | | | | | |
| AUTHORS | Maroto,F.G., Alonso,D.L., Garrido,J.-A.S., Ferron,M.V. and Ruiz,J.R. | | | | | |
| TITLE | Direct Submission | | | | | |
| JOURNAL | Submitted (10-SEP-2001) Biochemistry, Universidad de Almeria, | | | | | |
| REFERENCE | 2 (bases 1 to 1450) | | | | | |
| AUTHORS | Maroto,F.G., Alonso,D.L., Garrido,J.-A.S., Ferron,M.V. and Ruiz,J.R. | | | | | |
| TITLE | Direct Submission | | | | | |
| JOURNAL | Submitted (10-SEP-2001) Biochemistry, Universidad de Almeria, | | | | | |
| REFERENCE | 2 (bases 1 to 1450) | | | | | |
| AUTHORS | Maroto,F.G., Alonso,D.L., Garrido,J.-A.S., Ferron,M.V. and Ruiz,J.R. | | | | | |
| TITLE | Direct Submission | | | | | |
| JOURNAL | Submitted (10-SEP-2001) Biochemistry, Universidad de Almeria, | | | | | |
| REFERENCE | 2 (bases 1 to 1450)</ | | | | | |

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/db_xref="taxon:17391"
/feature="Echium gentianoides Webb ex Coigny.
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AGHYIVMNPRLKMGIVAGNCLSGISIGWKNHNAHIAACNSLDYDPOIYIPFL
VSSKLSLTSHPYEKKLTDFSLRPFVSHQWTFYVMGSAARVNVQSLIMLLTK
RNVFVRSOELLGLVFWIYVPLVSCLPNWCERIMFVVASLSVTGMQOVQFSLNHFA
SVYVGQKGNDFEKGCTGTLDISCPNMDVPHGLOQVVEHLEPKLPRCHLKISP
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Alignment Scores:
Pred. No.: 5, 2 Length: 1478
Score: 53.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-029-756-6 (1-8) x AY055117 (1-1478)

Qy 1 TptileGlyHisAspAlaGlyHis 8
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Db 502 TGGATTGGCATGATGCTGGGCAT 525

RESULT 3
AR076814 LOCUS 1684 bp DNA linear PAT 30-AUG-2000
DEFINITION Sequence 1 from patent US 5959175.
ACCESSION AR076814
VERSION AR076814.1 GI:10003560
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 1684)
AUTHORS
Thomas, T.L., Nunberg, A.N. and Beremand, P.D.
TITLE
Sunflower albumin 5' regulatory region for the modification of
plant seed lipid composition
JOURNAL
Patent: US 5959175-A 1 28-SEP-1999;
FEATURES
source
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 5, 91 Length: 1684
Score: 53.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-6 (1-8) x AR076814 (1-1684)

Qy 1 TptileGlyHisAspAlaGlyHis 8
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Db 508 TGGATTGGCATGATGCTGGGCAT 531

RESULT 4
AR084177 LOCUS 1684 bp DNA linear PAT 01-SEP-2000
DEFINITION Sequence 1 from patent US 5977436.
ACCESSION AR084177
VERSION AR084177.1 GI:10010948
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 1684)
AUTHORS
Thomas, T.L. and Li, Z.
TITLE
Oleusin 5' regulatory region for the modification of plant seed
lipid composition
JOURNAL
Patent: US 5977436-A 1 02-NOV-1999;
FEATURES
source
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 5, 91 Length: 1684
Score: 53.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-6 (1-8) x AR084177 (1-1684)

Qy 1 TptileGlyHisAspAlaGlyHis 8
|||||
Db 508 TGGATTGGCATGATGCTGGGCAT 531

RESULT 5
BD062571 LOCUS 1684 bp DNA linear PAT 27-AUG-2002
DEFINITION A sunflower albumin 5' regulatory region for the modification of
plant seed lipid composition.
ACCESSION BD062571
VERSION BD062571.1 GI:22608174
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 1684)
AUTHORS
Thomas, T.L., Beremand, P.D. and Nunberg, A.N.
TITLE
A sunflower albumin 5' regulatory region for the modification of
plant seed lipid composition
JOURNAL
Patent: JP 2001518795-A 1 16-OCT-2001;
COMMENT
RHONE-POULENC AGRO
PN JP 2001518795-A/1
PD 16-OCT-2001
PF 09-APR-1998 JP 1998543140
PR 09-APR-1997 US 08/831570
PI TERRY L THOMAS, PHILLIP D BEREMAND, ANDREW N NUNBERG PC
C12N15/82, C12N15/29, C12N15/53, A01H5/00, A01H5/10 CC Strandedness:
Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FT CDS 43..1387.
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source
1..1684
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
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Alignment Scores:
Pred. No.: 5.91 Length: 1684
Score: 53.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-6 (1-8) x BD062571 (1-1684)

Qy 1 TnpileGlyHisAspAlaGlyHis 8
Db 508 TGGATTGGACATGATGCTGGGCAT 531

RESULT 6
BD070919 LOCUS 1684 bp DNA linear PAT 27-AUG-2002
DEFINITION An oleosin 5'regulatory region for the modification of plant seed
lipid composition.
ACCESSION BD070919
VERSION BD070919.1 GI:22616522
KEYWORDS JP 2001519668-A/1.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1684)
AUTHORS Thomas,T.L. and Li,Z.
TITLE An oleosin 5'regulatory region for the modification of plant seed
lipid composition
JOURNAL RHONE POULENC AGRO
COMMENT OS Unidentified
PN JP 2001519668-A/1
PF 23-OCT-2001
PD 09-APR-1998 JP 1998543141
PI 09-APR-1997 US 08/831575
PR TERRY L THOMAS, ZHONGSEN LI
PC C12N15/82, C12N15/29, C12N15/53, A01H5/00, A01H5/10 CC
Strandedness: Double;
CC Topology: Linear;
CC An oleosin 5'regulatory region for the modification of plant
seed lipid
CC composition
FH Key Location/Qualifiers
FT CDS 43..1387.
FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Alignment Scores:
Pred. No.: 5.91 Length: 1684
Score: 53.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-6 (1-8) x BD070919 (1-1684)

Qy 1 TnpileGlyHisAspAlaGlyHis 8
Db 508 TGGATTGGACATGATGCTGGGCAT 531

RESULT 7
AR020904 LOCUS 1685 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 4 from patent US 5789220.
ACCESSION AR020904
VERSION AR020904.1 GI:3975519
KEYWORDS
```

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SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1685)
AUTHORS Thomas,T.L., Reddy,A.S., Nuccio,M., Nunberg,A.N. and Freysinet,G.L.
TITLE Production of .gamma.-linolenic acid by a .DELTA.6-desaturase
JOURNAL Patent: US 5789220-A 4 04-AUG-1998;
FEATURES Location/Qualifiers
source 1..1685
/mol_type="unassigned DNA"

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Alignment Scores:
Pred. No.: 5.91 Length: 1685
Score: 53.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-6 (1-8) x AR020904 (1-1685)

Qy 1 TnpileGlyHisAspAlaGlyHis 8
Db 509 TGGATTGGACATGATGCTGGGCAT 532

RESULT 8
I38430 LOCUS 1685 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 4 from patent US 5614393.
ACCESSION I38430
VERSION I38430.1 GI:2084484
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1685)
AUTHORS Thomas,T.L., Reddy,A.S., Nuccio,M., Nunberg,A.N. and Freysinet,G.L.
TITLE Production of .gamma.-linolenic acid by a .DELTA.6-desaturase
JOURNAL Patent: US 5614393-A 4 25-MAR-1997;
FEATURES Location/Qualifiers
source 1..1685
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 5.91 Length: 1685
Score: 53.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-6 (1-8) x I38430 (1-1685)

Qy 1 TnpileGlyHisAspAlaGlyHis 8
Db 509 TGGATTGGACATGATGCTGGGCAT 532

RESULT 9
AR200408 LOCUS 1685 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 4 from patent US 6355861.
ACCESSION AR200408
VERSION AR200408.1 GI:20250482
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
UNCLASSIFIED.
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REFERENCE 1 (bases 1 to 1685)
AUTHORS Thomas,T.L.
TITLE Production of gamma linolenic acid by a .DELTA.6-desaturase
JOURNAL Patent: US 6355861-A 4 12-MAR-2002;
FEATURES Location/Qualifiers
source 1..1685
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 5.91 Length: 1685
Score: 53.00 Matches: 8
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-6 (1-8) x AR200408 (1-1685)

Qy 1 TptleGlyHisAspAlaGlyHis 8
|||||
Db 509 TGGATTGGACATGATGCTGGGCAT 532

RESULT 10
LOCUS AR455421 1685 bp DNA linear PAT 20-FEB-2004
DEFINITION Sequence 4 from patent US 6683232.
ACCESSION AR455421
VERSION AR455421.1 GI:42689973
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1685)
AUTHORS Thomas,T.L.
TITLE Production of .gamma. linolenic acid by a .DELTA.6-desaturase
JOURNAL Patent: US 6683232-A 4 27-JAN-2004;
FEATURES Location/Qualifiers
source 1..1685
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 5.91 Length: 1685
Score: 53.00 Matches: 8
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-6 (1-8) x AR455421 (1-1685)

Qy 1 TptleGlyHisAspAlaGlyHis 8
|||||
Db 509 TGGATTGGACATGATGCTGGGCAT 532

RESULT 11
LOCUS AF007561 1695 bp mRNA linear PLN 05-JAN-1999
DEFINITION Borago officinalis delta 6-desaturase mRNA, complete cds.
ACCESSION AF007561
VERSION AF007561.1 GI:4102020
KEYWORDS Borago officinalis
SOURCE Borago officinalis
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Boraginaceae; Borago.

REFERENCE 1 (bases 1 to 1685)
AUTHORS Nunberg,A.N., Beremand,P.D. and Thomas,T.L.
TITLE Engineering of Plant Seed Oils to Produce Gamma Linolenic Acid

(GLA) Unpublished
2 (bases 1 to 1685)
Nunberg,A.N., Beremand,P.D. and Thomas,T.L.
TITLE Direct Submission
JOURNAL Submitted (09-JUN-1997) Biology, Texas A&M University, College
Station, TX 77843, USA
FEATURES Location/Qualifiers
source 1..1685
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/tissue_type="seed"
/dev_stage="12 day post pollination"
/note="membrane bound polyosomal RNA"
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/function="produces gamma linolenic acid from linoleic
acid"
/function="produces octadecatetraenoic acid from alpha
linolenic acid"
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/protein_id="AAD01410.1"
/db_xref="GI:4102021"
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AGHYVYVDSRLNKFMGIFANCLSGISIGWKNHNAHHIACHNSLEYDPSLOIYIPL
VVSSEFGSLTSHPEKRLTDSLRFPSVYQHKTEYPIMCAARLNMVYQSLJMLLTK
RVYRAQELGLGVFISWIWPLLVSLCPDNLWGERIMFVIASLSVTGMQVQPSLNHPSS
SNVYVKPKGNWFEKQTDGLDIDISCPMDWFGGLQFQIEHHLFPKPRCNLRKISP
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ORIGIN
Alignment Scores:
Pred. No.: 5.91 Length: 1685
Score: 53.00 Matches: 8
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-029-756-6 (1-8) x AF007561 (1-1685)

Qy 1 TptleGlyHisAspAlaGlyHis 8
|||||
Db 509 TGGATTGGACATGATGCTGGGCAT 532

RESULT 12
LOCUS AX951561 1687 bp DNA linear PAT 08-JAN-2004
DEFINITION Sequence 1 from Patent WO03093482.
ACCESSION AX951561
VERSION AX951561.1 GI:40781919
KEYWORDS Borago officinalis
SOURCE Borago officinalis
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Boraginaceae; Borago.

REFERENCE 1
AUTHORS Ciprus,P., Renz,A., Lerchl,J. and Kuijpers,A.M.
TITLE Method for producing multiple unsaturated fatty acids in plants
JOURNAL Patent: WO 03093482-A 1 13-NOV-2003;
BASF Plant Science GmbH (DE)
FEATURES Location/Qualifiers
source 1..1687
/organism="Borago officinalis"
/mol_type="unassigned DNA"
/db_xref="taxon:13363"
42..1388
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/db_xref="GI:40781920"
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SFLPKSLAGQEVTDFAVHPASTWKNLDRKFTFYGLKYDSVSEVSKDYRKLVPFEFSK
MGLYDKKGHIMFATLCFAMLFAMSVGLFCEGVLVHLFSGCLMGFLWTQSGWIGHD
AGHYMVVSDSLNFKMGIFANCLSGISIGWKNHNAHIAACNSLVDPLQVLPFL
VWSSKFGSLTSHFYERKLTFDLSLRFVSQHWTFYPMCAARLNNVQSLIMLLTK
RNVSYRAHLLGCLVFSIWIPLLVSLCLPNWGERIMFVIALSVTGMQVQFSLNHFS
SVYVKGKGNWFKQDGTLDISCPMNMDFHGLQFQIEHLLFPKPRCNLRKKISP
YVIBLCKHNLPPNYASFSPANEMTLRLNTALQARDITKPLPKNLVWEALHTHG"
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ORIGIN

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Alignment Scores:
Pred. No.: 5.92 Length: 1687
Score: 53.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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US-10-029-756-6 (1-8) x AX951561 (1-1687)

Qy 1 TripleGlyHisAspAlaGlyHis 8

Db 507 TGGATTGGACATGATGCTGGGCAT 530

RESULT 13

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BOU79010 1687 bp mRNA linear PLN 02-MAY-1997
LOCUS Borago officinalis delta 6 desaturase mRNA, complete cds.
DEFINITION
ACCESSION U79010
VERSION U79010.1 GI:2062402
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KEYWORDS

SOURCE

ORGANISM

Borago officinalis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamiales; Boraginaceae; Borago.

1 (bases 1 to 1687)

Sayanova,O., Smith,M.A., Lapinskas,P., Stobart,A.K., Dobson,G.,

Christie,W.W., Shewry,P.R. and Napier,J.A.

Expression of a borage desaturase cDNA containing an N-terminal

cytochrome b5 domain results in the accumulation of high levels of

delta6-desaturated fatty acids in transgenic tobacco

Proc. Natl. Acad. Sci. U.S.A. 94 (8), 4211-4216 (1997)

97268723

9108131

2 (bases 1 to 1687)

Sayanova,O., Smith,M.A., Shewry,P.R. and Napier,J.A.

Direct Submission

Submitted (20-NOV-1996) Cell Biology, IACR-Long Ashton Research

Station, Long Ashton, Bristol BS18 9AF, UK

Location/Qualifiers

1. .1687

/organism="Borago officinalis"

/mol_type="mRNA"

/db_xref="taxon:13363"

42. .1388

/function="haem-binding protein"

/codon_start=1

/product="delta 6 desaturase"

/protein_id="AAC49700.1"

/db_xref="GI:2062403"

/translation="MAAQIKKITYTSDELKNHDKPGDLWISIQKAYDVSDWKDHPGG

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AGHYMVVSDSLNFKMGIFANCLSGISIGWKNHNAHIAACNSLVDPLQVLPFL

VWSSKFGSLTSHFYERKLTFDLSLRFVSQHWTFYPMCAARLNNVQSLIMLLTK

RNVSYRAHLLGCLVFSIWIPLLVSLCLPNWGERIMFVIALSVTGMQVQFSLNHFS

SVYVKGKGNWFKQDGTLDISCPMNMDFHGLQFQIEHLLFPKPRCNLRKKISP

YVIBLCKHNLPPNYASFSPANEMTLRLNTALQARDITKPLPKNLVWEALHTHG"

ORIGIN

Alignment Scores:

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Pred. No.: 5.92 Length: 1687
Score: 53.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0
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US-10-029-756-6 (1-8) x BOU79010 (1-1687)

Qy 1 TripleGlyHisAspAlaGlyHis 8

Db 507 TGGATTGGACATGATGCTGGGCAT 530

RESULT 14

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AX824969 1362 bp DNA linear PAT 12-DEC-2003
LOCUS Sequence 1 from Patent WO03072784.
DEFINITION
ACCESSION AX824969
VERSION AX824969.1 GI:39750752
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KEYWORDS

SOURCE

ORGANISM

Primula farinosa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; Ericales; Primulaceae; Primula.

1

Napier,J.A. and Sayanova,O.

Delta 6minus;desaturases from primulaceae, expressing plants

and pufaminus;containing oils

Patent: WO 03072784-A 1 04-SEP-2003;

Rothamsted Experimental Station (GB)

Location/Qualifiers

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/organism="Primula farinosa"

/mol_type="unassigned DNA"

/db_xref="taxon:133892"

1. .1362

/notes="unnamed protein product"

/codon_start=1

/protein_id="CAE84827.1"

/db_xref="GI:39750753"

/translation="MANKSPNPKTYITSSDLKSHKAGDLWISIHQVVDVSSWAA

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WIGHSGHYRIMSDRKNNWFAQLISLNCLOGISIGWKNHNAHIAACNSLVDPLQVLPFL

YIPLLVSPKFFNSLTSRFDKLNFDGVSRLFVYQHWTFFYPVNCVARLNNLAQSF

TLFSSREVCHRAQEVFGLAVFWVWFPPLLSCLPNWGERIMFLLASVYTGTHQVQFSL

NHFSDDVYVGPVGNDFWFKQTAGTLNISCPAWMDHFGLOFQVHHLFPRMPRGQF

RKISPPVRDLCKKHNLPYNIASFPTKANVFTLKTALNTAIEARDLSNPLPKNMVWEALK

TLG"

ORIGIN

Alignment Scores:

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Pred. No.: 16.8 Length: 1362
Score: 50.00 Matches: 7
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 0
Query Match: 94.34% Indels: 0
DB: 6 Gaps: 0
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US-10-029-756-6 (1-8) x AX824969 (1-1362)

Qy 1 TripleGlyHisAspAlaGlyHis 8

Db 481 TGCATAGCTCAGCACTCTGGGCAT 504

RESULT 15

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AX824971 1362 bp DNA linear PAT 12-DEC-2003
LOCUS Sequence 3 from Patent WO03072784.
DEFINITION
ACCESSION AX824971
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VERSION      AX824971.1  GI:39750754
KEYWORDS
SOURCE       Primula vialii
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              asterids; Ericales; Primulaceae; Primula.
REFERENCE    1
AUTHORS      Napier,J.A. and Sayanova,O.
TITLE        Delta 6&minus;desaturases from primulaceae&comma; expressing plants
              and puf&minus;containing oils
JOURNAL      Patent: WO 03072784-A 3 04-SEP-2003;
              Rothamsted Experimental Station (GB)
FEATURES     Location/Qualifiers
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US-10-029-756-6 (1-8) x AX824971 (1-1362)

Oy      1  TrrileGlyHisAspAlaGlyHis 8
Db      481 TGGATAGTCACGACTCTGGGCAT 504

RESULT 16
AY234125      1410 bp  mRNA  linear  PLN 04-MAY-2003
LOCUS         Primula farinosa
DEFINITION    Primula farinosa fatty acid delta-6 desaturase mRNA, complete cds.
ACCESSION     AY234125
VERSION       AY234125.1  GI:30350276
KEYWORDS      Primula farinosa
SOURCE        Primula farinosa
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              asterids; Ericales; Primulaceae; Primula.
REFERENCE     1 (bases 1 to 1410)
AUTHORS       Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and
              Napier,J.A.
TITLE         Identification of Primula fatty acid Delta(6)-desaturases with n-3
              substrate preferences(1)
JOURNAL       FEBS Lett. 542 (1-3), 100-104 (2003)
MEDLINE       22615586
PUBMED        12729906
REFERENCE     2 (bases 1 to 1410)
AUTHORS       Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and
              Napier,J.A.
TITLE         Direct Submission
JOURNAL       Submitted (10-FEB-2003) Crop Performance & Improvement, Long Ashton
              Research Station, Long Ashton, Bristol BS41 9AF, UK
FEATURES     Location/Qualifiers
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US-10-029-756-6 (1-8) x AY234125 (1-1410)

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RESULT 17
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DEFINITION    Primula vialii
ACCESSION     AY234127
VERSION       AY234127.1  GI:30350280
KEYWORDS      Primula vialii
SOURCE        Primula vialii
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              asterids; Ericales; Primulaceae; Primula.
REFERENCE     1 (bases 1 to 1618)
AUTHORS       Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and
              Napier,J.A.
TITLE         Identification of Primula fatty acid Delta(6)-desaturases with n-3
              substrate preferences(1)
JOURNAL       FEBS Lett. 542 (1-3), 100-104 (2003)
MEDLINE       22615586
PUBMED        12729906
REFERENCE     2 (bases 1 to 1618)
AUTHORS       Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and
              Napier,J.A.
TITLE         Direct Submission
JOURNAL       Submitted (10-FEB-2003) Crop Performance & Improvement, Long Ashton
              Research Station, Long Ashton, Bristol BS41 9AF, UK
FEATURES     Location/Qualifiers
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Score: 50.00 Matches: 7
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 0
Query Match: 94.34% Indels: 0
DB: 8 Gaps: 0

US-10-029-756-6 (1-8) x AY234127 (1-1618)

Qy 1 TptileGlyHisAspAlaGlyHis 8
LOCUS
Db 737 TGGATAGTCACGACTCTGGGCAT 760

RESULT 18
AF031194 AF031194 1788 bp mRNA linear PLN 29-JAN-1999
DEFINITION
Triticum aestivum S276 (S276) mRNA, complete cds.
ACCESSION
AF031194
VERSION
AF031194.1 GI:4104055
KEYWORDS
Triticum aestivum (bread wheat)
ORGANISM
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE
1 (bases 1 to 1788)
Delhaize, E., Hebb, D.M., Gardner, R.C. and Richards, K.D.
Aluminum tolerance in yeast conferred by over-expression of wheat
genes
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 1788)
Delhaize, E., Hebb, D.M., Gardner, R.C. and Richards, K.D.
Direct Submission
JOURNAL
Submitted (23-OCT-1997) Plant Industry, CSIRO, Canberra, ACT 2601,
Australia
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intron
523..743
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Alignment Scores:
Pred. No.: 19.9 Length: 1618
Score: 50.00 Matches: 7
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 0
Query Match: 94.34% Indels: 0
DB: 8 Gaps: 0

US-10-029-756-6 (1-8) x AY234127 (1-1618)

Qy 1 TptileGlyHisAspAlaGlyHis 8
LOCUS
Db 737 TGGATAGTCACGACTCTGGGCAT 760

RESULT 18
AF031194 AF031194 1788 bp mRNA linear PLN 29-JAN-1999
DEFINITION
Triticum aestivum S276 (S276) mRNA, complete cds.
ACCESSION
AF031194
VERSION
AF031194.1 GI:4104055
KEYWORDS
Triticum aestivum (bread wheat)
ORGANISM
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE
1 (bases 1 to 1788)
Delhaize, E., Hebb, D.M., Gardner, R.C. and Richards, K.D.
Aluminum tolerance in yeast conferred by over-expression of wheat
genes
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 1788)
Delhaize, E., Hebb, D.M., Gardner, R.C. and Richards, K.D.
Direct Submission
JOURNAL
Submitted (23-OCT-1997) Plant Industry, CSIRO, Canberra, ACT 2601,
Australia
FEATURES
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Location/Qualifiers
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from GenBank Accession Number U79010"
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ORIGIN
Alignment Scores:
Pred. No.: 22 Length: 1788
Score: 50.00 Matches: 7
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 0
Query Match: 94.34% Indels: 0
DB: 8 Gaps: 0

US-10-029-756-6 (1-8) x AF031194 (1-1788)

Qy 1 TptileGlyHisAspAlaGlyHis 8
LOCUS
Db 646 TGGATTGGCCATGACTCCGCCAC 669

RESULT 19
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DEFINITION
Ricinun communis desaturase/cytochrome b5 protein mRNA, complete
cds.
ACCESSION
AF005096
VERSION
AF005096.1 GI:4101625
KEYWORDS
Ricinun communis (castor bean)
ORGANISM
Ricinun communis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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Acalyphaeae; Ricinus.
REFERENCE
1 (bases 1 to 1856)
Savanova, O., Smith, M.A., Lapinskas, P., Stobart, A.K., Dobson, G.,
Christie, W.W., Shewry, P.R. and Napier, J.A.
Expression of a borage desaturase cDNA containing an N-terminal
cytochrome b5 domain results in the accumulation of high levels of
delta6-desaturated fatty acids in transgenic tobacco
Proc. Natl. Acad. Sci. U.S.A. 94 (8), 4211-4216 (1997)
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2 (bases 1 to 1856)
Napier, J.A. and Shewry, P.R.
Direct Submission
JOURNAL
Submitted (22-MAY-1997) Cell Biology, IACR-Long Ashton Research
Station, Long Ashton, Bristol BS18 9AF, UK
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ORIGIN
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 8, 2005, 09:24:10 ; Search time 385.263 Seconds
(without alignments)
122.924 Million cell updates/sec

Title: US-10-029-756-6

Perfect score: 53

Sequence: 1 WIGHDAGH 8

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Fgapop 6.0, Fgapext 7.0
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Searched: 4390206 seqs, 2959870667 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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| 70 | 42 | 79.2 | 3419 | 5 AAS78145 | Aas78145 DNA encod |
| 71 | 42 | 79.2 | 3470 | 8 ACC46735 | Acc46735 Human dit |
| 72 | 42 | 79.2 | 4023 | 10 ADE31423 | Ade31423 Human dia |
| 73 | 42 | 79.2 | 4741 | 4 ABL22486 | Ab122486 Drosophill |
| 74 | 42 | 79.2 | 6005 | 4 ABL11164 | Ab11164 Drosophill |
| 75 | 42 | 79.2 | 8335 | 5 AAS78974 | Aas78974 DNA encod |
| 76 | 42 | 79.2 | 100762 | 12 ADQ59518 | Adq59518 Human can |
| 77 | 41 | 77.4 | 418 | 9 ACH20392 | Ach20392 Human adu |
| 78 | 41 | 77.4 | 476 | 6 ABL93274 | Ab193274 Arabidops |

| | | | | | | | | | | | | | |
|-------|------|------|--------|----|-------------|---------------------|-------|----|------|--------|----|-------------|---------------------|
| c 79 | 41 | 77.4 | 514 | 12 | ACH78188 | Ach78188 Human gen | c 152 | 40 | 75.5 | 723 | 13 | ADS56787 | Ads56787 Bacterial |
| c 80 | 41 | 77.4 | 544 | 12 | ADJ84393 | Adj84393 Human phe | c 153 | 40 | 75.5 | 780 | 4 | AAH06798 | Aah06798 Human cDN |
| c 81 | 41 | 77.4 | 564 | 4 | AAK63843 | Aak63843 Human imm | c 154 | 40 | 75.5 | 828 | 13 | ADR93383 | Adr93383 Novel S. |
| c 82 | 41 | 77.4 | 656 | 13 | ADS60395 | Ads60395 Bacterial | c 155 | 40 | 75.5 | 843 | 13 | ADS57548 | Ads57548 Bacterial |
| c 83 | 41 | 77.4 | 658 | 4 | AAH36243 | Aah36243 Human col | c 156 | 40 | 75.5 | 856 | 3 | AAC75808 | Aac75808 Human ORF |
| c 84 | 41 | 77.4 | 775 | 6 | ADG32419 | Adg32419 Cocoa ole | c 157 | 40 | 75.5 | 858 | 12 | ADQ21379 | Adq21379 Human sof |
| c 85 | 41 | 77.4 | 780 | 13 | ADS49622 | Ads49622 Bacterial | c 158 | 40 | 75.5 | 942 | 10 | ABX05802 | Abx05802 S. pneumo |
| c 86 | 41 | 77.4 | 800 | 13 | ADS55132 | Ads55132 Bacterial | c 159 | 40 | 75.5 | 960 | 8 | ABX24264 | Abx24264 Streptoco |
| c 87 | 41 | 77.4 | 816 | 4 | AAH82258 | Aaf82258 Bacillus | c 160 | 40 | 75.5 | 1176 | 13 | ADS56580 | Ads56580 Bacterial |
| c 88 | 41 | 77.4 | 921 | 10 | ADE81200 | Ade81200 Orf14 cod | c 161 | 40 | 75.5 | 1274 | 13 | ADS48415 | Ads48415 Bacterial |
| c 89 | 41 | 77.4 | 955 | 4 | AAH71706 | Aaf71706 Corynebact | c 162 | 40 | 75.5 | 1305 | 12 | ADJ40265 | Adj40265 Plant cDN |
| c 90 | 41 | 77.4 | 1143 | 8 | ADA69970 | Ada69970 Rice gene | c 163 | 40 | 75.5 | 1311 | 5 | AAS45093 | Aas45093 cDNA enco |
| c 91 | 41 | 77.4 | 1161 | 4 | AAK86046 | Aak86046 Human imm | c 164 | 40 | 75.5 | 1460 | 4 | AAC84336 | Aac84336 C. soroki |
| c 92 | 41 | 77.4 | 1311 | 2 | AAZ96369 | Aaz96369 S. pneumo | c 165 | 40 | 75.5 | 1460 | 4 | AAC84338 | Aac84338 C. soroki |
| c 93 | 41 | 77.4 | 1350 | 6 | ABZ12753 | Abz12753 Arabidops | c 166 | 40 | 75.5 | 1465 | 3 | AAC42244 | Aac42244 Arabidops |
| c 94 | 41 | 77.4 | 1461 | 6 | ABA01201 | Aba01201 Aldehydde- | c 167 | 40 | 75.5 | 1471 | 3 | AAD01349 | Aad01349 Florida b |
| c 95 | 41 | 77.4 | 1650 | 3 | AAC51462 | Aac51462 Arabidops | c 168 | 40 | 75.5 | 1523 | 3 | AZ439020 | Aaz439020 Mouse nov |
| c 96 | 41 | 77.4 | 1650 | 3 | AAC33846 | Aac33846 Arabidops | c 169 | 40 | 75.5 | 1594 | 3 | AZ44832 | Aaz44832 B. napus |
| c 97 | 41 | 77.4 | 1678 | 3 | AAZ44833 | Aaz44833 A. thalia | c 170 | 40 | 75.5 | 1696 | 12 | ADO15558 | Ado15558 Evening p |
| c 98 | 41 | 77.4 | 1756 | 4 | AAK86044 | Aak86044 Human imm | c 171 | 40 | 75.5 | 1702 | 6 | ABK49503 | Abk49503 DNA enco |
| c 99 | 41 | 77.4 | 1757 | 4 | AAK86045 | Aak86045 Human imm | c 172 | 40 | 75.5 | 1702 | 8 | ABX15367 | Abx15367 Evening p |
| c 100 | 41 | 77.4 | 1962 | 12 | ADO07822 | Ado07822 Mouse pol | c 173 | 40 | 75.5 | 1702 | 12 | ADO15556 | Ado15556 Evening p |
| c 101 | 41 | 77.4 | 2000 | 8 | ADA73284 | Ada73284 Rice gene | c 174 | 40 | 75.5 | 1702 | 12 | ADN49384 | Adn49384 Evening p |
| c 102 | 41 | 77.4 | 2466 | 3 | AAZ91853 | Aaz91853 Streptoco | c 175 | 40 | 75.5 | 1934 | 3 | AAD01352 | Aad01352 Soybean s |
| c 103 | 41 | 77.4 | 2466 | 12 | ADG67565 | Adg67565 Streptoco | c 176 | 40 | 75.5 | 2541 | 4 | ABL28071 | AbL28071 Drosophi |
| c 104 | 41 | 77.4 | 2466 | 12 | ADG67567 | Adg67567 Streptoco | c 177 | 40 | 75.5 | 2568 | 8 | ACA40424 | Aca40424 Prokaryot |
| c 105 | 41 | 77.4 | 2475 | 10 | ABX07903 | Abx07903 S. pneumo | c 178 | 40 | 75.5 | 2680 | 6 | AAS62282 | Aas62282 cDNA sequ |
| c 106 | 41 | 77.4 | 2505 | 13 | ADR93522 | Adr93522 Novel S. | c 179 | 40 | 75.5 | 3248 | 4 | AAH14518 | Aah14518 Human cDN |
| c 107 | 41 | 77.4 | 2550 | 10 | ADL24770 | Adl24770 Intestina | c 180 | 40 | 75.5 | 3248 | 13 | ACN40824 | Acn40824 Tumour-as |
| c 108 | 41 | 77.4 | 3057 | 5 | AAH67964 | Aah67964 C. glutami | c 181 | 40 | 75.5 | 3296 | 5 | ADL45170 | Adl45170 Human ova |
| c 109 | 41 | 77.4 | 3187 | 11 | ADL65624 | Adl65624 C. glutam | c 182 | 40 | 75.5 | 4540 | 6 | ABS56604 | Abs56604 S. macros |
| c 110 | 41 | 77.4 | 3549 | 6 | ABL58732 | AbL58732 Corynebact | c 183 | 40 | 75.5 | 5057 | 4 | ABL28070 | AbL28070 Drosophi |
| c 111 | 41 | 77.4 | 4530 | 4 | AAH99553 | Aah99553 Human pro | c 184 | 40 | 75.5 | 6825 | 10 | ADFS5397 | Adfs5397 Human DNA |
| c 112 | 41 | 77.4 | 4750 | 13 | ADR83446 | Adr83446 Human MOS | c 185 | 40 | 75.5 | 6827 | 2 | AAV52193 | Av52193 Streptoco |
| c 113 | 41 | 77.4 | 4763 | 13 | ACN38958 | Acn38958 Tumour-as | c 186 | 40 | 75.5 | 26309 | 4 | AAS59535 | Aas59535 Propionib |
| c 114 | 41 | 77.4 | 4965 | 2 | AAV52276 | Av52276 Streptoco | c 187 | 40 | 75.5 | 26309 | 8 | ACF64464 | Acf64464 Propionib |
| c 115 | 41 | 77.4 | 5095 | 4 | AAH02884 | Aah02884 Human she | c 188 | 40 | 75.5 | 110000 | 4 | AAI99682_10 | Contiuation (11 o |
| c 116 | 41 | 77.4 | 5108 | 1 | AAH60388 | Aan60388 Sequence | c 189 | 40 | 75.5 | 110000 | 4 | AAI99682_11 | Contiuation (12 o |
| c 117 | 41 | 77.4 | 5174 | 12 | ADQ83539 | Adq83539 Human tum | c 190 | 40 | 75.5 | 110000 | 4 | AAI99683_10 | Contiuation (12 o |
| c 118 | 41 | 77.4 | 5174 | 13 | ADQ84718 | Adq84718 Human tum | c 191 | 40 | 75.5 | 110000 | 4 | AAI99683_11 | Contiuation (12 o |
| c 119 | 41 | 77.4 | 5174 | 13 | ACN40463 | Acn40463 Tumour-as | c 192 | 40 | 75.5 | 110000 | 10 | ABS56454_00 | Ab56454 Streptoco |
| c 120 | 41 | 77.4 | 5175 | 12 | ADAF45426 | Adf45426 Human vas | c 193 | 40 | 75.5 | 127917 | 13 | ADRS2731 | Adrs2731 Drug ther |
| c 121 | 41 | 77.4 | 5175 | 12 | ADI28823 | Adi28823 Human mod | c 194 | 40 | 75.5 | 141912 | 10 | ACN86530 | Acn86530 Human GPC |
| c 122 | 41 | 77.4 | 5175 | 12 | ADK70429 | Adk70429 Respirato | c 195 | 40 | 75.5 | 233380 | 11 | ACN44282 | Acn44282 Human gen |
| c 123 | 41 | 77.4 | 5175 | 12 | ADN03813 | Adn03813 Antipsori | c 196 | 39 | 73.6 | 262 | 4 | AAK83296 | Aak83296 Human imm |
| c 124 | 41 | 77.4 | 5175 | 12 | ADO19241 | Ado19241 Human PRO | c 197 | 39 | 73.6 | 273 | 10 | ADD49985 | Add49985 Mammalian |
| c 125 | 41 | 77.4 | 5194 | 4 | ABA09043 | Aba09043 Human LDL | c 198 | 39 | 73.6 | 334 | 3 | AAC71797 | Aac71797 Single nu |
| c 126 | 41 | 77.4 | 5201 | 4 | AAH98389 | Aah98389 Human EST | c 199 | 39 | 73.6 | 334 | 3 | AAC71734 | Aac71734 Single nu |
| c 127 | 41 | 77.4 | 5214 | 12 | ADK70381 | Adk70381 Respirato | c 200 | 39 | 73.6 | 334 | 3 | AAC71743 | Aac71743 Single nu |
| c 128 | 41 | 77.4 | 5343 | 12 | ADQ22368 | Adq22368 Human sof | c 201 | 39 | 73.6 | 415 | 3 | AAC04445 | Aac04445 Human sec |
| c 129 | 41 | 77.4 | 5382 | 6 | ABL91141 | AbL91141 Hominidae | c 202 | 39 | 73.6 | 418 | 9 | ACH47722 | Ach47722 Human inf |
| c 130 | 41 | 77.4 | 5468 | 2 | AAQ06540 | Aaq06540 Human low | c 203 | 39 | 73.6 | 425 | 9 | ACH47830 | Ach47830 Human inf |
| c 131 | 41 | 77.4 | 5851 | 6 | ABN83957 | Abn83957 Human gen | c 204 | 39 | 73.6 | 426 | 9 | ACH46760 | Ach46760 Human inf |
| c 132 | 41 | 77.4 | 24167 | 5 | ABA16132 | Aba16132 Human ner | c 205 | 39 | 73.6 | 437 | 10 | ADE85546 | Ade85546 Farnesyl |
| c 133 | 41 | 77.4 | 29112 | 8 | AAS59609 | Aas59609 Propionib | c 206 | 39 | 73.6 | 454 | 5 | AAK87901 | Aak87901 Human dig |
| c 134 | 41 | 77.4 | 29112 | 8 | ACF64538 | Acf64538 Propionib | c 207 | 39 | 73.6 | 454 | 5 | AAS31717 | Aas31717 Human liv |
| c 135 | 41 | 77.4 | 5999 | 13 | ADR88249 | Adr88249 Human low | c 208 | 39 | 73.6 | 454 | 5 | ABN90072 | Abn90072 Human liv |
| c 136 | 41 | 77.4 | 72149 | 10 | ADE81173 | Ade81173 ML-2368 s | c 209 | 39 | 73.6 | 454 | 11 | ADJ14839 | Adj14839 Human liv |
| c 137 | 41 | 77.4 | 110000 | 10 | ABS56454_18 | Contiuation (19 o | c 210 | 39 | 73.6 | 477 | 9 | ACH43182 | Ach43182 Human foe |
| c 138 | 41 | 77.4 | 110000 | 10 | ABS56454_19 | Contiuation (20 o | c 211 | 39 | 73.6 | 496 | 6 | ABK62866 | Abk62866 Rat sequ |
| c 139 | 41 | 77.4 | 34980 | 5 | AAH68533 | Aah68533 C. glutami | c 212 | 39 | 73.6 | 496 | 10 | ADB56864 | Adb56864 Toxicity- |
| c 140 | 40.5 | 76.4 | 942 | 10 | ABQ80365 | Abq80365 A. fumiga | c 213 | 39 | 73.6 | 496 | 12 | ADP72150 | Adp72150 Renal tox |
| c 141 | 40.5 | 76.4 | 1002 | 10 | ABQ80365 | Abq80365 A. fumiga | c 214 | 39 | 73.6 | 521 | 3 | AAC32639 | Aac32639 Arabidops |
| c 142 | 40.5 | 76.4 | 384 | 4 | AAH13439 | Aal13439 Human bre | c 215 | 39 | 73.6 | 567 | 6 | ABN68155 | Abn68155 Streptoco |
| c 143 | 40 | 75.5 | 390 | 11 | ACN91287 | Acn91287 Breast ca | c 216 | 39 | 73.6 | 580 | 5 | AAS70360 | Aas70360 DNA enco |
| c 144 | 40 | 75.5 | 393 | 4 | AAI22309 | Aai22309 Human bre | c 217 | 39 | 73.6 | 662 | 13 | ADQ52982 | Adq52982 Novel can |
| c 145 | 40 | 75.5 | 413 | 5 | AAS45281 | Aas45281 cDNA enco | c 218 | 39 | 73.6 | 685 | 10 | ACD94064 | AcD94064 Human col |
| c 146 | 40 | 75.5 | 427 | 5 | ADI73727 | Adi73727 Human ova | c 219 | 39 | 73.6 | 796 | 4 | AAK89367 | Aak89367 Human dig |
| c 147 | 40 | 75.5 | 427 | 5 | ADI67330 | Adi67330 Human ova | c 220 | 39 | 73.6 | 796 | 5 | AAS31900 | Aas31900 Human liv |
| c 148 | 40 | 75.5 | 464 | 9 | ACH42387 | Ach42387 Human foe | c 221 | 39 | 73.6 | 796 | 6 | ABN90255 | Abn90255 Human liv |
| c 149 | 40 | 75.5 | 468 | 5 | ADL38964 | Adl38964 Human ova | c 222 | 39 | 73.6 | 796 | 11 | ADJ15168 | Adj15168 Human neu |
| c 150 | 40 | 75.5 | 575 | 11 | ACN83525 | Acn83525 Breast ca | c 223 | 39 | 73.6 | 902 | 4 | AAI94202 | Aai94202 Human neu |
| c 151 | 40 | 75.5 | 595 | 3 | AAH11470 | Aaf11470 Aspergill | c 224 | 39 | 73.6 | 943 | 10 | ADC87054 | Adc87054 Human GPC |

| | | | | | | | | | | | | | |
|-------|------|------|--------|----|-----------|-----------------------------|-------|----|------|-----|----|----------|--------------------|
| c 225 | 39 | 73.6 | 1192 | 10 | ADBS3230 | Adbs3230 Primary r | c 298 | 38 | 71.7 | 367 | 4 | AAI92907 | Aai92907 Human pol |
| c 226 | 39 | 73.6 | 1244 | 2 | AAV72448 | Aav72448 Mouse MDH | c 299 | 38 | 71.7 | 371 | 8 | ABZ36849 | Abz36849 Human gen |
| c 227 | 39 | 73.6 | 1390 | 6 | AAI42599 | Aai42599 Human eer | c 300 | 38 | 71.7 | 373 | 6 | ABN96255 | Abn96255 Gene #275 |
| c 228 | 39 | 73.6 | 1669 | 8 | ABZ24267 | Abz24267 Human SLC | c 301 | 38 | 71.7 | 379 | 3 | AAC79312 | Aac79312 Human lun |
| c 229 | 39 | 73.6 | 1674 | 8 | ABZ24266 | Abz24266 Human SLC | c 302 | 38 | 71.7 | 379 | 3 | AAD23388 | Aad23388 Human lun |
| c 230 | 39 | 73.6 | 1692 | 2 | AAT60974 | Aat60974 NLERK2 CD | c 303 | 38 | 71.7 | 379 | 10 | ADD66662 | Add66662 Human lun |
| c 231 | 39 | 73.6 | 1705 | 13 | ACN37636 | Acn37636 Tumour-as | c 304 | 38 | 71.7 | 379 | 10 | ADG87916 | Adg87916 Human lun |
| c 232 | 39 | 73.6 | 1821 | 3 | AAA62004 | Aaa62004 Hydrophob | c 305 | 38 | 71.7 | 384 | 5 | AAE80296 | Aae80296 DNA encod |
| c 233 | 39 | 73.6 | 1829 | 8 | ABZ24263 | Abz24263 Human SLC | c 306 | 38 | 71.7 | 400 | 4 | AAI81281 | Aai81281 Human pol |
| c 234 | 39 | 73.6 | 1831 | 13 | ADQ84960 | Adq84960 Human tum | c 307 | 38 | 71.7 | 404 | 4 | AAI81570 | Aai81570 CDNA enco |
| c 235 | 39 | 73.6 | 1832 | 8 | ABZ24265 | Abz24265 Human SLC | c 308 | 38 | 71.7 | 404 | 4 | AAI01153 | Aai01153 Human rep |
| c 236 | 39 | 73.6 | 1864 | 8 | ABZ24268 | Abz24268 Human SLC | c 309 | 38 | 71.7 | 404 | 4 | ABL96615 | Abi96615 Human tes |
| c 237 | 39 | 73.6 | 1866 | 10 | ACF67850 | Acf67850 Phototrab | c 310 | 38 | 71.7 | 405 | 2 | AAV63618 | Aav63618 Synthetic |
| c 238 | 39 | 73.6 | 1950 | 5 | ACAC85821 | Acac85821 hOAT2B DN | c 311 | 38 | 71.7 | 405 | 2 | AAZ09860 | Aaz09860 Synthetic |
| c 239 | 39 | 73.6 | 2000 | 12 | ADJ41525 | Adj41525 Plant cDN | c 312 | 38 | 71.7 | 406 | 2 | AAQ60129 | Aaq60129 Human bra |
| c 240 | 39 | 73.6 | 2052 | 4 | ABL07785 | Abi07785 Drosophi | c 313 | 38 | 71.7 | 420 | 2 | AAQ34090 | Aaq34090 Mycobacte |
| c 241 | 39 | 73.6 | 2112 | 3 | AAA62014 | Aaa62014 Hydrophob | c 314 | 38 | 71.7 | 431 | 6 | ABQ57922 | Abq57922 Human col |
| c 242 | 39 | 73.6 | 2136 | 8 | ABZ24264 | Abz24264 Human SLC | c 315 | 38 | 71.7 | 435 | 6 | ABN17451 | Abn17451 Human ORF |
| c 243 | 39 | 73.6 | 2153 | 4 | AAH17179 | Aah17179 Human cDN | c 316 | 38 | 71.7 | 459 | 3 | RAC08555 | Rac08555 Human sec |
| c 244 | 39 | 73.6 | 2235 | 6 | ABZ13084 | Abz13084 Arabidops | c 317 | 38 | 71.7 | 462 | 9 | ACH28524 | Ach28524 Human adu |
| c 245 | 39 | 73.6 | 2380 | 2 | AAV06355 | Aav06355 AL-2-shor | c 318 | 38 | 71.7 | 486 | 2 | AAQ34091 | Aaq34091 Mycobacte |
| c 246 | 39 | 73.6 | 2493 | 3 | AAA75034 | Aaa75034 DNA encod | c 319 | 38 | 71.7 | 486 | 3 | RAC01882 | Rac01882 Human sec |
| c 247 | 39 | 73.6 | 2501 | 5 | RAC85820 | Rac85820 hOAT2A DN | c 320 | 38 | 71.7 | 505 | 6 | ABN65709 | Abn65709 Human can |
| c 248 | 39 | 73.6 | 2502 | 3 | AAA75035 | Aaa75035 DNA encod | c 321 | 38 | 71.7 | 507 | 8 | ABZ53370 | Abz53370 Aspergill |
| c 249 | 39 | 73.6 | 2704 | 12 | ADQ64839 | Adq64839 Novel hum | c 322 | 38 | 71.7 | 520 | 4 | AAH72956 | Aah72956 Human eer |
| c 250 | 39 | 73.6 | 2788 | 6 | AAI71438 | Aai71438 Human exc | c 323 | 38 | 71.7 | 528 | 6 | ABN65938 | Abn65938 Human can |
| c 251 | 39 | 73.6 | 2855 | 13 | ADS09787 | Ads09787 Human the | c 324 | 38 | 71.7 | 537 | 11 | ADR69872 | Adr69872 Synthetic |
| c 252 | 39 | 73.6 | 2952 | 8 | ADA70942 | Ada70942 Rice gene | c 325 | 38 | 71.7 | 552 | 5 | AAH75734 | Aah75734 DNA encod |
| c 253 | 39 | 73.6 | 2966 | 4 | ABA09274 | Aba09274 Human liv | c 326 | 38 | 71.7 | 564 | 9 | ACH38770 | Ach38770 Human foe |
| c 254 | 39 | 73.6 | 2987 | 8 | ABX12546 | Abx12546 cDNA enco | c 327 | 38 | 71.7 | 579 | 6 | ABN64307 | Abn64307 Human can |
| c 255 | 39 | 73.6 | 3259 | 12 | ADQ25284 | Adq25284 Human sof | c 328 | 38 | 71.7 | 589 | 5 | AAH75735 | Aah75735 DNA encod |
| c 256 | 39 | 73.6 | 3394 | 6 | ABL67235 | Abi67235 Thyroid c | c 329 | 38 | 71.7 | 603 | 10 | ADF00843 | Adf00843 Bacterial |
| c 257 | 39 | 73.6 | 3394 | 8 | ABZ34869 | Abz34869 Coding se | c 330 | 38 | 71.7 | 621 | 8 | AAH54253 | Aah54253 Pseudom |
| c 258 | 39 | 73.6 | 3401 | 10 | ADD49973 | Add49973 Mammalian | c 331 | 38 | 71.7 | 621 | 8 | ACA42564 | ACA42564 Prokaryot |
| c 259 | 39 | 73.6 | 3575 | 11 | ADN95705 | Adn95705 Human BEC | c 332 | 38 | 71.7 | 622 | 10 | ADB50941 | Adb50941 Primary r |
| c 260 | 39 | 73.6 | 3575 | 13 | ADR25499 | Adr25499 Breast ca | c 333 | 38 | 71.7 | 624 | 11 | ABD06206 | Abd06206 Pseudom |
| c 261 | 39 | 73.6 | 4437 | 4 | ABL07784 | Abi07784 Drosophi | c 334 | 38 | 71.7 | 645 | 4 | ABL14295 | Abi14295 Drosophi |
| c 262 | 39 | 73.6 | 7016 | 4 | AAH57552 | Aah57552 Human bra | c 335 | 38 | 71.7 | 650 | 13 | ADQ51198 | Adq51198 Novel can |
| c 263 | 39 | 73.6 | 7016 | 4 | AAH57552 | Aah57552 Human bra | c 336 | 38 | 71.7 | 655 | 4 | AAH57552 | Aah57552 DNA encod |
| c 264 | 39 | 73.6 | 7443 | 13 | ADR84285 | Adr84285 Aspergill | c 337 | 38 | 71.7 | 679 | 13 | ADG88642 | Adg88642 Human hou |
| c 265 | 39 | 73.6 | 12595 | 4 | AAH42100 | Aah42100 Geomirc a | c 338 | 38 | 71.7 | 699 | 11 | ABD09304 | Abd09304 Pseudom |
| c 266 | 39 | 73.6 | 16607 | 4 | AAI04678 | Aai04678 Human rep | c 339 | 38 | 71.7 | 724 | 4 | AAH03782 | Aah03782 Human cDN |
| c 267 | 39 | 73.6 | 16607 | 4 | ABL97585 | Abi97585 Human tes | c 340 | 38 | 71.7 | 730 | 3 | AAA02336 | Aaa02336 Human col |
| c 268 | 39 | 73.6 | 16607 | 5 | ABA18349 | Aba18349 Human ner | c 341 | 38 | 71.7 | 747 | 13 | ADS56559 | Ads56559 Bacterial |
| c 269 | 39 | 73.6 | 22651 | 4 | AAK78202 | Aak78202 Human imm | c 342 | 38 | 71.7 | 753 | 13 | ADS92665 | Ads92665 Chitinase |
| c 270 | 39 | 73.6 | 38596 | 9 | ADA02957 | Ada02957 Mouse Dad | c 343 | 38 | 71.7 | 753 | 13 | ADS92693 | Ads92693 Chitinase |
| c 271 | 39 | 73.6 | 38596 | 10 | ADB72695 | Adb72695 Mouse Dad | c 344 | 38 | 71.7 | 754 | 3 | AAH12578 | Aah12578 Aspergill |
| c 272 | 39 | 73.6 | 38596 | 10 | ADC85437 | Adc85437 Mouse Dad | c 345 | 38 | 71.7 | 754 | 9 | ADA03917 | Ada03917 Human rec |
| c 273 | 39 | 73.6 | 38596 | 12 | ADM74552 | Adm74552 Murine ca | c 346 | 38 | 71.7 | 776 | 4 | AAH08301 | Aah08301 Human cDN |
| c 274 | 39 | 73.6 | 48853 | 13 | ABD33472 | Abd33472 Murine ca | c 347 | 38 | 71.7 | 780 | 13 | ADS92691 | Ads92691 Chitinase |
| c 275 | 39 | 73.6 | 60203 | 10 | ACF65383 | Acf65383 Continuation (5 of | c 348 | 38 | 71.7 | 795 | 10 | ADE28260 | Ade28260 Human MDD |
| c 276 | 39 | 73.6 | 110000 | 2 | AAV30458 | Aav30458 Continuation (5 of | c 349 | 38 | 71.7 | 833 | 9 | ADA03021 | Ada03021 Human RAC |
| c 277 | 39 | 73.6 | 110000 | 2 | AAV30458 | Aav30458 Continuation (5 of | c 350 | 38 | 71.7 | 833 | 10 | ADB72759 | Adb72759 Human RAC |
| c 278 | 39 | 73.6 | 110000 | 8 | ADQ53223 | Adq53223 Human chr | c 351 | 38 | 71.7 | 833 | 10 | ADC85501 | Adc85501 Human RAC |
| c 279 | 39 | 73.6 | 110000 | 10 | ACF67367 | Acf67367 Continuation (6 of | c 352 | 38 | 71.7 | 833 | 12 | ADM74616 | Adm74616 Human car |
| c 280 | 39 | 73.6 | 110000 | 13 | ABD32968 | Abd32968 Human can | c 353 | 38 | 71.7 | 834 | 11 | ABD09039 | Abd09039 Pseudom |
| c 281 | 39 | 73.6 | 112414 | 6 | ABL59091 | Abi59091 Nucleotid | c 354 | 38 | 71.7 | 859 | 12 | ADP13582 | Adp13582 Renal cel |
| c 282 | 39 | 73.6 | 129722 | 6 | ABQ88117 | Abq88117 Human ost | c 355 | 38 | 71.7 | 862 | 12 | ADQ84286 | Adq84286 Human tum |
| c 283 | 39 | 73.6 | 129722 | 12 | ADQ18027 | Adq18027 Human sof | c 356 | 38 | 71.7 | 862 | 12 | ADQ83607 | Adq83607 Human tum |
| c 284 | 39 | 73.6 | 137049 | 11 | ACN44646 | Acn44646 Human gen | c 357 | 38 | 71.7 | 862 | 13 | ADQ84033 | Adq84033 Human tum |
| c 285 | 39 | 73.6 | 157875 | 6 | ABK99972 | Abk99972 Human CAD | c 358 | 38 | 71.7 | 862 | 13 | ADQ85751 | Adq85751 Human tum |
| c 286 | 39 | 73.6 | 167163 | 10 | ADB82948 | Adb82948 Human PVT | c 359 | 38 | 71.7 | 862 | 13 | ADQ86826 | Adq86826 Human tum |
| c 287 | 39 | 73.6 | 313287 | 13 | ABD33100 | Abd33100 Human can | c 360 | 38 | 71.7 | 862 | 13 | ACN40555 | Acn40555 Tumour-as |
| c 288 | 39 | 73.6 | 349980 | 6 | ABQ81846 | Abq81846 Bifidobac | c 361 | 38 | 71.7 | 863 | 12 | ADP03024 | Adp03024 Human hou |
| c 289 | 39 | 73.6 | 349980 | 6 | ABQ81844 | Abq81844 Bifidobac | c 362 | 38 | 71.7 | 863 | 13 | ADS88522 | Ads88522 Human hou |
| c 290 | 38.5 | 72.6 | 38771 | 4 | AAK81036 | Aak81036 Human imm | c 363 | 38 | 71.7 | 894 | 11 | ABD09237 | Abd09237 Pseudom |
| c 291 | 38 | 71.7 | 121 | 3 | AAA45639 | Aaa45639 Human sec | c 364 | 38 | 71.7 | 901 | 13 | ADT07990 | Adt07990 Chicken o |
| c 292 | 38 | 71.7 | 136 | 2 | AAT20688 | Aat20688 Human gen | c 365 | 38 | 71.7 | 901 | 13 | ADS91448 | Ads91448 Fragment |
| c 293 | 38 | 71.7 | 187 | 3 | AAO2341 | Aao2341 Human sec | c 366 | 38 | 71.7 | 901 | 13 | ADT62577 | Adt62577 Chicken o |
| c 294 | 38 | 71.7 | 300 | 3 | AAO2341 | Aao2341 Human col | c 367 | 38 | 71.7 | 902 | 12 | ADI04138 | Adi04138 Chicken o |
| c 295 | 38 | 71.7 | 317 | 6 | ABV88166 | Abv88166 Human col | c 368 | 38 | 71.7 | 912 | 5 | AAH81092 | Aah81092 DNA encod |
| c 296 | 38 | 71.7 | 347 | 11 | ABD06085 | Abd06085 Pseudom | c 369 | 38 | 71.7 | 927 | 13 | ADT47059 | Adt47059 Bacterial |
| c 297 | 38 | 71.7 | 357 | 9 | ACH50288 | Ach50288 Human leu | c 370 | 38 | 71.7 | 939 | 3 | AAH93489 | Aah93489 Human sec |

| | | | | | | | | | | | | | |
|-------|----|------|------|----|-----------|---------------------|-------|----|------|------|----|----------|--------------------|
| c 371 | 38 | 71.7 | 1010 | 5 | AA575736 | AA875736 DNA encod | c 444 | 38 | 71.7 | 2686 | 13 | ADP55714 | Adp55714 Human PRO |
| c 372 | 38 | 71.7 | 1023 | 8 | ACA45475 | ACA45475 Prokaryot | c 445 | 38 | 71.7 | 2737 | 4 | AA05321 | AA05321 Human sec |
| c 373 | 38 | 71.7 | 1024 | 5 | AA545057 | Aa545057 cDNA enco | c 446 | 38 | 71.7 | 2814 | 10 | ADB69912 | Adb69912 C. neofor |
| c 374 | 38 | 71.7 | 1034 | 2 | AAV13052 | AAV13052 pBAR-EDN | c 447 | 38 | 71.7 | 2852 | 4 | ABL14294 | Ab114294 Drosophil |
| c 375 | 38 | 71.7 | 1041 | 13 | ADT43349 | Adt43349 Bacterial | c 448 | 38 | 71.7 | 2853 | 10 | ADB69551 | Adb69551 C. neofor |
| c 376 | 38 | 71.7 | 1050 | 13 | ADT44326 | Adt44326 Bacterial | c 449 | 38 | 71.7 | 2865 | 8 | ACA45858 | ACA45858 Prokaryot |
| c 377 | 38 | 71.7 | 1052 | 5 | AA545245 | Aa545245 cDNA enco | c 450 | 38 | 71.7 | 2879 | 4 | ABL27160 | Ab127160 Drosophil |
| c 378 | 38 | 71.7 | 1059 | 3 | AAA16661 | AAa16661 Human sec | c 451 | 38 | 71.7 | 3011 | 2 | AAV64132 | AAv64132 Drosophil |
| c 379 | 38 | 71.7 | 1134 | 4 | ABL07379 | Ab107379 Drosophil | c 452 | 38 | 71.7 | 3171 | 6 | ABK92214 | Abk92214 Prostata |
| c 380 | 38 | 71.7 | 1176 | 11 | ABD08967 | ABd08967 Pseudomon | c 453 | 38 | 71.7 | 3171 | 6 | ABN89393 | Abn89393 Human P-C |
| c 381 | 38 | 71.7 | 1197 | 5 | AAH74574 | AaH74574 Nucleotid | c 454 | 38 | 71.7 | 3171 | 6 | ABT07755 | Abt07755 Breast ca |
| c 382 | 38 | 71.7 | 1197 | 5 | AAH74575 | AaH74575 Nucleotid | c 455 | 38 | 71.7 | 3171 | 6 | ABK52038 | Abk52038 DNA encod |
| c 383 | 38 | 71.7 | 1197 | 5 | AAH74548 | AaH74548 Nucleotid | c 456 | 38 | 71.7 | 3171 | 6 | ABN97264 | Abn97264 Gene #376 |
| c 384 | 38 | 71.7 | 1197 | 13 | ADS58238 | AdS58238 Bacterial | c 457 | 38 | 71.7 | 3171 | 8 | ABZ24736 | Abz24736 Human P-C |
| c 385 | 38 | 71.7 | 1260 | 2 | AA50964 | AA50964 Pseudomon | c 458 | 38 | 71.7 | 3171 | 10 | ADD14795 | Add14795 Human src |
| c 386 | 38 | 71.7 | 1260 | 2 | AA039009 | Aa039009 Methionin | c 459 | 38 | 71.7 | 3171 | 10 | ACA56750 | ACA56750 Human sig |
| c 387 | 38 | 71.7 | 1279 | 2 | AA84990 | Aa84990 Human sec | c 460 | 38 | 71.7 | 3171 | 11 | ADN39464 | Adn39464 Cancer/an |
| c 388 | 38 | 71.7 | 1279 | 8 | ACD18916 | ACd18916 Novel hum | c 461 | 38 | 71.7 | 3171 | 11 | ADN39577 | Adn39577 Cancer/an |
| c 389 | 38 | 71.7 | 1279 | 12 | ADG78307 | Adg78307 Human sec | c 462 | 38 | 71.7 | 3171 | 11 | ADN39544 | Adn39544 Cancer/an |
| c 390 | 38 | 71.7 | 1279 | 12 | ADN60598 | Adn60598 Human sec | c 463 | 38 | 71.7 | 3171 | 11 | ADN39481 | Adn39481 Cancer/an |
| c 391 | 38 | 71.7 | 1299 | 2 | AAV63620 | AAv63620 Nucleic a | c 464 | 38 | 71.7 | 3171 | 12 | ADJ56546 | Adj56546 Human pol |
| c 392 | 38 | 71.7 | 1299 | 2 | AAZ03862 | AaZ03862 pET-11d-E | c 465 | 38 | 71.7 | 3171 | 12 | ADL06487 | Adl06487 Human tum |
| c 393 | 38 | 71.7 | 1320 | 2 | AA185643 | Aa185643 DNA encod | c 466 | 38 | 71.7 | 3171 | 12 | ADQ20014 | Adq20014 Human sof |
| c 394 | 38 | 71.7 | 1338 | 8 | AA49078 | AA49078 Thraustoc | c 467 | 38 | 71.7 | 3171 | 13 | ADR24808 | Adr24808 Breast ca |
| c 395 | 38 | 71.7 | 1367 | 13 | ABD33194 | ABd33194 Murine ca | c 468 | 38 | 71.7 | 3183 | 12 | ADO00912 | Ado00912 Human hom |
| c 396 | 38 | 71.7 | 1369 | 2 | AA511369 | AA511369 P. putida | c 469 | 38 | 71.7 | 3194 | 4 | ABA09022 | AbA09022 Human FGF |
| c 397 | 38 | 71.7 | 1369 | 2 | AA511370 | AA511370 P. putida | c 470 | 38 | 71.7 | 3194 | 4 | AAK52458 | AAk52458 Human pol |
| c 398 | 38 | 71.7 | 1369 | 2 | AA232211 | Aa232211 P. putida | c 471 | 38 | 71.7 | 3205 | 6 | ABQ81547 | Abq81547 Gene up-r |
| c 399 | 38 | 71.7 | 1369 | 2 | AA28097 | Aa28097 Methionin | c 472 | 38 | 71.7 | 3205 | 8 | ABX76155 | Abx76155 Lung canc |
| c 400 | 38 | 71.7 | 1387 | 13 | ADS48911 | AdS48911 Bacterial | c 473 | 38 | 71.7 | 3205 | 8 | ABX76399 | Abx76399 Lung canc |
| c 401 | 38 | 71.7 | 1416 | 4 | ABL30503 | Ab130503 Drosophil | c 474 | 38 | 71.7 | 3205 | 10 | ACC72821 | Acc72821 Human can |
| c 402 | 38 | 71.7 | 1417 | 3 | AA26301 | AA26301 Human sec | c 475 | 38 | 71.7 | 3205 | 11 | ADN39711 | Adn39711 Cancer/an |
| c 403 | 38 | 71.7 | 1417 | 8 | ADA33975 | AdA33975 Human sec | c 476 | 38 | 71.7 | 3205 | 11 | ADN39019 | Adn39019 Cancer/an |
| c 404 | 38 | 71.7 | 1417 | 8 | ACC50537 | ACc50537 Human sec | c 477 | 38 | 71.7 | 3205 | 12 | ADL70220 | Adl70220 Colon can |
| c 405 | 38 | 71.7 | 1417 | 10 | ADC73600 | Adc73600 Human sec | c 478 | 38 | 71.7 | 3205 | 12 | ADN59612 | Adn59612 Colon neo |
| c 406 | 38 | 71.7 | 1417 | 10 | ADD37635 | AdD37635 Human sec | c 479 | 38 | 71.7 | 3205 | 12 | ADN03947 | Adn03947 Antipsori |
| c 407 | 38 | 71.7 | 1417 | 10 | ADA56163 | AdA56163 Gene enco | c 480 | 38 | 71.7 | 3205 | 12 | ADO28656 | Ado28656 Human CAD |
| c 408 | 38 | 71.7 | 1425 | 6 | AA242497 | AA242497 t(2;22) t | c 481 | 38 | 71.7 | 3205 | 12 | ADP26910 | Adp26910 Human P-C |
| c 409 | 38 | 71.7 | 1427 | 6 | ABK34855 | ABk34855 Human cDN | c 482 | 38 | 71.7 | 3206 | 4 | AAH99681 | AaH99681 Human pro |
| c 410 | 38 | 71.7 | 1427 | 6 | ABK13115 | ABk13115 Human sec | c 483 | 38 | 71.7 | 3219 | 6 | AA27637 | AA27637 Human col |
| c 411 | 38 | 71.7 | 1427 | 6 | ABK13115 | ABk13115 Human sec | c 484 | 38 | 71.7 | 3266 | 12 | ADQ24084 | Adq24084 Human sof |
| c 412 | 38 | 71.7 | 1461 | 10 | ADD71204 | AdD71204 Human int | c 485 | 38 | 71.7 | 3281 | 2 | AAV64133 | AAv64133 Drosophil |
| c 413 | 38 | 71.7 | 1483 | 6 | ABZ35390 | ABz35390 Human enco | c 486 | 38 | 71.7 | 3578 | 4 | ABL30502 | Ab130502 Drosophil |
| c 414 | 38 | 71.7 | 1484 | 5 | AA545022 | Aa545022 cDNA enco | c 487 | 38 | 71.7 | 3599 | 4 | AA056638 | AA056638 Human sec |
| c 415 | 38 | 71.7 | 1516 | 11 | ADN95655 | Adn95655 Human BEC | c 488 | 38 | 71.7 | 3599 | 4 | AD085058 | Ad085058 Human sec |
| c 416 | 38 | 71.7 | 1520 | 2 | AA34093 | Aa34093 Mycobacte | c 489 | 38 | 71.7 | 3599 | 9 | ADB91447 | Adb91447 Human sec |
| c 417 | 38 | 71.7 | 1608 | 4 | AA523120 | AA523120 DNA encod | c 490 | 38 | 71.7 | 3599 | 10 | ADA56704 | Ada56704 Gene enco |
| c 418 | 38 | 71.7 | 1632 | 3 | AAZ55789 | AaZ55789 cDNA enco | c 491 | 38 | 71.7 | 3632 | 13 | ADR44020 | Adr44020 Human col |
| c 419 | 38 | 71.7 | 1686 | 9 | ADB06255 | AdB06255 Alloioococ | c 492 | 38 | 71.7 | 3665 | 4 | AA08490 | AA08490 Human sec |
| c 420 | 38 | 71.7 | 1753 | 2 | AAV04456 | AAv04456 Replicati | c 493 | 38 | 71.7 | 3763 | 4 | AAH16650 | AaH16650 Human cDN |
| c 421 | 38 | 71.7 | 1781 | 4 | AA506728 | AA506728 Polynucle | c 494 | 38 | 71.7 | 3777 | 9 | ACH03801 | Ach03801 Human cDN |
| c 422 | 38 | 71.7 | 1901 | 3 | AAZ44679 | AaZ44679 Rac liver | c 495 | 38 | 71.7 | 3884 | 10 | ADD24906 | Add24906 DNA encod |
| c 423 | 38 | 71.7 | 1910 | 10 | ADB57944 | AdB57944 Toxicity- | c 496 | 38 | 71.7 | 3906 | 10 | ADB69190 | Adb69190 C. neofor |
| c 424 | 38 | 71.7 | 1910 | 10 | ADB53450 | AdB53450 Primary r | c 497 | 38 | 71.7 | 3986 | 5 | ABV28780 | Abv28780 Human pro |
| c 425 | 38 | 71.7 | 1959 | 8 | ACA26531 | ACA26531 Prokaryot | c 498 | 38 | 71.7 | 3986 | 5 | ABV22948 | Abv22948 Human pro |
| c 426 | 38 | 71.7 | 1992 | 8 | ADA70741 | AdA70741 Rice gene | c 499 | 38 | 71.7 | 3989 | 10 | ADA53410 | Ada53410 Human cod |
| c 427 | 38 | 71.7 | 1992 | 9 | ADA48621 | AdA48621 Rice gene | c 500 | 38 | 71.7 | 4100 | 4 | AA527115 | Aa527115 cDNA enco |
| c 428 | 38 | 71.7 | 2000 | 6 | ABZ15274 | ABz15274 Arabidops | c 501 | 38 | 71.7 | 4100 | 10 | ADP93293 | Adp93293 Human cDN |
| c 429 | 38 | 71.7 | 2028 | 9 | ADA48343 | AdA48343 Rice gene | c 502 | 38 | 71.7 | 4112 | 6 | ABZ11824 | Abz11824 Human pol |
| c 430 | 38 | 71.7 | 2076 | 13 | ADT48722 | Adt48722 Bacterial | c 503 | 38 | 71.7 | 4112 | 12 | ADM44342 | Adm44342 Novel hum |
| c 431 | 38 | 71.7 | 2100 | 12 | ADP28102 | Adp28102 Human sec | c 504 | 38 | 71.7 | 4177 | 10 | ADE54313 | Ad54313 Human gen |
| c 432 | 38 | 71.7 | 2100 | 12 | ADP28195 | Adp28195 Human sec | c 505 | 38 | 71.7 | 4177 | 10 | ADE54317 | Ad54317 Human gen |
| c 433 | 38 | 71.7 | 2151 | 4 | ABL03193 | Ab103193 Drosophil | c 506 | 38 | 71.7 | 4217 | 6 | ABT10142 | Abt10142 Human bre |
| c 434 | 38 | 71.7 | 2316 | 11 | ABD08346 | ABd08346 Pseudomon | c 507 | 38 | 71.7 | 4217 | 10 | ADD67641 | Add67641 Human Ly6 |
| c 435 | 38 | 71.7 | 2364 | 8 | ABX63037 | ABx63037 Human cDN | c 508 | 38 | 71.7 | 4217 | 12 | ADQ21677 | Adq21677 Human sof |
| c 436 | 38 | 71.7 | 2379 | 4 | AAH15341 | AaH15341 Human cDN | c 509 | 38 | 71.7 | 4217 | 13 | ADR52722 | Adr52722 Drug ther |
| c 437 | 38 | 71.7 | 2412 | 13 | ADS55593 | AdS55593 Bacterial | c 510 | 38 | 71.7 | 4220 | 4 | ABL03192 | Ab103192 Drosophil |
| c 438 | 38 | 71.7 | 2412 | 13 | ADS550078 | AdS550078 Bacterial | c 511 | 38 | 71.7 | 4441 | 6 | ABX92073 | Abx92073 Lung spec |
| c 439 | 38 | 71.7 | 2433 | 4 | ABL04033 | Ab104033 Drosophil | c 512 | 38 | 71.7 | 4458 | 4 | AAI60755 | Aai60755 Human pol |
| c 440 | 38 | 71.7 | 2451 | 8 | ACA44102 | ACA44102 Prokaryot | c 513 | 38 | 71.7 | 4492 | 3 | AAI77245 | Aai77245 Human ORF |
| c 441 | 38 | 71.7 | 2530 | 5 | AA588011 | AA588011 DNA encod | c 514 | 38 | 71.7 | 4494 | 4 | AAI58969 | Aai58969 Human pol |
| c 442 | 38 | 71.7 | 2624 | 4 | AAI13348 | AAI13348 Human sec | c 515 | 38 | 71.7 | 4494 | 5 | ADQ99191 | Adq99191 DNA encod |
| c 443 | 38 | 71.7 | 2660 | 13 | ADR14030 | Adr14030 Human NF- | c 516 | 38 | 71.7 | 4494 | 9 | ADB48951 | Adb48951 Novel hum |

| | | | | | | | | | | | | | |
|-----|----|------|-------|----|----------|---------------------|-------|------|------|--------|----|----------|---------------------|
| 517 | 38 | 71.7 | 4520 | 4 | ABL09423 | Ab109423 Drosophila | 590 | 38 | 71.7 | 13255 | 8 | ADA41522 | Ada41522 Human sec |
| 518 | 38 | 71.7 | 4559 | 4 | AB118477 | Ab118477 Drosophila | 591 | 38 | 71.7 | 13255 | 10 | ADA57647 | Ada57647 BAC fragm |
| 519 | 38 | 71.7 | 4603 | 4 | AB104032 | Ab104032 Drosophila | c 592 | 38 | 71.7 | 14919 | 4 | AA163992 | AA163992 Human pol |
| 520 | 38 | 71.7 | 4615 | 2 | AAQ70724 | Aaq70724 TATA-bind | c 593 | 38 | 71.7 | 14919 | 4 | AA331670 | AA331670 Genomic s |
| 521 | 38 | 71.7 | 4615 | 2 | AAQ72210 | Aaq72210 Drosophila | c 594 | 38 | 71.7 | 14919 | 12 | ADM24707 | Adm24707 Human PRO |
| 522 | 38 | 71.7 | 4615 | 2 | AAQ79604 | Aaq79604 TATA-bind | c 595 | 38 | 71.7 | 17874 | 4 | AAK71070 | AAK71070 Human imm |
| 523 | 38 | 71.7 | 4625 | 4 | ABL07378 | Ab107378 Drosophila | c 596 | 38 | 71.7 | 19632 | 4 | AAK66943 | AAK66943 Human imm |
| 524 | 38 | 71.7 | 4934 | 5 | ADL45192 | Adl45192 Human ova | 597 | 38 | 71.7 | 23416 | 4 | ABL26670 | Ab126670 Drosophila |
| 525 | 38 | 71.7 | 4940 | 6 | ABX92006 | Abx92006 Lung spec | c 598 | 38 | 71.7 | 27204 | 11 | ACN44866 | Acn44866 Human gen |
| 526 | 38 | 71.7 | 5076 | 12 | ADH56432 | Adh56432 Human hyp | c 599 | 38 | 71.7 | 28564 | 10 | ADE63609 | Ad663609 Human gen |
| 527 | 38 | 71.7 | 5140 | 3 | AAZ29679 | Aaz29679 N. tabacu | 600 | 38 | 71.7 | 28829 | 13 | ABD33193 | Abd33193 Murine ca |
| 528 | 38 | 71.7 | 5140 | 6 | AB158338 | Ab158338 N. tabacu | c 601 | 38 | 71.7 | 30001 | 2 | AA61016 | AA61016 Total DNA |
| 529 | 38 | 71.7 | 5203 | 6 | ABL60880 | Ab160880 Human cyt | c 602 | 38 | 71.7 | 30001 | 2 | AA605110 | AA605110 S. aureof |
| 530 | 38 | 71.7 | 5345 | 4 | AA527696 | Aa527696 DNA encod | 603 | 38 | 71.7 | 31422 | 3 | AAA92302 | AAa92302 S. averm |
| 531 | 38 | 71.7 | 5345 | 4 | ABK42842 | Abk42842 Genomic s | 604 | 38 | 71.7 | 31422 | 3 | AAH79278 | AAh79278 Streptomy |
| 532 | 38 | 71.7 | 5345 | 4 | ADM20212 | Adm20212 Alternati | 605 | 38 | 71.7 | 32199 | 4 | AAK90296 | AAk90296 Human dig |
| 533 | 38 | 71.7 | 5345 | 9 | ADB60998 | Adb60998 Connectiv | 606 | 38 | 71.7 | 32199 | 4 | AA157673 | AA157673 Human col |
| 534 | 38 | 71.7 | 5345 | 10 | ADB94499 | Adb94499 Novel hum | 607 | 38 | 71.7 | 32199 | 6 | ABS99850 | ABs99850 Genomic D |
| 535 | 38 | 71.7 | 5385 | 12 | ADQ23484 | Adq23484 Human sof | 608 | 38 | 71.7 | 32199 | 10 | ADB93003 | Adb93003 Human col |
| 536 | 38 | 71.7 | 5748 | 3 | AAQ76580 | Aaq76580 Human ORF | 609 | 38 | 71.7 | 33481 | 4 | ABL04906 | Ab104906 Drosophila |
| 537 | 38 | 71.7 | 6132 | 10 | AD507519 | Ad507519 Novel cod | 610 | 38 | 71.7 | 38734 | 2 | AAZ32020 | AAz32020 Human MET |
| 538 | 38 | 71.7 | 6195 | 8 | ABZ74127 | Abz74127 Secreted | 611 | 38 | 71.7 | 38734 | 5 | AAQ90077 | AAq90077 AL021529 |
| 539 | 38 | 71.7 | 6195 | 8 | ADA98554 | Ada98554 Human sec | 612 | 38 | 71.7 | 38764 | 9 | ADA03020 | Ada03020 Human RAC |
| 540 | 38 | 71.7 | 6195 | 8 | ADA44292 | Ada44292 Human sec | 613 | 38 | 71.7 | 38764 | 10 | ADB72758 | Adb72758 Human RAC |
| 541 | 38 | 71.7 | 6195 | 10 | ADC20671 | Adc20671 Human sec | 614 | 38 | 71.7 | 38764 | 10 | ADC85500 | Adc85500 Human Rac |
| 542 | 38 | 71.7 | 6195 | 10 | ADC20782 | Adc20782 Human sec | 615 | 38 | 71.7 | 38764 | 12 | ADM74615 | Adm74615 Human car |
| 543 | 38 | 71.7 | 6195 | 10 | ADF10864 | Adf10864 Human sec | 616 | 38 | 71.7 | 43633 | 12 | ADQ59425 | Adq59425 Human can |
| 544 | 38 | 71.7 | 6234 | 2 | AAV64131 | Aav64131 St-H segm | 617 | 38 | 71.7 | 44242 | 4 | ABL11930 | Ab11930 Drosophila |
| 545 | 38 | 71.7 | 6240 | 4 | ABL06443 | Ab106443 Drosophila | c 618 | 38 | 71.7 | 46050 | 10 | ABX13974 | Abx13974 Human Ras |
| 546 | 38 | 71.7 | 6248 | 4 | AAH98460 | Aah98460 Murine ES | c 619 | 38 | 71.7 | 46275 | 6 | ABT10145 | Abt10145 Human bre |
| 547 | 38 | 71.7 | 6490 | 12 | ADJ27244 | Adj27244 Human TRI | c 620 | 38 | 71.7 | 46275 | 6 | ABT10145 | Abt10145 Human bre |
| 548 | 38 | 71.7 | 6625 | 6 | ABS67779 | Abs67779 Human rec | c 621 | 38 | 71.7 | 52479 | 9 | ADA02795 | Ada02795 Mouse Tnf |
| 549 | 38 | 71.7 | 6663 | 6 | ABL92102 | Ab192102 Human Tum | c 622 | 38 | 71.7 | 52479 | 10 | ADB72533 | Adb72533 Mouse Tnf |
| 550 | 38 | 71.7 | 6702 | 10 | ADA72027 | Ada72027 DNA encod | c 623 | 38 | 71.7 | 52479 | 10 | ADC85275 | Adc85275 Mouse Tnf |
| 551 | 38 | 71.7 | 6702 | 10 | ADN19207 | Adn19207 Human ins | c 624 | 38 | 71.7 | 52479 | 12 | ADM74390 | Adm74390 Murine ca |
| 552 | 38 | 71.7 | 6702 | 12 | ADN04791 | Adn04791 Antipeori | c 625 | 38 | 71.7 | 52479 | 11 | ACN44396 | Acn44396 Mouse gen |
| 553 | 38 | 71.7 | 6702 | 12 | ADQ07978 | Adq07978 Human tum | c 626 | 38 | 71.7 | 66681 | 13 | ABD33333 | Abd33333 Murine ca |
| 554 | 38 | 71.7 | 6702 | 13 | ACN38608 | Acn38608 Tumour-as | c 627 | 38 | 71.7 | 68196 | 13 | ABD32800 | Abd32800 Human can |
| 555 | 38 | 71.7 | 6702 | 13 | ADP24833 | Adp24833 PRO poly | c 628 | 38 | 71.7 | 80557 | 6 | ABX09142 | Abx09142 Mycobacte |
| 556 | 38 | 71.7 | 6729 | 4 | ADQ05595 | Adq05595 Human sec | 629 | 38 | 71.7 | 95001 | 12 | ADH56439 | Adh56439 Human hyp |
| 557 | 38 | 71.7 | 6729 | 9 | ADB91309 | Adb91309 Human sec | 630 | 38 | 71.7 | 100608 | 13 | ABD32769 | Abd32769 Human can |
| 558 | 38 | 71.7 | 6729 | 10 | ADA56398 | Ada56398 Gene enco | 631 | 38 | 71.7 | 109453 | 13 | ABD32728 | Abd32728 Mouse can |
| 559 | 38 | 71.7 | 6756 | 2 | AAQ11174 | Aaq11174 Sequence, | 632 | 38 | 71.7 | 110000 | 4 | AA199682 | AA199682_18 |
| 560 | 38 | 71.7 | 6756 | 2 | AAQ11174 | Aaq11174 Aspergill | c 633 | 38 | 71.7 | 110000 | 4 | AA199682 | AA199682_28 |
| 561 | 38 | 71.7 | 6756 | 8 | ABX13436 | Abx13436 Plasmid | 634 | 38 | 71.7 | 110000 | 4 | AA199683 | AA199683_18 |
| 562 | 38 | 71.7 | 6759 | 2 | AAV63619 | Aav63619 Nucleic a | c 635 | 38 | 71.7 | 110000 | 4 | AA199683 | AA199683_28 |
| 563 | 38 | 71.7 | 6799 | 2 | AAZ09861 | Aaz09861 pET-11d-E | c 636 | 38 | 71.7 | 110000 | 9 | ADB12064 | ADB12064_00 |
| 564 | 38 | 71.7 | 7080 | 2 | AAV33621 | Aav33621 Plasmid p | c 637 | 38 | 71.7 | 110000 | 11 | ADM27081 | ADM27081_13 |
| 565 | 38 | 71.7 | 7389 | 4 | AA527788 | Aa527788 DNA encod | c 638 | 38 | 71.7 | 110000 | 12 | ADN46845 | ADN46845_10 |
| 566 | 38 | 71.7 | 7389 | 10 | ADB94591 | Adb94591 Novel hum | 639 | 38 | 71.7 | 110000 | 12 | ADN47591 | ADN47591_10 |
| 567 | 38 | 71.7 | 9525 | 4 | ABL09422 | Ab109422 Drosophila | c 640 | 38 | 71.7 | 110000 | 12 | ADN46123 | ADN46123_10 |
| 568 | 38 | 71.7 | 9678 | 12 | AD104103 | Ad104103 Vector pt | 641 | 38 | 71.7 | 110000 | 12 | ADN47209 | ADN47209_10 |
| 569 | 38 | 71.7 | 9933 | 4 | ABL06442 | Ab106442 Drosophila | c 642 | 38 | 71.7 | 110000 | 12 | ADN46464 | ADN46464_10 |
| 570 | 38 | 71.7 | 10083 | 4 | ABL18476 | Ab118476 Drosophila | c 643 | 38 | 71.7 | 110000 | 12 | ADN47960 | ADN47960_10 |
| 571 | 38 | 71.7 | 10297 | 12 | AD104127 | Ad104127 Vector pt | 644 | 38 | 71.7 | 110000 | 13 | ABD32721 | ABD32721_0 |
| 572 | 38 | 71.7 | 10297 | 13 | ADT08018 | Adt08018 Transposo | c 645 | 38 | 71.7 | 122614 | 11 | ACN44998 | Acn44998 Human gen |
| 573 | 38 | 71.7 | 10401 | 12 | ADJ81642 | Adj81642 Human tyr | 646 | 38 | 71.7 | 128668 | 11 | ACN44074 | Acn44074 Human gen |
| 574 | 38 | 71.7 | 10512 | 12 | AD104129 | Ad104129 Vector pt | c 647 | 38 | 71.7 | 131239 | 12 | ADQ21179 | Adq21179 Human sof |
| 575 | 38 | 71.7 | 10512 | 13 | ADT08015 | Adt08015 Transposo | c 648 | 38 | 71.7 | 14723 | 11 | ACN44898 | Acn44898 Human gen |
| 576 | 38 | 71.7 | 11101 | 6 | ABN83947 | Abn83947 Human tra | c 649 | 38 | 71.7 | 212331 | 11 | ACN44598 | Acn44598 Human gen |
| 577 | 38 | 71.7 | 11308 | 8 | AA59625 | Aa59625 Propionib | c 650 | 38 | 71.7 | 247461 | 13 | ABD33153 | Abd33153 Murine ca |
| 578 | 38 | 71.7 | 11308 | 8 | ACF64554 | Acf64554 Propionib | 651 | 38 | 71.7 | 299598 | 12 | ADQ59380 | Adq59380 Human can |
| 579 | 38 | 71.7 | 11332 | 12 | AD104141 | Ad104141 Vector pt | c 652 | 38 | 71.7 | 312477 | 12 | ADP69744 | Adp69744 Human ROC |
| 580 | 38 | 71.7 | 11964 | 13 | ADT62603 | Adt62603 Transposo | c 653 | 38 | 71.7 | 321491 | 11 | ACN44202 | Acn44202 Human gen |
| 581 | 38 | 71.7 | 11964 | 13 | ADT62603 | Adt62603 Transposo | c 654 | 38 | 71.7 | 32602 | 13 | ABD32843 | Abd32843 Human can |
| 582 | 38 | 71.7 | 11967 | 13 | ADT62604 | Adt62604 Transposo | c 655 | 37.5 | 70.8 | 777 | 6 | ABQ55513 | ABq55513 Human ova |
| 583 | 38 | 71.7 | 11967 | 13 | ADT62604 | Adt62604 Transposo | c 656 | 37.5 | 70.8 | 3624 | 12 | ADO28604 | Ado28604 Human myo |
| 584 | 38 | 71.7 | 12155 | 4 | ABL06990 | Ab106990 Drosophila | c 657 | 37.5 | 70.8 | 5043 | 10 | ADC27727 | Adc27727 Human col |
| 585 | 38 | 71.7 | 12339 | 13 | ADT62607 | Adt62607 Transposo | c 658 | 37.5 | 70.8 | 5046 | 10 | ADC27640 | Adc27640 Human col |
| 586 | 38 | 71.7 | 12339 | 13 | ADT62607 | Adt62607 Transposo | c 659 | 37.5 | 70.8 | 29871 | 13 | ADS36480 | Ad36480 Human aut |
| 587 | 38 | 71.7 | 12342 | 13 | ADS91479 | Ad91479 Transposo | 660 | 37.5 | 70.8 | 321019 | 13 | ADS36450 | Ad36450 Human aut |
| 588 | 38 | 71.7 | 12342 | 13 | ADS91479 | Ad91479 Transposo | 661 | 37.5 | 70.8 | 329019 | 13 | ADS32707 | Ad32707 Human can |
| 589 | 38 | 71.7 | 12355 | 4 | AAK76842 | Aak76842 Human imm | c 662 | 37 | 69.8 | 55 | 2 | AAQ41963 | AAq41963 Ig delta |

| | | | | | | | | | | | | | |
|-------|----|------|-----|----|-----------|---------------------|-------|----|------|-----|----|-----------|---------------------|
| 663 | 37 | 69.8 | 84 | 12 | ADP22732 | Adp22732 Human HAR | 736 | 37 | 69.8 | 507 | 2 | AAQ20697 | AaQ20697 OSF.1 gen |
| 664 | 37 | 69.8 | 153 | 4 | AAI22253 | Aai22253 Probe #12 | 737 | 37 | 69.8 | 507 | 3 | AAZ91785 | Aaz91785 Human PTN |
| 665 | 37 | 69.8 | 153 | 4 | ABA67331 | Aba67331 Human foe | 738 | 37 | 69.8 | 513 | 4 | Aai70201 | Aai70201 Human ple |
| 666 | 37 | 69.8 | 153 | 4 | AAI47545 | Aai47545 Probe #16 | 739 | 37 | 69.8 | 513 | 5 | AAF85304 | Aaf85304 Nucleotid |
| 667 | 37 | 69.8 | 153 | 4 | ABA49419 | Aba49419 Human bre | c 740 | 37 | 69.8 | 567 | 12 | ACH69875 | Ach69875 Human gen |
| 668 | 37 | 69.8 | 153 | 4 | ABA34422 | Aba34422 Probe #12 | c 741 | 37 | 69.8 | 582 | 4 | Aai18338 | Aai18338 Probe #82 |
| 669 | 37 | 69.8 | 153 | 4 | AAK41505 | Aak41505 Human bra | c 742 | 37 | 69.8 | 582 | 4 | ABA63339 | Aba63339 Human foe |
| 670 | 37 | 69.8 | 153 | 4 | AAK15764 | Aak15764 Human bon | c 743 | 37 | 69.8 | 582 | 4 | Aai143453 | Aai143453 Probe #12 |
| 671 | 37 | 69.8 | 153 | 4 | ABA41094 | Aba41094 Human liv | c 744 | 37 | 69.8 | 582 | 4 | ABA30543 | Aba30543 Probe #90 |
| 672 | 37 | 69.8 | 153 | 5 | AAI07950 | Aai07950 Probe #79 | c 745 | 37 | 69.8 | 582 | 4 | AAK37582 | Aak37582 Human bon |
| 673 | 37 | 69.8 | 153 | 6 | ABS15510 | Abs15510 Human gen | c 746 | 37 | 69.8 | 582 | 4 | AAK11881 | Aak11881 Human bra |
| 674 | 37 | 69.8 | 198 | 12 | ACH85073 | Ach85073 Human gen | c 747 | 37 | 69.8 | 582 | 4 | ABS37242 | Abs37242 Human liv |
| 675 | 37 | 69.8 | 222 | 4 | AAK44202 | Aak44202 Human bon | c 748 | 37 | 69.8 | 582 | 6 | ABS11567 | Abs11567 Human gen |
| 676 | 37 | 69.8 | 222 | 4 | ABS43859 | Abs43859 Human liv | 749 | 37 | 69.8 | 583 | 12 | ACH78772 | Ach78772 Human gen |
| 677 | 37 | 69.8 | 222 | 6 | ABS18438 | Abs18438 Human gen | c 750 | 37 | 69.8 | 595 | 5 | AAH82488 | Aah82488 Human ova |
| 678 | 37 | 69.8 | 259 | 3 | AAAI0181 | Aaai0181 Rat liver | 751 | 37 | 69.8 | 596 | 12 | ACH71317 | Ach71317 Human gen |
| 679 | 37 | 69.8 | 280 | 10 | ABX86931 | Abx86931 Corn ear- | c 752 | 37 | 69.8 | 600 | 5 | ADL44070 | Adl44070 Human ova |
| c 680 | 37 | 69.8 | 297 | 9 | ADA58057 | Ada58057 Maize fru | c 753 | 37 | 69.8 | 603 | 6 | ABQ55800 | Abq55800 Human ova |
| c 681 | 37 | 69.8 | 297 | 12 | ADP60854 | Adp60854 Maize car | 754 | 37 | 69.8 | 604 | 8 | ABX71006 | Abx71006 Novel hum |
| 682 | 37 | 69.8 | 304 | 2 | AAV63639 | Aav63639 Contig 35 | 755 | 37 | 69.8 | 607 | 13 | ACN47396 | Acn47396 Cotton pr |
| 683 | 37 | 69.8 | 304 | 2 | AAK00906 | Aak00906 Human des | 756 | 37 | 69.8 | 618 | 5 | AAS91283 | Aas91283 DNA encod |
| 684 | 37 | 69.8 | 304 | 2 | AAV82638 | Aav82638 Contig 35 | c 757 | 37 | 69.8 | 654 | 5 | AAS76099 | Aas76099 DNA encod |
| 685 | 37 | 69.8 | 304 | 3 | AAA14590 | Aaa14590 Nucleotid | c 758 | 37 | 69.8 | 665 | 5 | ADI72547 | Adi72547 Human ova |
| 686 | 37 | 69.8 | 304 | 3 | AAA09449 | Aaa09449 Human con | c 759 | 37 | 69.8 | 665 | 5 | ADL37686 | Adl37686 Human ova |
| 687 | 37 | 69.8 | 304 | 3 | AAA49935 | Aaa49935 Human del | c 760 | 37 | 69.8 | 696 | 8 | ACF39378 | Acf39378 Mycobacte |
| 688 | 37 | 69.8 | 304 | 6 | ABS76709 | Abs76709 Human des | c 761 | 37 | 69.8 | 699 | 11 | ABD12355 | Abd12355 Pseudomon |
| 689 | 37 | 69.8 | 304 | 6 | ABS71822 | Abs71822 Human del | c 762 | 37 | 69.8 | 705 | 8 | ADA50534 | Ada50534 Human pro |
| c 690 | 37 | 69.8 | 327 | 2 | AAI68134 | Aai68134 H. pylori | c 763 | 37 | 69.8 | 711 | 4 | AAH04911 | Aah04911 Human cDN |
| 691 | 37 | 69.8 | 333 | 4 | ABK41734 | Abk41734 cDNA enco | c 764 | 37 | 69.8 | 714 | 2 | AAZ06674 | Aaz06674 Pig Facto |
| 692 | 37 | 69.8 | 333 | 9 | ADB59401 | Adb59401 Connectiv | c 765 | 37 | 69.8 | 725 | 12 | ACH87523 | Ach87523 Human gen |
| 693 | 37 | 69.8 | 392 | 2 | AAV68572 | Aav68572 Partial h | 766 | 37 | 69.8 | 730 | 4 | AAK82227 | Aak82227 Human imm |
| c 694 | 37 | 69.8 | 394 | 5 | AAS66625 | Aas66625 DNA encod | c 767 | 37 | 69.8 | 738 | 2 | AAK30478 | Aak30478 H. pylori |
| c 695 | 37 | 69.8 | 395 | 10 | ADD33825 | Add33825 Mouse mit | 768 | 37 | 69.8 | 753 | 12 | ACH92032 | Ach92032 Human gen |
| 696 | 37 | 69.8 | 401 | 6 | ABN25585 | Abn25585 Human ORF | 769 | 37 | 69.8 | 760 | 4 | AAK93705 | Aak93705 Human cDN |
| 697 | 37 | 69.8 | 401 | 12 | ADP91287 | Adp91287 Cotton ex | 770 | 37 | 69.8 | 760 | 12 | ADL30132 | Adl30132 3' end of |
| 698 | 37 | 69.8 | 410 | 9 | ACH31241 | Ach31241 Human bon | 771 | 37 | 69.8 | 774 | 4 | AAH05182 | Aah05182 Human cDN |
| c 699 | 37 | 69.8 | 412 | 6 | ABQ98404 | Abq98404 Human ORF | 772 | 37 | 69.8 | 783 | 2 | AAV69512 | Aav69512 Banana fr |
| 700 | 37 | 69.8 | 414 | 9 | ACH29878 | Ach29878 Human tes | 773 | 37 | 69.8 | 808 | 4 | AAK93646 | Aak93646 Human cDN |
| c 701 | 37 | 69.8 | 431 | 8 | ABX44733 | Abx44733 Bovine ES | 774 | 37 | 69.8 | 808 | 4 | AAK91979 | Aak91979 Human cDN |
| 702 | 37 | 69.8 | 447 | 4 | AAI13015 | Aai13015 Probe #29 | 775 | 37 | 69.8 | 808 | 12 | ADL28406 | Adl28406 5' end of |
| 703 | 37 | 69.8 | 447 | 4 | ABA54715 | Aba54715 Human foe | 776 | 37 | 69.8 | 808 | 12 | ADL30073 | Adl30073 3' end of |
| 704 | 37 | 69.8 | 447 | 4 | AAI34369 | Aai34369 Probe #30 | 777 | 37 | 69.8 | 816 | 3 | AAA46661 | Aaa46661 cDNA of a |
| 705 | 37 | 69.8 | 447 | 4 | ABA44265 | Aba44265 Human bre | 778 | 37 | 69.8 | 816 | 3 | AAA46673 | Aaa46673 cDNA of a |
| 706 | 37 | 69.8 | 447 | 4 | ABA24495 | Aba24495 Probe #29 | 779 | 37 | 69.8 | 822 | 2 | AAQ20696 | Aaq20696 Human OSF |
| 707 | 37 | 69.8 | 447 | 4 | AAK28447 | Aak28447 Human bon | c 780 | 37 | 69.8 | 828 | 2 | AAV59796 | Aav59796 Human sec |
| 708 | 37 | 69.8 | 447 | 4 | AAK02998 | Aak02998 Human bra | c 781 | 37 | 69.8 | 828 | 6 | ABS73790 | Abs73790 Human cDN |
| 709 | 37 | 69.8 | 447 | 4 | ABS28042 | Abs28042 Human liv | c 782 | 37 | 69.8 | 828 | 9 | ACD82933 | Acd82933 cDNA sequ |
| 710 | 37 | 69.8 | 447 | 5 | AAI02931 | Aai02931 Probe #29 | c 783 | 37 | 69.8 | 828 | 10 | ADI23018 | Adi23018 cDNA enco |
| 711 | 37 | 69.8 | 447 | 6 | ABS02955 | Abs02955 Human gen | c 784 | 37 | 69.8 | 828 | 12 | ADH74020 | Adh74020 Human sec |
| 712 | 37 | 69.8 | 453 | 9 | ACH41883 | Ach41883 Human foe | c 785 | 37 | 69.8 | 831 | 11 | ABD12562 | Abd12562 Pseudomon |
| c 713 | 37 | 69.8 | 455 | 3 | AAK07014 | Aak07014 Human sec | 786 | 37 | 69.8 | 831 | 11 | ABD12562 | Abd12562 Pseudomon |
| c 714 | 37 | 69.8 | 475 | 4 | AAI16336 | Aai16336 Probe #62 | 787 | 37 | 69.8 | 832 | 4 | AAK93707 | Aak93707 Human cDN |
| c 715 | 37 | 69.8 | 475 | 4 | ABA59160 | Aba59160 Human foe | 788 | 37 | 69.8 | 832 | 4 | AAK92044 | Aak92044 Human cDN |
| c 716 | 37 | 69.8 | 475 | 4 | AAI38911 | Aai38911 Probe #75 | 789 | 37 | 69.8 | 832 | 12 | ADL30134 | Adl30134 3' end of |
| c 717 | 37 | 69.8 | 475 | 4 | ABA27933 | Aba27933 Probe #63 | 790 | 37 | 69.8 | 832 | 12 | ADL28471 | Adl28471 5' end of |
| 718 | 37 | 69.8 | 475 | 4 | AAK31107 | Aak31107 Human bon | c 791 | 37 | 69.8 | 834 | 13 | ADS49928 | Ads49928 Bacterial |
| c 719 | 37 | 69.8 | 475 | 4 | AAK33116 | Aak33116 Human bon | c 792 | 37 | 69.8 | 835 | 5 | AAF94058 | Aaf94058 Primer sp |
| c 720 | 37 | 69.8 | 475 | 4 | AAK07348 | Aak07348 Human bra | c 793 | 37 | 69.8 | 843 | 13 | ADS55443 | Ads55443 Bacterial |
| c 721 | 37 | 69.8 | 475 | 4 | ABS32853 | Abs32853 Human liv | c 794 | 37 | 69.8 | 852 | 8 | ACA27078 | Aca27078 Prokaryot |
| 722 | 37 | 69.8 | 475 | 4 | ABS30787 | Abs30787 Human liv | 795 | 37 | 69.8 | 864 | 3 | AAA49944 | Aaa49944 Putative |
| c 723 | 37 | 69.8 | 475 | 6 | ABS07933 | Abs07933 Human gen | 796 | 37 | 69.8 | 864 | 6 | ABS76714 | Abs76714 Human cDN |
| 724 | 37 | 69.8 | 475 | 6 | ABS05859 | Abs05859 Human gen | 797 | 37 | 69.8 | 864 | 6 | ABS71827 | Abs71827 Human del |
| c 725 | 37 | 69.8 | 477 | 4 | AAI98720 | Aai98720 Human exc | 798 | 37 | 69.8 | 890 | 4 | AAK93978 | Aak93978 Human cDN |
| c 726 | 37 | 69.8 | 477 | 5 | AAI63116 | Aai63116 Human kid | 799 | 37 | 69.8 | 890 | 4 | AAK91991 | Aak91991 Human cDN |
| c 727 | 37 | 69.8 | 479 | 9 | ACH13126 | Ach13126 Human adu | 800 | 37 | 69.8 | 890 | 12 | ADL28418 | Adl28418 5' end of |
| c 728 | 37 | 69.8 | 492 | 4 | AAAS23930 | Aaas23930 Human ova | 801 | 37 | 69.8 | 890 | 12 | ADL30405 | Adl30405 5' end of |
| 729 | 37 | 69.8 | 493 | 6 | ABS69532 | Abs69532 Novel mur | 802 | 37 | 69.8 | 900 | 8 | ABS252402 | Abs252402 Aspergill |
| c 730 | 37 | 69.8 | 494 | 10 | ADB50671 | Adb50671 Primary r | 803 | 37 | 69.8 | 912 | 5 | AAS70559 | Aas70559 DNA encod |
| c 731 | 37 | 69.8 | 496 | 10 | ADH28970 | Adh28970 Human chr | c 804 | 37 | 69.8 | 912 | 5 | AAS66812 | Aas66812 DNA encod |
| 732 | 37 | 69.8 | 498 | 3 | ACG62329 | Acg62329 Contig HE | c 805 | 37 | 69.8 | 914 | 5 | AAK83170 | Aak83170 DNA encod |
| c 733 | 37 | 69.8 | 500 | 6 | ABA05271 | Aba05271 Human Ig- | c 806 | 37 | 69.8 | 914 | 5 | AAV63640 | Aav63640 Contig 38 |
| c 734 | 37 | 69.8 | 500 | 10 | ADE97362 | Ade97362 Human ger | 807 | 37 | 69.8 | 918 | 2 | AAK00907 | Aak00907 Human des |
| c 735 | 37 | 69.8 | 500 | 12 | ACH73812 | Ach73812 Human gen | 808 | 37 | 69.8 | 918 | 2 | AAV82639 | Aav82639 Contig 38 |

| | | | | | | | | | | | | | |
|-------|----|------|------|----|-----------|---------------------|-------|----|------|------|----|----------|---------------------|
| 809 | 37 | 69.8 | 918 | 3 | AAA14591 | Aaa14591 Nucleotid | 882 | 37 | 69.8 | 1575 | 6 | ABL90108 | Ab190108 Human pol |
| 810 | 37 | 69.8 | 918 | 3 | AAA09450 | Aaa09450 Human con | c 883 | 37 | 69.8 | 1580 | 7 | ADS31114 | Ad31114 Human gen |
| 811 | 37 | 69.8 | 918 | 3 | AAA49936 | Aaa49936 Human del | c 884 | 37 | 69.8 | 1590 | 8 | ACA37980 | Ac37980 Prokaryot |
| 812 | 37 | 69.8 | 918 | 6 | ABS76710 | Ab576710 Human des | c 885 | 37 | 69.8 | 1606 | 10 | ADA52622 | Ad52622 Human cod |
| 813 | 37 | 69.8 | 918 | 6 | ABS71823 | Ab571823 Human des | c 886 | 37 | 69.8 | 1621 | 10 | ADF82405 | Adf82405 Leukaemia |
| 814 | 37 | 69.8 | 960 | 3 | AAA49951 | Aaa49951 Human del | c 887 | 37 | 69.8 | 1686 | 4 | AAF63836 | Aaf63836 Human sec |
| 815 | 37 | 69.8 | 960 | 6 | ABS76727 | Ab576727 Human des | c 888 | 37 | 69.8 | 1686 | 13 | ADR99928 | Adr99928 Immune re |
| 816 | 37 | 69.8 | 960 | 6 | ABS71840 | Ab571840 Human del | c 889 | 37 | 69.8 | 1692 | 6 | ABQ90404 | Abq90404 M. capsul |
| 817 | 37 | 69.8 | 961 | 2 | AAQ13151 | Aaql3151 Heparin-b | c 890 | 37 | 69.8 | 1716 | 4 | AAH17528 | Aah17528 Human cDN |
| 818 | 37 | 69.8 | 966 | 13 | ADR96646 | Adr96646 M. tuberc | c 891 | 37 | 69.8 | 1749 | 4 | AAI61154 | Aai61154 Human pol |
| c 819 | 37 | 69.8 | 981 | 6 | ABK31789 | Abk31789 DNA encod | c 892 | 37 | 69.8 | 1787 | 5 | AA574236 | Aa574236 DNA encod |
| 820 | 37 | 69.8 | 981 | 6 | ABS76726 | Ab576726 Human cDN | c 893 | 37 | 69.8 | 1843 | 2 | AAV63642 | Aav63642 Contig 25 |
| 821 | 37 | 69.8 | 990 | 6 | ABS71839 | Ab571839 Human del | c 894 | 37 | 69.8 | 1843 | 2 | AA00909 | Aa00909 Human des |
| 822 | 37 | 69.8 | 999 | 13 | ADT44325 | Adt44325 Bacterial | c 895 | 37 | 69.8 | 1843 | 2 | AAV82641 | Aav82641 Contig 25 |
| 823 | 37 | 69.8 | 1001 | 2 | AAQ67396 | Aaql67396 HARP like | c 896 | 37 | 69.8 | 1843 | 3 | AAA14593 | Aaa14593 Nucleotid |
| 824 | 37 | 69.8 | 1014 | 13 | ADR99931 | Adr99931 Immune re | c 897 | 37 | 69.8 | 1843 | 3 | AAA09452 | Aaa09452 Human con |
| 825 | 37 | 69.8 | 1020 | 13 | AAF16150 | Aaf16150 Human pro | c 898 | 37 | 69.8 | 1843 | 3 | AAA49938 | Aaa49938 Human del |
| 826 | 37 | 69.8 | 1029 | 6 | AB167217 | Ab167217 Thyroid c | c 899 | 37 | 69.8 | 1843 | 6 | ABS76712 | Ab576712 Human des |
| 827 | 37 | 69.8 | 1029 | 6 | ABT10913 | Abt10913 Human bre | c 900 | 37 | 69.8 | 1843 | 6 | ABS71825 | Ab571825 Human del |
| 828 | 37 | 69.8 | 1029 | 12 | ADQ19929 | Adq19929 Human sof | c 901 | 37 | 69.8 | 1856 | 4 | AAH15766 | Aah15766 Human cDN |
| 829 | 37 | 69.8 | 1041 | 13 | ADT45348 | Adt45348 Bacterial | c 902 | 37 | 69.8 | 1917 | 8 | ACA37855 | Ac37855 Prokaryot |
| 830 | 37 | 69.8 | 1056 | 13 | ADS47995 | Ad547995 Bacterial | c 903 | 37 | 69.8 | 1928 | 8 | ABX93652 | Abx93652 cDNA enco |
| 831 | 37 | 69.8 | 1077 | 10 | RAAS58792 | Rad58792 Saprolegi | c 904 | 37 | 69.8 | 1928 | 10 | ADF69392 | Adf69392 Human del |
| 832 | 37 | 69.8 | 1077 | 13 | ADR20168 | Adr20168 Saprolegn | c 905 | 37 | 69.8 | 1940 | 4 | AAI59087 | Aai59087 Human pol |
| 833 | 37 | 69.8 | 1080 | 13 | ADS48002 | Ad548002 Bacterial | c 906 | 37 | 69.8 | 1940 | 5 | ADQ99310 | Adq99310 DNA encod |
| 834 | 37 | 69.8 | 1095 | 13 | ADS58661 | Ad558661 Bacterial | c 907 | 37 | 69.8 | 1940 | 9 | ADB49070 | Adb49070 Novel hum |
| c 835 | 37 | 69.8 | 1115 | 3 | AA51801 | Aa51801 Arabidops | c 908 | 37 | 69.8 | 1946 | 4 | AAH17649 | Aah17649 Human cDN |
| 836 | 37 | 69.8 | 1131 | 11 | ACF69599 | Adf69599 C. elegan | c 909 | 37 | 69.8 | 1972 | 6 | ABK35347 | Abk35347 Human cDN |
| 837 | 37 | 69.8 | 1136 | 11 | ACN88800 | Acn88800 Breast ca | c 910 | 37 | 69.8 | 1974 | 8 | ACC59952 | Acc59952 Human IRA |
| 838 | 37 | 69.8 | 1137 | 2 | AAV68561 | Aav68561 Human hea | c 911 | 37 | 69.8 | 1975 | 2 | AAI10640 | Aai10640 Streess ac |
| 839 | 37 | 69.8 | 1137 | 10 | ADE25556 | Ad525556 Human LLP | c 912 | 37 | 69.8 | 1975 | 6 | ABL88414 | Ab188414 Pain regu |
| 840 | 37 | 69.8 | 1137 | 10 | ADG14395 | Adg14395 Human LLP | c 913 | 37 | 69.8 | 1986 | 2 | AAI10641 | Aai10641 Streess ac |
| 841 | 37 | 69.8 | 1146 | 2 | AAV68564 | Aav68564 Human hea | c 914 | 37 | 69.8 | 2000 | 6 | ABZ15493 | Abz15493 Arabidops |
| 842 | 37 | 69.8 | 1233 | 2 | AAV68562 | Aav68562 Human kid | c 915 | 37 | 69.8 | 2001 | 12 | ADM47683 | Adm47683 Polynucle |
| 843 | 37 | 69.8 | 1236 | 2 | AAV68566 | Aav68566 Human hea | c 916 | 37 | 69.8 | 2046 | 4 | AAI59631 | Aai59631 Human cel |
| 844 | 37 | 69.8 | 1238 | 5 | ADL63377 | Adl63377 Human ova | c 917 | 37 | 69.8 | 2074 | 4 | AAI59368 | Aai59368 Human pol |
| 845 | 37 | 69.8 | 1242 | 5 | ADL63377 | Adl63377 Human kid | c 918 | 37 | 69.8 | 2080 | 4 | AAK94270 | Aak94270 Human ful |
| c 846 | 37 | 69.8 | 1250 | 6 | ABK86148 | Abk86148 cDNA enco | c 919 | 37 | 69.8 | 2080 | 12 | ADL30865 | Adl30865 Full leng |
| c 847 | 37 | 69.8 | 1269 | 8 | ABT16045 | Abt16045 NOVX rela | c 920 | 37 | 69.8 | 2090 | 4 | AAH45810 | Aah45810 Chlorella |
| c 848 | 37 | 69.8 | 1269 | 8 | ACA43466 | Ac43466 Prokaryot | c 921 | 37 | 69.8 | 2112 | 13 | ADQ17622 | Adq17622 Breast ca |
| c 849 | 37 | 69.8 | 1269 | 12 | ADO41691 | Ado41691 Novel hum | c 922 | 37 | 69.8 | 2112 | 13 | ADR25642 | Adr25642 Human NF- |
| 850 | 37 | 69.8 | 1332 | 2 | AAV68567 | Aav68567 Human kid | c 923 | 37 | 69.8 | 2112 | 13 | ADR14338 | Adr14338 Human NF- |
| 851 | 37 | 69.8 | 1335 | 3 | AAA49932 | Aaa49932 Human del | c 924 | 37 | 69.8 | 2140 | 13 | ADR07456 | Adr07456 Full leng |
| 852 | 37 | 69.8 | 1335 | 3 | AAAD19402 | Aad19402 Rat delta | c 925 | 37 | 69.8 | 2180 | 8 | ACA57993 | Ac57993 cDNA enco |
| 853 | 37 | 69.8 | 1335 | 4 | AAAD19403 | Aad19403 Human del | c 926 | 37 | 69.8 | 2224 | 4 | ABL09971 | Ab109971 Drosophi |
| 854 | 37 | 69.8 | 1335 | 5 | AAI66599 | Aai66599 Rat fatty | c 927 | 37 | 69.8 | 2236 | 4 | AAK94234 | Aak94234 Human ful |
| 855 | 37 | 69.8 | 1335 | 5 | AAI66599 | Aai66599 Rat fatty | c 928 | 37 | 69.8 | 2236 | 12 | ADL30793 | Adl30793 Full leng |
| 856 | 37 | 69.8 | 1335 | 5 | AAI66599 | Aai66599 Rat fatty | c 929 | 37 | 69.8 | 2236 | 8 | ACA37098 | Ac37098 Prokaryot |
| 857 | 37 | 69.8 | 1335 | 6 | ABS76706 | Ab576706 Human cDN | c 930 | 37 | 69.8 | 2257 | 2 | AAV63643 | Aav63643 Contig 25 |
| 858 | 37 | 69.8 | 1335 | 6 | ABS71819 | Ab571819 Human del | c 931 | 37 | 69.8 | 2257 | 2 | AA00910 | Aa00910 Human des |
| 859 | 37 | 69.8 | 1344 | 6 | AAAD31178 | Aad31178 Rat delta | c 932 | 37 | 69.8 | 2257 | 2 | AAV82642 | Aav82642 Contig 25 |
| 860 | 37 | 69.8 | 1383 | 2 | AAQ22960 | Aaq22960 Sequence | c 933 | 37 | 69.8 | 2257 | 3 | AAA14594 | Aaa14594 Nucleotid |
| 861 | 37 | 69.8 | 1383 | 2 | AAQ38811 | Aaq38811 Heparin-b | c 934 | 37 | 69.8 | 2257 | 3 | AAA09453 | Aaa09453 Human con |
| 862 | 37 | 69.8 | 1383 | 2 | AAQ61628 | Aaq61628 HBNF gene | c 935 | 37 | 69.8 | 2257 | 3 | AAA49939 | Aaa49939 Human del |
| 863 | 37 | 69.8 | 1383 | 2 | AAI2736 | Aai2736 Human ple | c 936 | 37 | 69.8 | 2257 | 6 | ABS76713 | Ab576713 Human del |
| 864 | 37 | 69.8 | 1383 | 3 | AAZ38456 | Aaz38456 Human ple | c 937 | 37 | 69.8 | 2257 | 6 | ABS71826 | Ab571826 Human del |
| c 865 | 37 | 69.8 | 1398 | 6 | ABZ14279 | Abz14279 Arabidops | c 938 | 37 | 69.8 | 2307 | 8 | ABZ35968 | Abz35968 Human sec |
| c 866 | 37 | 69.8 | 1398 | 12 | ADN74696 | Adn74696 Thale cre | c 939 | 37 | 69.8 | 2354 | 10 | ADA52542 | Ada52542 Human cod |
| 867 | 37 | 69.8 | 1400 | 13 | ADR14576 | Adr14576 Human NF- | c 940 | 37 | 69.8 | 2363 | 11 | ADM02625 | Adm02625 Human cDN |
| c 868 | 37 | 69.8 | 1442 | 6 | ABK63626 | Abk63626 Rat seque | c 941 | 37 | 69.8 | 2376 | 5 | AA591752 | Aa591752 DNA encod |
| c 869 | 37 | 69.8 | 1442 | 10 | ADB58034 | Ad58034 Toxicity- | c 942 | 37 | 69.8 | 2376 | 5 | AA566688 | Aa566688 DNA encod |
| c 870 | 37 | 69.8 | 1442 | 10 | ADB52506 | Ad52506 Primary r | c 943 | 37 | 69.8 | 2376 | 8 | ACD05933 | Ac05933 Novel hum |
| c 871 | 37 | 69.8 | 1442 | 10 | ADB79828 | Adb79828 Rat aldol | c 944 | 37 | 69.8 | 2469 | 8 | ACA37489 | Ac37489 Prokaryot |
| c 872 | 37 | 69.8 | 1442 | 10 | ABT41789 | Abt41789 Toxicity | c 945 | 37 | 69.8 | 2558 | 4 | AAK94786 | Aak94786 Human ful |
| c 873 | 37 | 69.8 | 1442 | 12 | ADP72631 | Adp72631 Renal tox | c 946 | 37 | 69.8 | 2558 | 12 | ADL31861 | Adl31861 Full leng |
| 874 | 37 | 69.8 | 1445 | 13 | ADS51471 | Ad551471 Bacterial | c 947 | 37 | 69.8 | 2614 | 3 | AACT6207 | Aac76207 Human ORF |
| 875 | 37 | 69.8 | 1464 | 4 | AAAF60969 | Aaf60969 P. putida | c 948 | 37 | 69.8 | 2618 | 10 | ADB63382 | Adb63382 Human cDN |
| 876 | 37 | 69.8 | 1474 | 3 | AAAF21845 | Aaf21845 Human bre | c 949 | 37 | 69.8 | 2621 | 10 | ABT10758 | Abt10758 Human bre |
| c 877 | 37 | 69.8 | 1489 | 10 | AAAD53959 | Aad53959 Synchocy | c 950 | 37 | 69.8 | 2621 | 8 | ACA89908 | Ac89908 Gene diff |
| c 878 | 37 | 69.8 | 1533 | 3 | AAAC42592 | Aac42592 Arabidops | c 951 | 37 | 69.8 | 2627 | 5 | AA586072 | Aa586072 DNA encod |
| c 879 | 37 | 69.8 | 1550 | 11 | ADJ130775 | Adj130775 Human cDN | c 952 | 37 | 69.8 | 2629 | 4 | AAH99666 | Aah99666 Human pro |
| 880 | 37 | 69.8 | 1554 | 4 | ABL12149 | Ab12149 Drosophi | c 953 | 37 | 69.8 | 2650 | 8 | AAH48137 | Aah48137 Human ple |
| 881 | 37 | 69.8 | 1575 | 4 | AAAF60968 | Aaf60968 P. putida | c 954 | 37 | 69.8 | 2650 | 12 | ADN06011 | Adn06011 Antipbri |

```
955 37 69.8 2657 8 ABZ34742 Coding se
956 37 69.8 2657 8 ACF12925 Human cer
957 37 69.8 2661 8 ACA37430 Prokaryot
958 37 69.8 2680 2 AAZ34023 Human PRO
959 37 69.8 2680 3 AAA88516 Human PRO
960 37 69.8 2680 3 AAC78492 Human PRO
961 37 69.8 2680 4 AAC91556 Human PRO
962 37 69.8 2680 4 ABK69967 cDNA enco
963 37 69.8 2680 8 ACA63591 Novel hum
964 37 69.8 2680 8 ACA71755 Human sec
965 37 69.8 2680 8 ABX92395 cDNA enco
966 37 69.8 2680 8 ACA66136 Human cDN
967 37 69.8 2680 9 ADA01281 Human PRO
968 37 69.8 2680 9 ADA43710 Human cDN
969 37 69.8 2680 9 ADA43478 Human cDN
970 37 69.8 2680 9 ADA24695 Novel hum
971 37 69.8 2680 9 ADA01153 Human PRO
972 37 69.8 2680 9 ACD29737 Novel hum
973 37 69.8 2680 9 ADA12356 Human cDN
974 37 69.8 2680 9 ACD23152 Novel hum
975 37 69.8 2680 9 ADA01037 Human cDN
976 37 69.8 2680 9 ADA43594 Human cDN
977 37 69.8 2680 9 ADA06856 Human PRO
978 37 69.8 2680 9 ADA08344 Novel hum
979 37 69.8 2680 9 ADB99637 Human PRO
980 37 69.8 2680 9 ADB88920 Human PRO
981 37 69.8 2680 9 ADB66075 Human cDN
982 37 69.8 2680 10 ADB73662 Human PRO
983 37 69.8 2680 10 ADB99753 Human PRO
984 37 69.8 2680 10 ADB76378 Human PRO
985 37 69.8 2680 10 ADB99408 Novel hum
986 37 69.8 2680 10 ADB65959 Human cDN
987 37 69.8 2680 10 ADC43804 Human cDN
988 37 69.8 2680 10 ADC61564 Human cDN
989 37 69.8 2680 10 ADC63528 Human cDN
990 37 69.8 2680 10 ADC66628 Human cDN
991 37 69.8 2680 10 ADC68752 Human cDN
992 37 69.8 2680 10 ADC82812 Human cDN
993 37 69.8 2680 10 ADC67877 Human cDN
994 37 69.8 2680 10 ADC41197 Human cDN
995 37 69.8 2680 10 ADC67252 Human cDN
996 37 69.8 2680 10 ADC23357 Human cDN
997 37 69.8 2680 10 ADC26050 Human PRO
998 37 69.8 2680 10 ADC62188 Human cDN
999 37 69.8 2680 10 ADC41821 Human cDN
1000 37 69.8 2680 10 ADE04877 Human PRO

Abz34742 Coding se
Acf12925 Human cer
Aca37430 Prokaryot
Aaz34023 Human PRO
Aaa88516 Human PRO
Aac78492 Human PRO
Aac91556 Human PRO
Abk69967 cDNA enco
Aca63591 Novel hum
Aca71755 Human sec
Abx92395 cDNA enco
Aca66136 Human cDN
Ada01281 Human PRO
Ada43710 Human cDN
Ada43478 Human cDN
Ada24695 Novel hum
Ada01153 Human PRO
Acd29737 Novel hum
Ada12356 Human cDN
Acd23152 Novel hum
Ada01037 Human cDN
Ada43594 Human cDN
Ada06856 Human PRO
Ada08344 Novel hum
Adb99637 Human PRO
Adb88920 Human PRO
Adb66075 Human cDN
Adb73662 Human PRO
Adb99753 Human PRO
Adb76378 Human PRO
Adb99408 Novel hum
Adb65959 Human cDN
Adc43804 Human cDN
Adc61564 Human cDN
Adc63528 Human cDN
Adc66628 Human cDN
Adc68752 Human cDN
Adc82812 Human cDN
Adc67877 Human cDN
Adc41197 Human cDN
Adc67252 Human cDN
Adc23357 Human cDN
Adc26050 Human PRO
Adc62188 Human cDN
Adc41821 Human cDN
Ade04877 Human PRO

ALIGNMENTS

RESULT 1
AAV34398
ID AAV34398 standard; DNA; 1684 BP.
AC
AC AAV34398;
DT 02-MAR-1999 (first entry)
DE
DE Borage delta-6 desaturase gene.
KW Upstream region; regulatory region; sunflower; albumin; seed; expression;
KW lipid metabolism; delta-6 desaturase; transgenic plant; ds.
OS Borage officinalis.
XX
XX Key Location/Qualifiers
XX CDS 43..1389
XX FT /*tag= a
XX FT primer_bind product= "delta-6 desaturase"
XX FT primer_bind complement(616..632)
XX FT primer_bind /*tag= b
XX FT primer_bind 1165..1181
XX FT primer_bind /*tag= c

XX WO9845460-A1.
XX PN
XX 15-OCT-1998.
XX PD
XX 09-APR-1998; 98WO-US007178.
XX PF
XX 09-APR-1997; 97US-00831570.
XX PR
XX (RHON ) RHONE-POULENC AGROCHIMIE.
XX Thomas TL, Beremand PD, Nunberg AN;
XX WPI; 1998-583201/49.
XX P-PSDB; AAW67471.
XX New sunflower albumin 5' regulatory region - useful for directing altered
XX lipid metabolism in plant seeds.
XX Example 2; Fig 1; 38pp; English.
XX This sequence is the gene encoding the borage (Borago officinalis) delta-
XX 6 desaturase enzyme. The lipid metabolism gene is an example of a
XX heterologous gene which can be expressed at high levels in a seed-
XX specific manner in transgenic plants, when placed under control of the
XX sunflower albumin gene 5' regulatory region (AAV34397)
XX SQ Sequence 1684 BP; 430 A; 277 C; 358 G; 619 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.11 Length: 1684
Score: 53.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-6 (1-8) x AAV34398 (1-1684)
Qy 1 TrrlleGlyHisAepAlaGlyHis 8
Db 508 TGGATTGGACATGATGCTGGGCAT 531
RESULT 2
AAV24917
ID AAV24917 standard; cDNA; 1684 BP.
XX
XX AC AAV24917;
XX
XX DT 21-JUN-1999 (first entry)
XX
XX DE Borage delta-6 desaturase cDNA.
XX
XX KW Delta-6 desaturase; borage; oleosin; AtS21; promoter; transgenic plant;
XX seed; lipid; fatty acid; oilseed; vegetable oil; gamma-linolenic acid;
XX octadecatetraenoic acid; ds.
XX OS Borage officinalis.
XX
XX Key Location/Qualifiers
XX CDS 43..1389
XX FT /*tag= a
XX
XX PN WO9845461-A1.
XX
XX PD 15-OCT-1998.
XX
XX PF 09-APR-1998; 98WO-US007179.
XX
XX PR 09-APR-1997; 97US-00831575.
XX
XX PA (RHON ) RHONE-POULENC AGROCHIMIE.
XX
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PI Thomas TL, Li Z;
XX WPI; 1999-180333/15.
DR P-PSDB; AAW98130.
XX
XX Nucleic acid containing oleosin 5'-regulatory region - useful for
PT modulating fatty acid synthesis and lipid metabolism in plants,
PT particularly to increase content of gamma-linolenic acid.
XX
XX Example 2; Page 59-61; 101pp; English.
XX
XX The present sequence encodes borage delta-6 desaturase (see AAW98130), an
CC enzyme that catalyses the conversion of linoleic acid to gamma-linolenic
CC acid (GLA). Delta-6 desaturase cDNA was isolated from a borage membrane-
CC bound polysomal cDNA library using a partial clone, obtained from an EST
CC database search, as probe. The borage delta-6 desaturase nucleic acid can
CC be operably linked to the seed-specific 5' regulatory region (see
CC AAX24916) of the Arabidopsis thaliana oleosin AtS21 gene in claimed
CC expression cassettes of the invention. Transgenic plants, e.g. sunflower,
CC soybean, maize, tobacco, cotton, peanut, oilseed rape or Arabidopsis are
CC obtained that show increased levels of GLA or octadecatetraenoic acid.
CC The levels of desirable fatty acids in oilseed crops can be manipulated
CC to provide seed oils of use in human health and industrial applications
XX
SQ Sequence 1684 BP; 430 A; 277 C; 358 G; 619 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.11 Length: 1684
Score: 53.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-6 (1-8) x AAX24917 (1-1684)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 508 TGGATTGGACATGATGCTGGGCAT 531

RESULT 3
AAT30395
ID AAT30395 standard; DNA; 1685 BP.
XX
AC AAT30395;
XX
DT 15-SEP-1996 (first entry)
XX
DE Borage delta-6-desaturase gene.
XX
KW Delta-6-desaturase; gamma-linolenic acid; transgenic plant; borage;
KW polyunsaturated fatty acid; octadecatetraenoic acid; chilling resistance;
KW oilseed; ss; ds.
XX
OS Borage officinalis.
XX
FH Key Location/Qualifiers
FT CDS 44..1390
FT /*tag= a
FT
XX WO9621022-A2.
XX
XX 11-JUL-1996.
XX
XX 28-DEC-1995; 95WO-IB001167.
XX
XX 30-DEC-1994; 94US-00366779.
XX
XX (RHON ) RHONE POULENC AGROCHIMIE.
XX
XX Thomas TL, Reddy AS, Nuccio M, Nunberg AN, Freysinet GL;
XX WPI; 1996-333997/33.
XX
DR

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DR P-PSDB; AAR98455.
XX
XX Transgenic plants comprising the borage delta-6-desaturase gene - show
PT increased production of gamma linolenic acid and having increased
PT resistance to chilling.
XX
XX Claim 2; Page 51-52; 75pp; English.
XX
XX A DNA clone (AAT30395) codes for borage delta-6-desaturase (AAR98455),
CC which catalyses the conversion of linoleic acid to gamma-linolenic acid
CC (GLA). It was isolated from a borage membrane-bound polysomal library
CC using probes based on abundantly expressed seed storage protein cDNAs and
CC with an isolated partial cDNA clone. The gene can be incorporated into a
CC vector, pref. incorporating a tissue-specific promoter, for the
CC expression of delta-6-desaturase in transgenic plants, esp. sunflower,
CC soybean, maize, tobacco, peanut, carrot or oilseed rape, resulting in
CC increased GLA prodn. Alteration of plant lipids may also lead to improved
CC chilling resistance
XX
SQ Sequence 1685 BP; 431 A; 277 C; 357 G; 620 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.11 Length: 1685
Score: 53.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-6 (1-8) x AAT30395 (1-1685)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 509 TGGATTGGACATGATGCTGGGCAT 532

RESULT 4
ABK49502
ID ABK49502 standard; DNA; 1685 BP.
XX
AC ABK49502;
XX
DT 15-JUL-2002 (first entry)
XX
DE DNA encoding Borage officinalis delta6-desaturase.
XX
KW delta6-desaturase; sunflower; soybean; maize; tobacco; peanut; carrot;
KW oil seed rape; gamma linolenic acid; GLA; chilling tolerance; gene; ds;
KW borage.
XX
OS Borage officinalis.
XX
FH Key Location/Qualifiers
FT CDS 44..1390
FT /*tag= a
FT /product= "delta6-desaturase"
FT /transl_except= (pos:1151..1153, aa:Ser)
XX
XX US6355861-B1.
XX
XX 12-MAR-2002.
XX
XX 19-SEP-1997; 97US-00934254.
XX
XX 10-OCT-1991; 91US-00774475.
XX
XX 08-JAN-1992; 92US-00817919.
XX
XX 13-OCT-1992; 92US-00959952.
XX
XX 14-SEP-1994; 94US-00307382.
XX
XX 28-JAN-1997; 97US-00789936.
XX
XX (RHON ) RHONE-POULENC AGROCHIMIE.
XX
XX Thomas TL;
XX
XX

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DR WPI; 2002-380944/41.
 DR P-PSDB; AAU79830.
 XX
 PT Novel nucleic acid encoding evening primrose delta6-desaturase which
 PT converts linoleic acid to gamma linolenic acid useful for producing gamma
 PT linolenic acid in transgenic plant or bacteria.
 XX
 PS Example 9; Col 29-32; 53pp; English.
 XX
 CC The invention describes an isolated nucleic acid encoding an evening
 CC primrose Delta6-desaturase. The nucleic acid and a vector expressing the
 CC nucleic acid are useful for producing a plant such as sunflower, soybean,
 CC maize, tobacco, peanut, carrot or oil seed rape plant, with increased
 CC gamma linolenic acid (GLA) content, and also for inducing or increasing
 CC production of GLA in a bacteria or plant deficient, lacking in or
 CC producing low levels of GLA. The nucleic acid is also useful for inducing
 CC chilling tolerance in plants. This sequence encodes the borage delta6
 CC desaturase involved in the production of gamma linoleic acid
 XX
 SQ Sequence 1685 BP; 431 A; 277 C; 357 G; 620 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 6.11 Length: 1685
 Score: 53.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-10-029-756-6 (1-8) x ABK49502 (1-1685)
 Qy 1 TtpIleGlyHisAspAlaGlyHis 8
 Db 509 TGGATTGGACATGATGCTGGGCAT 532
 RESULT 5
 ABX15366
 ID ABX15366 standard; cDNA; 1685 BP.
 XX
 AC ABX15366;
 XX
 DT 17-APR-2003 (first entry)
 XX
 DE Borage delta-6-desaturase #1 cDNA.
 XX
 KW Delta-6-desaturase; gene; ss; delta-12-desaturase; sunflower; soybean;
 KW maize; tobacco; peanut; carrot; oil seed rape; gamma-linolenic acid; GLA;
 KW octadecatetraenoic acid; alpha-linolenic acid; delta-15-desaturase;
 KW borage.
 XX
 OS Borage officinalis.
 XX
 FH Key Location/Qualifiers
 FT CDS 44..1390
 FT /*tag= a
 FT /product= "Borage delta-6-desaturase #1"
 FT /trans_except= (pos:1151..1153, aa:Ser)
 XX
 XX US2002108147-A1.
 XX
 XX 08-AUG-2002.
 XX
 XX 21-DEC-2001; 2001US-00029756.
 XX
 XX 10-OCT-1991; 91US-00774475.
 XX 08-JAN-1992; 92US-00817919.
 XX 13-OCT-1992; 92US-00959952.
 XX 14-SEP-1994; 94US-00307382.
 XX 28-JAN-1997; 97US-00789936.
 XX 19-SEP-1997; 97US-00934254.
 XX
 XX (THOM/) THOMAS T L.
 XX

PI Thomas TL;
 XX
 DR WPI; 2003-066659/06.
 DR P-PSDB; ABG73095.
 XX
 PT Novel nucleic acid encoding evening primrose delta-6-desaturase, useful
 PT for producing plant with increased gamma linolenic acid content, and for
 PT inducing octadecatetraenoic acid production in plant.
 XX
 PS Example 9; Fig 5A; 55pp; English.
 XX
 CC The invention relates to a nucleic acid encoding an evening primrose
 CC delta-6-desaturase polypeptide. The nucleic acid, a vector comprising the
 CC nucleic acid or a nucleic acid encoding delta-12-desaturase, is useful
 CC for producing a plant (such as sunflower, soybean, maize, tobacco,
 CC peanut, carrot or oil seed rape plant) with increased gamma-linolenic
 CC acid (GLA) content by transforming a plant cell with the nucleic acid or
 CC vector and regenerating a plant with increased GLA content from the plant
 CC cell, for inducing or increasing production of GLA in an organism lacking
 CC in or producing low levels of GLA and for inducing production of
 CC octadecatetraenoic acid in at least one of a plant deficient or lacking
 CC in or producing low levels of octadecatetraenoic acid, a bacterium which
 CC produces alpha-linolenic acid or a bacterium which exhibits a delta-15-
 CC desaturase activity on a GLA substrate. This sequence represents cDNA
 CC encoding a borage delta-6-desaturase polypeptide
 XX
 SQ Sequence 1685 BP; 431 A; 277 C; 357 G; 620 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 6.11 Length: 1685
 Score: 53.00 Matches: 8
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0
 US-10-029-756-6 (1-8) x ABX15366 (1-1685)
 Qy 1 TtpIleGlyHisAspAlaGlyHis 8
 Db 509 TGGATTGGACATGATGCTGGGCAT 532
 RESULT 6
 AD015534
 ID AD015534 standard; cDNA; 1685 BP.
 XX
 AC AD015534;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Borage cDNA encoding delta6-desaturase.
 XX
 KW Delta6-desaturase; ss; gene; linolenic acid; gamma linolenic acid;
 KW essential fatty acid; arachidonic acid; prostaglandin;
 KW hypercholesterolaemia; atherosclerosis; coronary disease;
 KW delta12-desaturase; borage; plant.
 XX
 OS Borage officinalis.
 XX
 XX US6683232-B1.
 XX
 XX 27-JAN-2004.
 XX
 XX 10-OCT-2000; 2000US-00685775.
 XX
 XX 10-OCT-1991; 91US-00774475.
 XX 08-JAN-1992; 92US-00817919.
 XX 13-OCT-1992; 92US-00959952.
 XX 14-SEP-1994; 94US-00307382.
 XX 28-JAN-1997; 97US-00789936.
 XX 19-SEP-1997; 97US-00934254.
 XX
 XX (RHON) RHONE-POULENC AGROCHIMIE.
 XX

PN WO200032790-A2.
 XX
 PD 08-JUN-2000.
 XX
 XX 02-DEC-1999; 99WO-US028589.
 XX PF
 XX 03-DEC-1998; 98US-0110784P.
 XX PR
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 XX PA
 XX Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;
 XX PI
 XX WPI; 2000-412336/35.
 XX DR
 XX P-PSDB; RAY71553.
 XX DR
 XX Polynucleotide encoding delta-6 desaturase enzyme useful for producing
 PT transgenic plants and for producing antibodies specific to which is
 PT useful for screening cDNA expression libraries.
 XX
 XX Claim 2; Page 44-45; 57pp; English.
 XX
 CC The present sequence is a cDNA encoding sphingolipid desaturase derived
 CC from a contig of clones sf11.pk0012.c5 and sf11.pk0031.d11 isolated from
 CC soybean immature flower cDNA library, sf11. The present sequence is
 CC useful for producing transgenic plants having altered levels of
 CC sphingolipid desaturase which in turn would alter the fatty acid
 CC composition. The enzyme is useful for producing polyclonal or monoclonal
 CC antibodies. The polynucleotide is also useful as a primer or probe for
 CC screening cDNA libraries to isolate desired full-length cDNA clones
 XX
 SQ Sequence 880 BP; 162 A; 267 C; 184 G; 251 T; 0 U; 16 Other;

Alignment Scores:
 Pred. No.: 10.6 Length: 880
 Score: 50.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 87.50% Mismatches: 0
 Query Match: 94.34% Indels: 0
 DB: 3 Gaps: 0

US-10-029-756-6 (1-8) x AAD01351 (1-880)
 Qy 1 TrpIleGlyHisAspAlaGlyHis 8
 Db 267 TGGATAGCCACGACTCGGCCAT 290

RESULT 9
 ADI26234
 ID ADI26234 standard; DNA; 1362 BP.
 XX
 AC ADI26234;
 XX
 XX 06-MAY-2004 (first entry)
 XX
 XX Primula vialii delta6-desaturase gene SeqID3.
 XX
 KW delta6-desaturase; omega3-fatty acid; oil; lipid; free fatty acid;
 KW animal feed; food; cosmetic; pharmaceutical; arachidonic acid;
 KW omega-6 family; gene; ds; plant.
 XX
 OS Primula vialii.
 XX
 XX Key Location/Qualifiers
 FH CDS 1..1362
 FT /*tag= a
 FT /product= "Aleruritia farinosa delta6-desaturase"
 XX
 XX GB2385852-A.
 XX
 XX 03-SEP-2003.
 XX
 XX 27-FEB-2002; 2002GB-00004676.
 XX

PR 27-FEB-2002; 2002GB-00004676.
 XX
 PA (ROTH-) ROTHAMSTED EXPERIMENTAL STATION.
 XX
 PI Napier JA, Sayanova O;
 XX WPI; 2003-699784/67.
 XX DR P-PSDB; ADI26235.
 XX
 XX New nucleic acid encoding delta6-desaturase and the encoded enzyme,
 PT useful for preparing transgenic plants with increased production of omega
 PT -3 fatty acids.
 XX
 XX Claim 2; SEQ ID NO 3; 51pp; English.
 XX
 CC This invention relates to a novel DNA sequence that encodes a protein
 CC with delta6-desaturase activity that specifically converts omega3-fatty
 CC acids. Transgenic organisms, specifically plants, that contain the DNA of
 CC the invention are used for production of omega-3 fatty acids, as oils,
 CC lipids or free fatty acids, useful in animal feeds, foods, cosmetics and
 CC pharmaceuticals. The invention can also be used in homology screening to
 CC isolate other genomic sequences, and as antisense reagents, ribozymes or
 CC other inhibitory molecules to prevent expression of delta6-desaturase,
 CC for example where oils of higher saturated fatty acid contents are
 CC required. Plants that express the DNA of the invention have an increased
 CC content of omega-3 fatty acids, without formation of unwanted by-products
 CC (particularly arachidonic acid or other members of the omega-6 family).
 CC The protein has activity towards omega-3 acids at least 1.5, particularly
 CC 5, times greater than against omega-6 acids. The present sequence is that
 CC of a delta6-desaturase gene of the invention.
 XX
 SQ Sequence 1362 BP; 300 A; 385 C; 338 G; 339 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 17 Length: 1362
 Score: 50.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 87.50% Mismatches: 0
 Query Match: 94.34% Indels: 0
 DB: 10 Gaps: 0

US-10-029-756-6 (1-8) x ADI26234 (1-1362)
 Qy 1 TrpIleGlyHisAspAlaGlyHis 8
 Db 481 TGGATAGGTCCGACTCTGGCCAT 504

RESULT 10
 ADI26232
 ID ADI26232 standard; DNA; 1362 BP.
 XX
 AC ADI26232;
 XX
 XX 06-MAY-2004 (first entry)
 XX
 XX Aletris farinosa delta6-desaturase gene SeqID1.
 XX
 KW delta6-desaturase; omega3-fatty acid; oil; lipid; free fatty acid;
 KW animal feed; food; cosmetic; pharmaceutical; arachidonic acid;
 KW omega-6 family; gene; ds; plant.
 XX
 OS Aletris farinosa.
 XX
 XX Key Location/Qualifiers
 FH CDS 1..1362
 FT /*tag= a
 FT /product= "Aleruritia farinosa delta6-desaturase"
 XX
 XX GB2385852-A.
 XX
 XX 03-SEP-2003.
 XX
 XX 27-FEB-2002; 2002GB-00004676.
 XX

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XX PR 27-FEB-2002; 2002GB-00004676.
XX PA (ROTH-) ROTHAMSTED EXPERIMENTAL STATION.
XX PI Napier JA, Sayanova O;
XX WPI; 2003-699784/67.
XX DR P-PSDB; ADI26233.
XX PT New nucleic acid encoding delta6-desaturase and the encoded enzyme,
XX PT useful for preparing transgenic plants with increased production of omega
XX PT -3 fatty acids.
XX PS Claim 2; SEQ ID NO 1; Sipp; English.
XX CC This invention relates to a novel DNA sequence that encodes a protein
XX CC with delta6-desaturase activity that specifically converts omega3-fatty
XX CC acids. Transgenic organisms, specifically plants, that contain the DNA of
XX CC the invention are used for production of omega-3 fatty acids, as oils,
XX CC lipids or free fatty acids, useful in animal feeds, foods, cosmetics and
XX CC pharmaceuticals. The invention can also be used in homology screening to
XX CC isolate other genomic sequences, and as antisense reagents, ribozymes or
XX CC other inhibitory molecules to prevent expression of delta6-desaturase,
XX CC for example where oils of higher saturated fatty acid contents are
XX CC required. Plants that express the DNA of the invention have an increased
XX CC content of omega-3 fatty acids, without formation of unwanted by-products
XX CC (particularly arachidonic acid or other members of the omega-6 family).
XX CC The protein has activity towards omega-3 acids at least 1.5, particularly
XX CC 5, times greater than against omega-6 acids. The present sequence is that
XX CC of a delta6-desaturase gene of the invention.
XX SQ Sequence 1362 BP; 294 A; 376 C; 329 G; 363 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 17 Length: 1362
Score: 50.00 Matches: 7
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 0
Query Match: 94.34% Indels: 0
DB: 10 Gaps: 0

US-10-029-756-6 (1-8) x ADI26232 (1-1362)
Oy 1 TptleGlyHisAspAlaGlyHis 8
Db 481 TGGATAGTCACGACTCTGGGCAT 504

RESULT 11
ADR60098
ID ADR60098 standard; CDNA; 1503 BP.
XX AC ADR60098;
XX DT 02-DEC-2004 (first entry)
XX DE Cotton cDNA sequence, SEQ ID 879.
XX KW Cotton; ss; plant; cold tolerance; growth rate; cell cycle pathway;
XX KW drought tolerance; plant disease resistance; galactomannan; lignin;
XX KW plant growth regulator; heat tolerance; herbicide tolerance;
XX KW homologous recombination; extreme osmotic condition tolerance;
XX KW pathogen resistance; pest resistance; yield; photosynthesis; seed oil;
XX KW stress resistance.
XX OS Gossypium hirsutum.
XX PN US2004181830-A1.
XX PD 16-SEP-2004.
XX XX 29-JAN-2004; 2004US-00767795.
XX XX

```

```

PR 07-MAY-2001; 2001US-00849529.
PR 12-DEC-2001; 2001US-00021323.
XX (KOVA/) KOVALIC D K.
XX PA (ZHOU/) ZHOU Y.
XX PI (CAOY/) CAO Y.
XX PI Kovalic DK, Zhou Y, Cao Y;
XX WPI; 2004-667718/65.
XX DR
XX PT New recombinant nucleic acid molecules and polypeptides from Gossypium
XX PT hirsutum, useful for producing plants with improved biological
XX PT characteristics (e.g. improved plant cold or drought tolerance).
XX PS Claim 1; SEQ ID NO 879; 14pp; English.
XX CC The invention relates to a recombinant polynucleotide comprising any of
XX CC the 58798 Cotton plant cDNA sequences mentioned in the specification.
XX CC Also a recombinant polypeptide comprising any of the 58798 amino acid
XX CC sequences mentioned in the specification and producing a plant having an
XX CC improved property. Producing a plant having an improved property
XX CC comprises transforming a plant with a recombinant construct comprising a
XX CC promoter region functional in a plant cell operably joined to a
XX CC polynucleotide comprising a coding sequence for a polypeptide associated
XX CC with the property, and growing the transformed plant. The polypeptide is
XX CC useful for improving plant cold tolerance, manipulating growth rate in
XX CC plant cells by modification of the cell cycle pathway, improving plant
XX CC drought tolerance, providing increased resistance to plant disease,
XX CC producing galactomannan (or lignin or plant growth regulators), improving
XX CC plant heat tolerance, improving plant tolerance to herbicides, increasing
XX CC the rate of homologous recombination in plants, improving plant tolerance
XX CC to extreme osmotic conditions or to pathogens or pests, improving yield
XX CC by modification of photosynthesis, modifying seed oil or protein yield
XX CC and/or content, improving yield by modification of carbohydrate, nitrogen
XX CC or phosphorus use and/or uptake, or improving yield by providing improved
XX CC plant growth and development under at least one stress condition. The
XX CC polynucleotide and polypeptide may also be used in recombinant DNA
XX CC constructs, in physical arrays of molecules, as plant breeding markers,
XX CC or in computer-based storage and analysis systems. The present sequence
XX CC is a Cotton plant cDNA of the invention. NOTE: The sequence data for this
XX CC patent did not form part of the printed specification, but was obtained
XX CC in electronic format directly from USPTO at
XX CC seqdata.uspto.gov/sequence.html?DocID=20040181830. However only 6585
XX CC polynucleotide sequences were available, the remaining 52213
XX CC polynucleotides and all 58798 protein sequences were not present.
XX SQ Sequence 1503 BP; 406 A; 292 C; 295 G; 510 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 18.9 Length: 1503
Score: 50.00 Matches: 7
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 87.50% Mismatches: 0
Query Match: 94.34% Indels: 0
DB: 13 Gaps: 0

US-10-029-756-6 (1-8) x ADR60098 (1-1503)
Oy 1 TptleGlyHisAspAlaGlyHis 8
Db 566 TGGATAGTCACGACTCTGGGCAT 589

RESULT 12
AAD01353
ID AAD01353 standard; CDNA; 1972 BP.
XX AC AAD01353;
XX DT 12-OCT-2000 (first entry)
XX DE Wheat sphingolipid desaturase cDNA #1.
XX XX

```

KW Wheat; sphingolipid desaturase; membrane-bound desaturase;
 KW transgenic plant; fatty acid; ss.
 OS

XX Triticum aestivum.

XX Key Location/Qualifiers
 XX CDS 124..1533

FT /*tag= a
 FT /product= "sphingolipid desaturase"

XX WO200032790-A2.

XX PN 08-JUN-2000.

XX PD 02-DEC-1999; 99WO-US028589.

XX PF 03-DEC-1998; 98US-0110784P.

XX PR (DUPO) DU PONT DE NEMOURS & CO E I.

XX PA Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;

XX PI WPI; 2000-412336/35.

XX DR P-PSDB; AAY71555.

XX PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing
 XX transgenic plants and for producing antibodies specific to which is
 XX useful for screening cDNA expression libraries.

XX PS Disclosure; Page 48-49; 57pp; English.

XX CC The present sequence is a cDNA encoding sphingolipid desaturase from
 CC clone wrel.pk0004.c7.fis isolated from wheat etiolated seedling root cDNA
 CC library, wrel. The present sequence is useful for producing transgenic
 CC plants having altered levels of sphingolipid desaturase which in turn
 CC would alter the fatty acid composition. The enzyme is useful for
 CC producing polyclonal or monoclonal antibodies. The polynucleotide is also
 CC useful as primer or probe for screening cDNA libraries to isolate desired
 CC full-length cDNA clones

XX SQ Sequence 1972 BP; 382 A; 616 C; 490 G; 484 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 25.4 Length: 1972
 Score: 50.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 87.50% Mismatches: 0
 Query Match: 94.34% Indels: 0
 DB: 3 Gaps: 0

US-10-029-756-6 (1-8) x AAD01353 (1-1972)

Qy 1 TtpIleGlyHisAspAlaGlyHis 8

Db 649 TGGATTGGCCATGACTCGGCCAC 672

RESULT 13

AAD01350

ID AAD01350 standard; cDNA; 1764 BP.

XX AAD01350;

XX DT 12-OCT-2000 (first entry)

XX DE Corn sphingolipid desaturase cDNA.

XX KW Corn; sphingolipid desaturase; membrane-bound desaturase;

XX transgenic plant; fatty acid; ss.

XX OS Zea mays.

XX Key Location/Qualifiers

XX FH CDS 89..1477

FT

FT /*tag= a
 FT /product= "Sphingolipid desaturase"

XX WO200032790-A2.

XX PN 08-JUN-2000.

XX PD 02-DEC-1999; 99WO-US028589.

XX PF 03-DEC-1998; 98US-0110784P.

XX PR (DUPO) DU PONT DE NEMOURS & CO E I.

XX PA Cahoon EB, Cahoon RE, Hitz WD, Kinney AJ;

XX PI WPI; 2000-412336/35.

XX DR P-PSDB; AAY71552.

XX PT Polynucleotide encoding delta-6 desaturase enzyme useful for producing
 XX transgenic plants and for producing antibodies specific to which is
 XX useful for screening cDNA expression libraries.

XX PS Claim 2; Page 41-42; 57pp; English.

XX CC The present sequence is a cDNA encoding sphingolipid desaturase from
 CC clone cdelc.pk001.c8.fis isolated from corn developing embryo cDNA
 CC library, cdelc. The present sequence is useful for producing transgenic
 CC plants having altered levels of sphingolipid desaturase which in turn
 CC would alter the fatty acid composition. The enzyme is useful for
 CC producing polyclonal or monoclonal antibodies. The polynucleotide is also
 CC useful as primer or probe for screening cDNA libraries to isolate desired
 CC full-length cDNA clones

XX SQ Sequence 1764 BP; 310 A; 602 C; 456 G; 396 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 78.7 Length: 1764
 Score: 47.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 2
 Best Local Similarity: 75.00% Mismatches: 0
 Query Match: 88.68% Indels: 0
 DB: 3 Gaps: 0

US-10-029-756-6 (1-8) x AAD01350 (1-1764)

Qy 1 TtpIleGlyHisAspAlaGlyHis 8

Db 593 TGGATGGGCCACGACTCGGCCAC 616

RESULT 14

ADJ48284

ID ADJ48284 standard; DNA; 2054 BP.

XX AC ADJ48284;

XX DT 06-MAY-2004 (first entry)

XX DE Maize oil-associated gene #102.

XX KW ds; maize; plant; oil-associated gene; transgenic; enhanced seed oil;
 XX vegetable oil.

XX OS Zea mays.

XX PN US2004025202-A1.

XX PD 05-FEB-2004.

XX PF 14-MAR-2003; 2003US-00389566.

XX PR 15-MAR-2002; 2002US-0365301P.

XX PR 26-JUN-2002; 2002US-0391786P.

XX PR 26-JUN-2002; 2002US-0392018P.

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XX (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEUX J R.
PA (ROGE/) ROGERS J A.
XX
XX Laurie CC, Ravanello M, Savage T, Ledoux JR, Rogers JA;
XX WPI; 2004-142683/14.
XX
XX Novel recombinant DNA construct comprising a promoter functional in
XX plants operably linked to an oil-associated gene for producing transgenic
XX plant seed.
XX
XX Example 1; SEQ ID NO 288; 22pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
XX promoter functional in plants operably linked to an oil-associated gene.
XX The construct is useful for transgenic plant seed which has in its genome
XX the construct, that is functional in the plant to transcribe the oil-
XX associated gene. The transgenic plant seed grows into a plant having
XX enhanced seed oil as compared to wild type. The construct is useful for
XX producing hybrid maize seed. The transgenic plant seed is useful for
XX producing vegetable oil. The present sequence represents a maize oil-
XX associated gene.
XX
XX SQ Sequence 2054 BP; 343 A; 692 C; 538 G; 481 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 92.8 Length: 2054
Score: 47.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 75.00% Mismatches: 0
Query Match: 88.68% Indels: 0
DB: 12 Gaps: 0

US-10-029-756-6 (1-8) x ADJ48284 (1-2054)

QY 1 TrpIleGlyHisAspAlaGlyHis 8
|||:::|||||:::|||||
Db 667 TGGATGGGCCACGACTCGGGCCAC 690

RESULT 15
AAS46880
ID AAS46880 standard; cDNA; 649 BP.
XX
XX AAS46880;
AC
XX
XX 18-DEC-2001 (first entry)
DT
XX
XX Human G protein-coupled receptor (GPCR) cDNA #62.
DE
XX
XX Human; G protein-coupled receptor; GPCR; mental disorder; schizophrenia;
XX neurological disorder; metabolic disorder; cancer; rheumatoid arthritis;
XX thyroid disorder; neurodegenerative disorder; cardiovascular disorder;
XX renal failure; autoimmune disorder; hyperproliferative disorder; HIV; ss;
XX human immunodeficiency virus; viral infection; neuroprotective;
XX immunostimulant; neuroleptic; nootropic; tranquiliser; antidepressant;
XX anorectic; gene therapy.
XX
XX Homo sapiens.
OS
XX
XX WO200168858-A2.
PN
XX
XX 20-SEP-2001.
PD
XX
XX 16-MAR-2001; 2001WO-US008456.
XX
XX 16-MAR-2000; 2000US-0187783P.
XX
XX 16-MAR-2000; 2000US-0189907P.
XX
XX 16-MAR-2000; 2000US-0189917P.
XX
XX 16-MAR-2000; 2000US-0189918P.

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PR 16-MAR-2000; 2000US-0189960P.
PR 29-MAR-2000; 2000US-0192155P.
PR 29-MAR-2000; 2000US-0192234P.
PR 29-MAR-2000; 2000US-0192830P.
PR 29-MAR-2000; 2000US-0192916P.
PR 29-MAR-2000; 2000US-0192933P.
PR 29-MAR-2000; 2000US-0192933P.
PR 29-MAR-2000; 2000US-0192945P.
XX
XX (PHAA ) PHARMACIA & UPJOHN CO.
XX
XX Vogeli G;
XX
XX WPI; 2001-607458/69.
XX P-PSDB; AAU29441.
XX
XX Nucleic acid encoding G-protein coupled receptors, useful for the
XX prevention, diagnosis and treatment of mental disorders.
XX
XX Claim 4; Page 80; 274pp; English.
XX
XX Sequences AAS46819-AAS46946 represent cDNA molecules encoding human G
XX protein-coupled receptor (GPCR) polypeptides. The protein and DNA
XX sequences of the invention can be used to identify compounds which bind
XX to GPCR polypeptides and in screening for compounds that modulate GPCR
XX activity. By screening a human subject for the presence of mutations in
XX GPCR DNA, a GPCR-related disorder or a genetic predisposition can be
XX diagnosed. The sequences can also be used for treatment and prevention of
XX mental disorders such as schizophrenia, neurological disorders such as
XX manic depression, metabolic disorders such as obesity, cancer, rheumatoid
XX arthritis, thyroid disorders such as myxoedema, neurodegenerative
XX disorders such as Parkinson's disease, cardiovascular disorders such as
XX atherosclerosis, renal failure, autoimmune disorders, hyperproliferative
XX disorders such as psoriasis and viral infections such as those caused by
XX HIV
XX
XX SQ Sequence 649 BP; 197 A; 122 C; 166 G; 164 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 40.6 Length: 649
Score: 46.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 75.00% Mismatches: 0
Query Match: 86.79% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x AAS46880 (1-649)

QY 1 TrpIleGlyHisAspAlaGlyHis 8
|||:::|||||:::|||||
Db 428 TGGGTAGGGTATGATCTGGGCAT 451

RESULT 16
ABK81658
ID ABK81658 standard; DNA; 649 BP.
XX
XX ABK81658;
AC
XX
XX 13-AUG-2002 (first entry)
DT
XX
XX cDNA encoding novel G protein coupled receptor (nGCPR-x) #62.
DE
XX
XX G protein coupled receptor; nGCPR-x; immune response; thyroid disorder;
XX mental disorder; thyrotoxicosis; myxoedema; inflammatory condition;
XX Crohn's disease; cell differentiation; homeostasis; rheumatoid arthritis;
XX renal failure; autoimmune disorder; movement disorder; CNS disorder;
XX viral infection; human immunodeficiency virus; HIV; metabolic disorder;
XX cardiovascular disorder; diabetes; obesity; anorexia; cardiomyopathy;
XX poriferative disease; cancer; psoriasis; lung cancer; hormonal disorder;
XX sexual dysfunction; gene; ss.
XX
XX Homo sapiens.
OS
XX

```

PN US2002058306-A1.
 XX 16-MAY-2002.
 PD
 XX
 PF 16-MAR-2001; 2001US-00811284.
 XX
 XX 16-MAR-2000; 2000US-0189783P.
 PR 16-MAR-2000; 2000US-0189907P.
 PR 16-MAR-2000; 2000US-0189917P.
 PR 16-MAR-2000; 2000US-0189918P.
 PR 16-MAR-2000; 2000US-0189960P.
 PR 24-MAR-2000; 2000US-01921155P.
 PR 27-MAR-2000; 2000US-0192234P.
 PR 29-MAR-2000; 2000US-0192830P.
 PR 29-MAR-2000; 2000US-0192916P.
 PR 29-MAR-2000; 2000US-0192923P.
 PR 29-MAR-2000; 2000US-0192933P.
 PR 29-MAR-2000; 2000US-0192935P.
 PR 29-MAR-2000; 2000US-0192945P.
 XX
 XX (VOGE/) VOGELI G.
 PA
 XX
 XX Vogeli G;
 PI
 XX
 XX WPI; 2002-434856/46.
 DR P-PSDB; ABG60729.
 DR
 XX
 XX New isolated nucleic acid encoding a G protein coupled receptor for
 PT producing the receptor which can induce an immune response in a mammal.
 PT
 XX
 XX Claim 4; Page 53; 216pp; English.
 PS
 XX
 XX The invention describes an isolated nucleic acid (I) comprising a
 CC sequence encoding a portion of a G protein coupled receptor (ngPCR-x).
 CC (I) is used to produce a recombinant ngPCR-x polypeptide. A polypeptide
 CC encoded by (I) is used to induce an immune response in a mammal. ngPCR-x
 CC is used to identify a compound that binds to it and/or modulates it's
 CC activity. (I) is used to identify animal homologues of ngPCR-x. (I) can
 CC be used to diagnose a human subject as having a brain or genetic
 CC predisposition disorder, such as a mental disorder. (I) is used to screen
 CC for an ngPCR-x related disorder including thyroid disorders (e.g.
 CC thyrotoxicosis, myxoedema), renal failure, inflammatory conditions (e.g.
 CC Crohn's disease), diseases related to cell differentiation and
 CC homeostasis, rheumatoid arthritis, autoimmune disorders, movement
 CC disorders, CNS disorders, viral infections (e.g. Human immunodeficiency
 CC virus), metabolic and cardiovascular disorders (e.g. diabetes, obesity,
 CC anorexia, cardiomyopathies), proliferative diseases and cancers (e.g.
 CC psoriasis, lung cancer), hormonal disorders, sexual dysfunction and
 CC hereditary mental disorders in a human patient. A host cell comprising
 CC (I) is used to screen for a modulator of ngPCR-x activity. ngPCR-x is
 CC used to identify compounds that can treat mental disorders. The
 CC polypeptide encoded by (I) is used to purify a G protein from a sample.
 CC This sequence encodes a novel G protein coupled receptor (ngPCR-x)
 CC protein described in the invention
 XX
 XX Sequence 649 BP; 197 A; 122 C; 166 G; 164 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 40.6 Length: 649
 Score: 46.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 2
 Best Local Similarity: 75.00% Mismatches: 0
 Query Match: 86.79% Indels: 0
 DB: 6 Gaps: 0
 US-10-029-756-6 (1-8) x ABK81658 (1-649)
 Qy 1 TrpIleGlyHisAspAlaGlyHis 8
 Db 428 TGGTAGGGTATGATGCTGGGCAAT 451
 RESULT 17
 ADP65987

ID ADP65987 standard; DNA; 533 BP.
 XX
 AC ADP65987;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Mouse EST sequence #145 DNA.
 XX
 XX autoimmune disease; arthritis; gene expression analysis;
 KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
 KW antirheumatic; osteopathic; antigout; antinflammatory; dermatological;
 KW immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;
 KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
 KW immune; ds; mouse; murine.
 XX
 OS Mus musculus.
 XX
 XX W02003072827-A1.
 PN
 XX
 XX 04-SEP-2003.
 PD
 XX
 XX 31-OCT-2002; 2002WO-US035433.
 PF
 XX
 XX 31-OCT-2001; 2001US-0336220P.
 PR
 XX
 XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 PA
 XX
 XX Hirsch R, Thorton SL;
 PI
 XX
 XX WPI; 2003-712740/67.
 DR
 XX GENBANK; AI893697.
 DR
 XX
 XX Diagnosing and analyzing autoimmune disease using gene expression
 PT profiles and microarray technology, useful for diagnosing and treating
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
 PT gout.
 XX
 XX Disclosure; Page; 56pp; English.
 PS
 XX
 XX The invention relates to a novel method for diagnosing and analysing
 CC autoimmune disease or arthritides. The method comprises obtaining a
 CC patient sample containing mRNA, analysing gene expression using the mRNA
 CC that results in a gene expression signature of the mRNA, and using that
 CC gene expression signature to diagnose or analyse the autoimmune disease
 CC or arthritides in the patient, where gene expression of at least 60% of
 CC the genes correlates with that of the gene signature. The invention
 CC further comprises: a treatment of rheumatoid arthritis; identification of
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal;
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
 CC analyses of autoimmune disease or rheumatoid arthritis; screening the
 CC efficacy of a candidate drug in vitro for the treatment of collagen-
 CC induced arthritis; and reducing the symptoms associated with collagen-
 CC induced arthritis. The compositions of the invention have the following
 CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
 CC antigout, antinflammatory, dermatological, and immunomodulatory. The
 CC methods and compositions of the present invention are useful for
 CC diagnosing and treating autoimmune disease or arthritides, such as
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
 CC immune disease caused by an infectious agent. This polynucleotide
 CC represents a DNA sequence relating to the genes used in the analysis and
 CC treatment of autoimmune diseases or arthritides. Note: This sequence is
 CC not shown in the specification. It has been supplied in an electronic
 CC format from WIPO.
 XX
 XX Sequence 533 BP; 121 A; 135 C; 151 G; 126 T; 0 U; 0 Other;
 SQ
 Alignment Scores:
 Pred. No.: 49.8 Length: 533
 Score: 45.00 Matches: 6
 Percent Similarity: 87.50% Conservative: 1
 Best Local Similarity: 75.00% Mismatches: 1

Query Match: 84.91% Indels: 0
DB: 11 Gaps: 0

US-10-029-756-6 (1-8) x ADP65987 (1-533)

QY 1 TTPILLEGlyHieAspAlaGlyHis 8
||||:|||||
Db 301 TGGCTGGGACATGACCATGCTCAC 324

RESULT 18

AAC83979/c

ID AAC83979 standard; cDNA; 1697 BP.

XX

AC AAC83979;

XX

DT 02-MAR-2001 (first entry)

XX

DE Murine organic anion transporter 6 coding sequence.

XX

KW Murine; organic anion transporter 6; mOATP6; cancer; inflammation;
cardiovascular disease; central nervous system disorder; kidney disease;
KW liver disease; autoimmune disease; ss.

XX

OS Mus sp.

XX WO200070048-A1.

PN

PD

XX

XX

PF 15-MAY-2000; 2000WO-US013316.

XX

PR 14-MAY-1999; 99US-0134137P.

XX

PR 12-MAY-2000; 2000US-00570293.

XX

PA (SMTK) SMITHKLINE BEECHAM CORP.

XX

PA (SMTK) SMITHKLINE BEECHAM PLC.

XX

PI Feild J, Yue L, Ellens H;

XX

DR WPI; 2001-016235/02.

XX

DR P-PSDB; AAB49401.

XX

PS Claim 1; Page 27-28; 32pp; English.

XX

CC The present sequence is the coding sequence for murine organic anion
transporter 6 (mOATP6). mOATP6 protein is useful for screening compounds
CC which inhibit or stimulate the function of mOATP6 and also compounds that
CC neither agonise nor antagonise OATP6. The identified agonists and
CC antagonists are useful for prevention and treatment of human diseases,
CC including cancer, inflammation, cardiovascular disease, central nervous
CC system disorders, kidney diseases, liver disease and autoimmune diseases
XX
SQ Sequence 1697 BP; 316 A; 475 C; 496 G; 410 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 174 Length: 1697
Score: 45.00 Matches: 6
Percent Similarity: 87.50% Conservative: 1
Best Local Similarity: 75.00% Mismatches: 1
Query Match: 84.91% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x AAC83979 (1-1697)

QY 1 TTPILLEGlyHieAspAlaGlyHis 8

||||:|||||

Db 187 TGGCTGGGACATGACCATGCTCAC 164

RESULT 19

AAL54074
ID AAL54074 standard; DNA; 197997 BP.
XX
AC AAL54074;
XX
DT 25-SEP-2003 (first entry)
XX
DE Human transporter protein encoding genomic DNA.
XX
KW Neuroprotective; immune; drug screening; tissue typing; expression;
KW pharmacogenomic analysis; transporter protein; brain; muscle; human;
KW human therapeutic target; transgenic animal; gene; ds.
XX
OS Homo sapiens.
XX
FH Key
FH variation
FT
FT Location/Qualifiers
FT replace(1418,A)
FT /*tag= y
FT
FT /standard_name= "Single nucleotide polymorphism"
FT CDS
FT 2001..195996
FT /*tag= a
FT /product= "Human transporter protein"
FT /note= "This coding region contains 11 introns"
FT exon
FT 2001..2580
FT /*tag= b
FT
FT /number= 1
FT variation
FT replace(2360,G)
FT /*tag= z
FT
FT /standard_name= "Single nucleotide polymorphism"
FT intron
FT 2581..66087
FT /*tag= c
FT
FT /number= 1
FT variation
FT replace(4407,G)
FT /*tag= aa
FT
FT /standard_name= "Single nucleotide polymorphism"
FT variation
FT replace(5864,G)
FT /*tag= ab
FT
FT /standard_name= "Single nucleotide polymorphism"
FT variation
FT replace(6728,T)
FT /*tag= ac
FT
FT /standard_name= "Single nucleotide polymorphism"
FT variation
FT replace(6874,T)
FT /*tag= ad
FT
FT /standard_name= "Single nucleotide polymorphism"
FT variation
FT replace(7162,T)
FT /*tag= ae
FT
FT /standard_name= "Single nucleotide polymorphism"
FT variation
FT replace(7665,A)
FT /*tag= af
FT
FT /standard_name= "Single nucleotide polymorphism"
FT variation
FT replace(8358,A)
FT /*tag= ag
FT
FT /standard_name= "Single nucleotide polymorphism"
FT variation
FT replace(8364,T)
FT /*tag= ah
FT
FT /standard_name= "Single nucleotide polymorphism"
FT variation
FT replace(8755,C)
FT /*tag= ai
FT
FT /standard_name= "Single nucleotide polymorphism"
FT variation
FT replace(9082,T)
FT /*tag= aj
FT
FT /standard_name= "Single nucleotide polymorphism"
FT variation
FT replace(9211,A)
FT /*tag= ak
FT
FT /standard_name= "Single nucleotide polymorphism"
FT variation
FT replace(9739,A)
FT /*tag= al
FT
FT /standard_name= "Single nucleotide polymorphism"
FT variation
FT replace(9802,T)
FT /*tag= am
FT
FT /standard_name= "Single nucleotide polymorphism"
FT variation
FT replace(10716,A)
FT /*tag= an

```
FT /standard_name= "Single nucleotide polymorphism"
FT replace(10814,G)
FT /*tag= ao
FT /standard_name= "Single nucleotide polymorphism"
FT replace(11136,C)
FT /*tag= ap
FT /standard_name= "Single nucleotide polymorphism"
FT replace(11364,G)
FT /*tag= aq
FT /standard_name= "Single nucleotide polymorphism"
FT replace(11471,G)
FT /*tag= ar
FT /standard_name= "Single nucleotide polymorphism"
FT replace(11628,G)
FT /*tag= as
FT /standard_name= "Single nucleotide polymorphism"
FT replace(12029,G)
FT /*tag= at
FT /standard_name= "Single nucleotide polymorphism"
FT replace(12349,C)
FT /*tag= au
FT /standard_name= "Single nucleotide polymorphism"
FT replace(12579,G)
FT /*tag= av
FT /standard_name= "Single nucleotide polymorphism"
FT replace(12663,G)
FT /*tag= aw
FT /standard_name= "Single nucleotide polymorphism"
FT replace(12891,T)
FT /*tag= ax
FT /standard_name= "Single nucleotide polymorphism"
FT replace(12961,A)
FT /*tag= ay
FT /standard_name= "Single nucleotide polymorphism"
FT replace(13062,G)
FT /*tag= az
FT /standard_name= "Single nucleotide polymorphism"
FT replace(13352,G)
FT /*tag= ba
FT /standard_name= "Single nucleotide polymorphism"
FT replace(13474,R)
FT /*tag= bb
FT /standard_name= "Single nucleotide polymorphism"
FT replace(13899,G)
FT /*tag= bc
FT /standard_name= "Single nucleotide polymorphism"
FT replace(14334,C)
FT /*tag= bd
FT /standard_name= "Single nucleotide polymorphism"
FT replace(14421,A)
FT /*tag= be
FT /standard_name= "Single nucleotide polymorphism"
FT replace(14569,G)
FT /*tag= bf
FT /standard_name= "Single nucleotide polymorphism"
FT replace(14794,A)
FT /*tag= bg
FT /standard_name= "Single nucleotide polymorphism"
FT replace(14980,T)
FT /*tag= bh
FT /standard_name= "Single nucleotide polymorphism"
FT replace(16099,G)
FT /*tag= bi
FT /standard_name= "Single nucleotide polymorphism"
FT replace(16055,G)
FT /*tag= bj
FT /standard_name= "Single nucleotide polymorphism"
FT replace(21114,C)
FT /*tag= bk
FT /standard_name= "Single nucleotide polymorphism"
FT replace(21566,A)
FT /*tag= bl
FT /standard_name= "Single nucleotide polymorphism"
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FT variation
FT replace(21713,C)
FT /*tag= bm
FT /standard_name= "Single nucleotide polymorphism"
FT replace(21957,T)
FT /*tag= bn
FT /standard_name= "Single nucleotide polymorphism"
FT replace(22489,C)
FT /*tag= bo
FT /standard_name= "Single nucleotide polymorphism"
FT replace(22637,C)
FT /*tag= bp
FT /standard_name= "Single nucleotide polymorphism"
FT replace(24154,A)
FT /*tag= bq
FT /standard_name= "Single nucleotide polymorphism"
FT replace(25140,G)
FT /*tag= br
FT /standard_name= "Single nucleotide polymorphism"
FT replace(25433,T)
FT /*tag= bs
FT /standard_name= "Single nucleotide polymorphism"
FT replace(26675,T)
FT /*tag= bt
FT /standard_name= "Single nucleotide polymorphism"
FT replace(26871,T)
FT /*tag= bu
FT /standard_name= "Single nucleotide polymorphism"
FT replace(26877,A)
FT /*tag= bv
FT /standard_name= "Single nucleotide polymorphism"
FT replace(27968,A)
FT /*tag= bw
FT /standard_name= "Single nucleotide polymorphism"
FT replace(28071,A)
FT /*tag= bx
FT /standard_name= "Single nucleotide polymorphism"
FT replace(28995,G)
FT /*tag= by
FT /standard_name= "Single nucleotide polymorphism"
FT replace(29184,A)
FT /*tag= bz
FT /standard_name= "Single nucleotide polymorphism"
FT replace(29198,T)
FT /*tag= ca
FT /standard_name= "Single nucleotide polymorphism"
FT replace(30098,A)
FT /*tag= cb
FT /standard_name= "Single nucleotide polymorphism"
FT replace(30387,G)
FT /*tag= cc
FT /standard_name= "Single nucleotide polymorphism"
FT replace(30401,T)
FT /*tag= cd
FT /standard_name= "Single nucleotide polymorphism"
FT replace(30468,G)
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Alignment Scores:
Pred. No.: 2.97e+04 Length: 197997
Score: 45.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 75.00% Mismatches: 0
Query Match: 84.91% Indels: 0
DB: 10 Gaps: 0
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US-10-029-756-6 (1-8) x AAL54074 (1-197997)

```
Qy 1 TrpIleGlyHisaePalaglyHis 8
Db 185026 TGGGTCGGGCATGATCTGGAAT 185049
RESULT 20
ABL14177/c
ID ABL14177 standard; cDNA; 2734 BP.
```

XX AC ABL14177;
 XX DT 26-MAR-2002 (first entry)
 XX DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 37013.
 XX KW Drosophila; developmental biology; cell signalling; insecticide;
 XX KW pharmaceutical; gene; ss.
 XX OS Drosophila melanogaster.
 XX PN WO200171042-A2.
 XX PD 27-SEP-2001.
 XX PF 23-MAR-2001; 2001WO-US009231.
 XX PR 23-MAR-2000; 2000US-0191637P.
 XX PR 11-JUL-2000; 2000US-00614150.
 XX PA (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX DR WPI; 2001-656860/75.
 XX DR P-PSDB; ABB70074.
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
 XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
 XX PT interactions.
 XX PS Claim 1; SEQ ID NO 37013; 21pp + Sequence Listing; English.
 XX CC The invention relates to an isolated nucleic acid detection reagent
 XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
 XX CC useful in developmental biology and in elucidating cell signalling and
 XX CC cell-cell interactions in higher eukaryotes for the development of
 XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
 XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 XX CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 XX CC ABB72072). The sequence data for this patent did not form part of the
 XX CC printed specification, but was obtained in electronic format directly
 XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 2734 BP; 719 A; 760 C; 749 G; 506 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 442 Length: 2734
 Score: 44.00 Matches: 6
 Percent Similarity: 87.50% Conservative: 1
 Best Local Similarity: 75.00% Mismatches: 1
 Query Match: 83.02% Indels: 0
 DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x ABL14177 (1-2734)
 QY 1 TtpileGlyHisAspAlaGlyHis 8
 DB 704 TGGATGGGGCATTTCAGCTGGGCAT 681

RESULT 21
 ABL14176/c
 ID ABL14176 standard; cDNA; 5679 BP.
 XX AC ABL14176;
 XX DT 26-MAR-2002 (first entry)
 XX DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 37010.
 XX KW Drosophila; developmental biology; cell signalling; insecticide;
 XX KW pharmaceutical; gene; ss.

XX OS Drosophila melanogaster.
 XX PN WO200171042-A2.
 XX PD 27-SEP-2001.
 XX PF 23-MAR-2001; 2001WO-US009231.
 XX PR 23-MAR-2000; 2000US-0191637P.
 XX PR 11-JUL-2000; 2000US-00614150.
 XX PA (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX DR WPI; 2001-656860/75.
 XX DR P-PSDB; ABB70073.
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
 XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
 XX PT interactions.
 XX PS Claim 1; SEQ ID NO 37010; 21pp + Sequence Listing; English.
 XX CC The invention relates to an isolated nucleic acid detection reagent
 XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
 XX CC useful in developmental biology and in elucidating cell signalling and
 XX CC cell-cell interactions in higher eukaryotes for the development of
 XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
 XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 XX CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 XX CC ABB72072). The sequence data for this patent did not form part of the
 XX CC printed specification, but was obtained in electronic format directly
 XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 5679 BP; 1627 A; 1375 C; 1297 G; 1380 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 974 Length: 5679
 Score: 44.00 Matches: 6
 Percent Similarity: 87.50% Conservative: 1
 Best Local Similarity: 75.00% Mismatches: 1
 Query Match: 83.02% Indels: 0
 DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x ABL14176 (1-5679)
 QY 1 TtpileGlyHisAspAlaGlyHis 8
 DB 2023 TGGATGGGGCATTTCAGCTGGGCAT 2000

RESULT 22
 ABL1186/c
 ID ABL1186 standard; DNA; 472 BP.
 XX AC ABL1186;
 XX DT 26-JUN-2003 (first entry)
 XX DE Toxicity modelling related rat gene SEQ ID No 888.
 XX KW Toxic effect; gene expression profile; renal toxicity; toxicity marker;
 XX KW database; drug screening; toxicity assay; rat; ds.
 XX OS Rattus norvegicus.
 XX PN WO200295000-A2.
 XX PD 28-NOV-2002.
 XX PF 22-MAY-2002; 2002WO-US016173.
 XX XX

PR 22-MAY-2001; 2001US-0292335P.
PR 13-JUN-2001; 2001US-0297523P.
PR 19-JUN-2001; 2001US-0298925P.
PR 10-JUL-2001; 2001US-0303807P.
PR 10-JUL-2001; 2001US-0303808P.
PR 10-JUL-2001; 2001US-0303810P.
PR 28-AUG-2001; 2001US-0315047P.
PR 27-SEP-2001; 2001US-0324928P.
PR 22-OCT-2001; 2001US-0330462P.
PR 01-NOV-2001; 2001US-0330867P.
PR 21-NOV-2001; 2001US-0331805P.
PR 06-DEC-2001; 2001US-0336114P.
PR 19-DEC-2001; 2001US-0340873P.
PR 21-FEB-2002; 2002US-0357842P.
PR 21-FEB-2002; 2002US-0357843P.
PR 21-FEB-2002; 2002US-0357844P.
PR 15-MAR-2002; 2002US-0364113P.
PR 08-APR-2002; 2002US-0370114P.
PR 08-APR-2002; 2002US-0370206P.
PR 08-APR-2002; 2002US-0370247P.
PR 17-APR-2002; 2002US-0372794P.
PR 21-APR-2002; 2002US-0371679P.
XX (GENE-) GENE LOGIC INC.
XX
XX Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Elashoff M;
XX WPI; 2003-148464/14.
DR
XX Predicting at least one toxic effect of a compound, useful for toxicity
PT modeling, comprises preparing a gene expression profile of a tissue or
PT cell sample exposed to the compound, and comparing the gene expression
PT profile to a database.
XX
XX Example 4; Page; 446pp; English.
XX
XX The invention relates to a novel method of predicting at least one toxic
CC effect of a compound. The method comprises a gene expression profile of a
CC tissue or cell sample exposed to the compound, and comparing the gene
CC expression profile to a database comprising at least part of the data or
CC information given in the specification. The methods are useful for
CC predicting at least one toxic effect of a compound, predicting the
CC progression of a toxic effect of a compound, predicting the renal
CC toxicity of a compound, or identifying toxicity markers in tissues or
CC cells exposed to known renal toxin. The genes are useful as toxicity
CC markers in drug screening and toxicity assays, in monitoring disease or
CC physiological states, or disease progression. This polynucleotide
CC represents a rat DNA sequence relating to the toxic effect database
CC described in the specification. NOTE: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from the World Intellectual Property
CC Organization
XX
SQ Sequence 472 BP; 131 A; 100 C; 126 G; 115 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 101 Length: 472
Score: 43.00 Matches: 5
Percent Similarity: 87.50% Conservative: 2
Best Local Similarity: 62.50% Mismatches: 1
Query Match: 81.13% Indels: 0
DB: 10 Gaps: 0
US-10-029-756-6 (1-8) x ABT41186 (1-472)
Qy 1 TrpIleGlyHisAspAlaGlyHis 8
|||:|||||:|||||:|||||
Db 463 TGGGTGGGCCATCAATCTGGCCAT 440
RESULT 23
ABD06890
ID ABD06890 standard; DNA; 1152 BP.
XX

AC ABD06890;
XX
DT 29-JUL-2004 (first entry)
XX
XX Pseudomonas aeruginosa polynucleotide #5494.
DE
XX Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KW antibacterial.
XX
XX Pseudomonas aeruginosa.
OS
XX US6551795-B1.
PN
XX 22-APR-2003.
PD
XX 18-FEB-1999; 99US-00252991.
PF
XX 18-FEB-1998; 98US-0074788P.
PR
XX 27-JUL-1998; 98US-0094190P.
PR
XX (GENO-) GENOME THERAPEUTICS CORP.
PA
XX Rubenfield MJ, Nolling J, Deloughery C, Bush D;
PI WPI; 2003-615309/58.
XX P-PSDB; ABO73319.
DR
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
PT
XX Disclosure; SEQ ID NO 5494; 455pp; English.
PS
XX The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABD01397-ABD17967 represent P. aeruginosa polynucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html
XX
SQ Sequence 1152 BP; 156 A; 437 C; 371 G; 188 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 325 Length: 1152
Score: 42.50 Matches: 8
Percent Similarity: 88.89% Conservative: 0
Best Local Similarity: 88.89% Mismatches: 0
Query Match: 80.19% Indels: 1
DB: 11 Gaps: 1
US-10-029-756-6 (1-8) x ABD06890 (1-1152)
Qy 1 Trp---IleGlyHisAspAlaGlyHis 8
|||:|||||:|||||:|||||
Db 1075 TGGAGCATTTGGCCATGACGAGGCAC 1101
RESULT 24
ACH87364
ID ACH87364 standard; DNA; 475 BP.
XX
XX ACH87364;
XX
DT 29-JUL-2004 (first entry)

XX Human genome derived single exon probe #20559.
 DE Human; probe; ss; gene expression; single exon probe; microarray;
 XX alternative splicing event; genomic alteration.
 KW Homo sapiens.
 OS
 XX
 XX US2003194704-A1.
 FN
 PD 16-OCT-2003.
 XX
 XX 03-APR-2002; 2002US-00029386.
 XX
 XX 03-APR-2002; 2002US-00029386.
 XX
 XX (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANZ/) HANZEL D K.
 XX
 XX Penn SG, Rank DR, Hanzel DK;
 XX WPI; 2004-119264/12.
 XX
 XX New human genome-derived single exon nucleic acid probes useful for human
 FT gene expression analysis, for identifying or characterizing alternative
 FT splicing events, for assessing genomic alterations or as tools for
 FT surveying tissues.
 XX
 PS Claim 1; SEQ ID NO 20559; 80pp; English.
 XX
 XX The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridises under high stringency conditions to a nucleic acid molecule
 CC expressed in human cells or tissues. Also included are a spatially-
 CC addressable set of single exon nucleic acid probes for measuring human
 CC gene expression (comprising a plurality of single exon nucleic acid
 CC probes cited above, where each of the plurality of probes is separately
 CC and addressably isolatable or amplifiable from the plurality), a single
 CC exon microarray for measuring human gene expression, a method of
 CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subscription, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above. The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterising
 CC alternative splicing events, in detecting and characterising gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docID=20030194704
 XX
 SQ Sequence 475 BP; 106 A; 107 C; 164 G; 98 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 154 Length: 475
 Score: 42.00 Matches: 6
 Percent Similarity: 75.00% Conservative: 0

Best Local Similarity: 75.00% Mismatches: 2
 Query Match: 79.25% Indels: 0
 DB: 12 Gaps: 0
 US-10-029-756-6 (1-8) x ACH87364 (1-475)
 QY 1 TptileGlyHisAspAlaGlyHis 8
 Db 356 TGGATAGGGCATTCCATTGGCCAC 379
 RESULT 25
 ACH82639
 ID ACH82639 standard; DNA; 487 BP.
 XX
 AC ACH82639;
 DT 29-JUL-2004 (first entry)
 XX
 DE Human genome derived single exon probe #15834.
 XX
 KW Human; probe; ss; gene expression; single exon probe; microarray;
 KW alternative splicing event; genomic alteration.
 XX
 OS Homo sapiens.
 XX
 XX US2003194704-A1.
 XX
 PD 16-OCT-2003.
 XX
 XX 03-APR-2002; 2002US-00029386.
 XX
 XX 03-APR-2002; 2002US-00029386.
 XX
 XX (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANZ/) HANZEL D K.
 XX
 XX Penn SG, Rank DR, Hanzel DK;
 XX WPI; 2004-119264/12.
 XX
 XX New human genome-derived single exon nucleic acid probes useful for human
 FT gene expression analysis, for identifying or characterizing alternative
 FT splicing events, for assessing genomic alterations or as tools for
 FT surveying tissues.
 XX
 PS Claim 1; SEQ ID NO 15834; 80pp; English.
 XX
 XX The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridises under high stringency conditions to a nucleic acid molecule
 CC expressed in human cells or tissues. Also included are a spatially-
 CC addressable set of single exon nucleic acid probes for measuring human
 CC gene expression (comprising a plurality of single exon nucleic acid
 CC probes cited above, where each of the plurality of probes is separately
 CC and addressably isolatable or amplifiable from the plurality), a single
 CC exon microarray for measuring human gene expression, a method of
 CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subscription, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above. The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their

CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterising
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030194704

XX SQ Sequence 487 BP; 119 A; 113 C; 112 G; 143 T; 0 U; 0 Other;

Alignment Scores: Length: 487
Pred. No.: 158 Matches: 6
Score: 42.00 Conservative: 0
Percent Similarity: 75.00% Mismatches: 2
Best Local Similarity: 75.00% Indels: 0
Query Match: 79.25% Gaps: 0
DB: 12

US-10-029-756-6 (1-8) x ACH82639 (1-487)

Qy 1 TpileGlyHisAspAlaGlyHis 8
 |||||
Db 58 TGGATTGGGCACAGCATGGGCCAC 81

RESULT 26

ABQ60110/c

ID ABQ60110 standard; cDNA; 498 BP.

XX AC ABQ60110;

XX DT 02-AUG-2002 (first entry)

XX DE Human colon cancer related nucleotide sequence SEQ ID NO:3805.

XX KW Human; colon cancer; cancer; tissue profiling; forensic; mapping;

XX KW Genetic analysis; diagnostic; antisense therapy; gene; ss.

XX OS Homo sapiens.

XX PN WO200229086-A2.

XX PD 11-APR-2002.

XX PF 02-OCT-2001; 2001WO-US030732.

XX PR 02-OCT-2000; 2000US-0237271P.

XX PA (FARB) BAYER CORP.

XX PI Burgess C, Astle JH, Carroll E, Catino TJ, Dwivedi P, Molino GA;
XX PI Thiaglingam A, Lewis ME;

XX DR WPI; 2002-426115/45.

XX PT New isolated nucleic acid that is differentially expressed in cancer
XX PT tissues useful for determining the presence of colon cancer in a cell or
XX PT tissue type, and in antisense therapy.

XX PS Claim 1; Fig 1; 796pp; English.

XX CC ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially
XX CC expressed in cancer tissues. ABB78993 to ABB79004 represent proteins
XX CC encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be
XX CC used in antisense therapy. An antibody immunoreactive with a polypeptide
XX CC encoded by (I) is useful for detecting cancer in a patient sample, and
XX CC for detecting the presence or absence of a polynucleotide encoded by a
XX CC nucleic acid which hybridises to (I) in a cell. A probe/primer derived
XX CC from (I) can be used for determining the presence of a nucleic acid which
XX CC hybridises to (I), and for determining the phenotype of cells in a sample
XX CC of cells from a patient. (I) is useful for determining the presence of

CC colon cancer in a cell or tissue type, for determining the presence or
CC state of other type of cancer, in antisense therapy, to generate
CC macroarrays on a solid surface, to identify a chromosome on which the
CC corresponding gene resides, and in tissue profiling, forensics, genetic
CC analysis, mapping and diagnostic applications. (I) can be used to raise
CC antibodies, and to screen for peptide analogues and antagonists
XX SQ Sequence 498 BP; 138 A; 137 C; 105 G; 118 T; 0 U; 0 Other;

Alignment Scores: Length: 498
Pred. No.: 162 Matches: 6
Score: 42.00 Conservative: 0
Percent Similarity: 75.00% Mismatches: 2
Best Local Similarity: 75.00% Indels: 0
Query Match: 79.25% Gaps: 0
DB: 6

US-10-029-756-6 (1-8) x ABQ60110 (1-498)

Qy 1 TpileGlyHisAspAlaGlyHis 8
 |||||
Db 161 TGGATTGGGCACAGCATGGGCCAC 138

RESULT 27

ACH77282/c

ID ACH77282 standard; DNA; 521 BP.

XX AC ACH77282;

XX DT 29-JUL-2004 (first entry)

XX DE Human genome derived single exon probe #10477.

XX KW Human; probe; ss; gene expression; single exon probe; microarray;

XX KW alternative splicing event; genomic alteration.

XX OS Homo sapiens.

XX PN US2003194704-A1.

XX PD 16-OCT-2003.

XX PF 03-APR-2002; 2002US-00029386.

XX PR 03-APR-2002; 2002US-00029386.

XX PA (PENN/) PENN S G.

XX PA (RANK/) RANK D R.

XX PA (HANZ/) HANZEL D K.

XX PI Penn SG, Rank DR, Hanzel DK;

XX DR WPI; 2004-119264/12.

XX PT New human genome-derived single exon nucleic acid probes useful for human
XX PT gene expression analysis, for identifying or characterizing alternative
XX PT splicing events, for assessing genomic alterations or as tools for
XX PT surveying tissues.

XX PS Claim 15; SEQ ID NO 10477; 80pp; English.

XX CC The invention relates to a nucleic acid probe for measuring human gene
XX CC expression, comprising any of the 27,400 fully defined nucleotide
XX CC sequences in the specification, or their complements or fragments, and
XX CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
XX CC fully defined in the specification. The probe is a single exon probe that
XX CC hybridises under high stringency conditions to a nucleic acid molecule
XX CC expressed in human cells or tissues. Also included are a spatially-
XX CC addressable set of single exon nucleic acid probes for measuring human
XX CC gene expression (comprising a plurality of single exon nucleic acid
XX CC probes cited above, where each of the plurality of probes is separately
XX CC and addressably isolatable or amplifiable from the plurality), a single
XX CC exon microarray for measuring human gene expression, a method of

CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subsequence, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above. The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterizing
 CC alternative splicing events, in detecting and characterizing gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704
 XX SQ Sequence 521 BP; 118 A; 165 C; 119 G; 119 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 170 Length: 521
 Score: 42.00 Matches: 6
 Percent Similarity: 75.00% Conservative: 0
 Best Local Similarity: 75.00% Mismatches: 2
 Query Match: 79.25% Indels: 0
 DB: 12 Gaps: 0

US-10-029-756-6 (1-8) x ACH77282 (1-521)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
 |||||
 Db 69 TGGATAGGCGCATTCATTGGCCAC 46

RESULT 28
 ABZ34667
 ID ABZ34667 standard; cDNA; 522 BP.
 AC ABZ34667;
 XX
 DT 04-FEB-2003 (first entry)
 DE Coding sequence SEQ ID 25, downregulated in osteogenesis.
 XX
 KW Osteopathic; osteogenesis modulator; gene therapy; osteogenesis;
 KW osteoporosis; bone disease; downregulator; human; ss.
 XX Homo sapiens.
 OS
 XX WO200281745-A2.
 FN
 XX 17-OCT-2002.
 PD
 XX 05-APR-2002; 2002WO-IB002211.
 PF
 XX 05-APR-2001; 2001US-0281400P.
 PR
 XX (AVET) AVENTIS PHARMA SA.

XX Garcia T, Roman Roman S, Baron R, Call K, Theilhaber J;
 PI Connolly T, Jackson A, Bushnell SE, Rawadi G;
 XX WPI; 2003-058567/05.
 DR
 XX Novel isolated nucleic acid upregulated/downregulated in osteogenesis,
 PT useful for bone disease therapy in subject.
 XX

PS Claim 27; Page 93; 237pp; English.
 XX The present invention relates to novel nucleotide sequences, which are
 CC differentially expressed in models of osteogenesis upon being put in
 CC contact with a stimulator of osteogenesis. The present sequence is one
 CC such sequence. This sequence can be used for diagnosing osteoporosis/bone
 CC disease in a patient, promoting osteogenesis and/or preventing
 CC osteoporosis/bone disease. The present sequence encodes a secreted
 CC protein
 XX SQ Sequence 522 BP; 154 A; 120 C; 153 G; 95 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 170 Length: 522
 Score: 42.00 Matches: 6
 Percent Similarity: 75.00% Conservative: 0
 Best Local Similarity: 75.00% Mismatches: 2
 Query Match: 79.25% Indels: 0
 DB: 8 Gaps: 0

US-10-029-756-6 (1-8) x ABZ34667 (1-522)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
 |||||
 Db 194 TGGATTGGGCACCCGGGAGGCAC 217

RESULT 29
 ADB57297
 ID ADB57297 standard; DNA; 539 BP.
 XX
 AC ADB57297;
 XX
 DT 04-DEC-2003 (first entry)
 DE Toxicity-related gene, SEQ ID 2323.
 XX
 KW Toxic; toxin; gene expression profile; hepatotoxicity; liver;
 KW drug screening; toxicity assay; da.
 XX Unidentified.
 OS
 XX WO2003064624-A2.
 FN
 XX 07-AUG-2003.
 PD
 XX 31-JAN-2003; 2003WO-US003194.
 PF
 XX 31-JAN-2002; 2002US-00060087.
 PR
 PR 15-MAR-2002; 2002US-0364045P.
 PR 15-MAR-2002; 2002US-0364055P.
 PR 30-DEC-2002; 2002US-0436643P.
 XX
 XX (GENE-) GENE LOGIC INC.
 PA
 XX Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Elashoff M;
 PI WPI; 2003-689530/65.

XX Predicting a toxic effect of a compound, useful in identifying toxicity
 PT markers in liver tissues or cells for drug screening and toxicity assays,
 PT comprises preparing gene expression profile of tissue or cells exposed to
 PT the compound.
 XX
 PS Claim 1; SEQ ID NO 2323; 1156pp; English.

XX The present invention relates to a method for predicting a toxic effect
 CC of a compound. The method comprises preparing a gene expression profile
 CC of a tissue or cell sample exposed to the compound, and comparing the
 CC gene expression profile to a database comprising SEQ ID 1-4925, where
 CC differential expression of the gene indicates at least one toxic effect.
 CC The method is useful for predicting at least one toxic effect of a
 CC compound, predicting hepatotoxicity or the progression of a toxic effect
 CC of a compound, identifying an agent that modulates the onset or

XX New human genome-derived single exon nucleic acid probe for measuring human gene
 PT gene expression analysis, for identifying or characterizing alternative
 PT splicing events, for assessing genomic alterations or as tools for
 PT surveying tissues.
 XX Claim 15; SEQ ID NO 6847; 80pp; English.
 XX The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridises under high stringency conditions to a nucleic acid molecule
 CC expressed in human cells or tissues. Also included are a spatially-
 CC addressable set of single exon nucleic acid probes for measuring human
 CC gene expression (comprising a plurality of single exon nucleic acid
 CC probes cited above, where each of the plurality of probes is separately
 CC and addressably isolatable or amplifiable from the plurality), a single
 CC exon microarray for measuring human gene expression, a method of
 CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subscription, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above. The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterising
 CC alternative splicing events, in detecting and characterising gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704
 XX
 SQ Sequence 565 BP; 126 A; 135 C; 202 G; 102 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 186 Length: 565
 Score: 42.00 Matches: 6
 Percent Similarity: 75.00% Conservative: 0
 Best Local Similarity: 75.00% Mismatches: 2
 Query Match: 79.25% Indels: 0
 DB: 12 Gaps: 0

US-10-029-756-6 (1-8) x ACH73652 (1-565)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
 |||||
 Db 241 TGGATAGGGCATTCATTGGCCAC 264
 |||||

RESULT 32
 ACH90983/c
 ID ACH90983 standard; DNA; 571 BP.
 XX
 AC ACH90983;
 XX
 XX 29-JUL-2004 (first entry)
 XX
 XX Human genome derived single exon probe #24178.
 DE
 XX Human; probe; ss; gene expression; single exon probe; microarray;
 KW alternative splicing event; genomic alteration.
 XX

OS Homo sapiens.
 XX US2003194704-A1.
 PN
 XX 16-OCT-2003.
 PD
 XX
 XX 03-APR-2002; 2002US-00029386.
 PF
 XX 03-APR-2002; 2002US-00029386.
 PR
 XX (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANZ/) HANZEL D K.
 XX
 XX Penn SG, Rank DR, Hanzel DK;
 PI WPI; 2004-119264/12.
 XX
 XX New human genome-derived single exon nucleic acid probes useful for human
 PT gene expression analysis, for identifying or characterizing alternative
 PT splicing events, for assessing genomic alterations or as tools for
 PT surveying tissues.
 XX
 PS Claim 1; SEQ ID NO 24178; 80pp; English.
 XX
 CC The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridises under high stringency conditions to a nucleic acid molecule
 CC expressed in human cells or tissues. Also included are a spatially-
 CC addressable set of single exon nucleic acid probes for measuring human
 CC gene expression (comprising a plurality of single exon nucleic acid
 CC probes cited above, where each of the plurality of probes is separately
 CC and addressably isolatable or amplifiable from the plurality), a single
 CC exon microarray for measuring human gene expression, a method of
 CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC methods of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subscription, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above. The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterising
 CC alternative splicing events, in detecting and characterising gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704
 XX
 SQ Sequence 571 BP; 105 A; 203 C; 137 G; 126 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 188 Length: 571
 Score: 42.00 Matches: 6
 Percent Similarity: 75.00% Conservative: 0
 Best Local Similarity: 75.00% Mismatches: 2
 Query Match: 79.25% Indels: 0
 DB: 12 Gaps: 0

US-10-029-756-6 (1-8) x ACH90983 (1-571)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
 Db 320 TGGATAGGCATTCCTATGGCCAC 297
 RESULT 33
 ACH68939 standard; DNA; 589 BP.
 XX
 AC ACH68939;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Human genome derived single exon probe #2134.
 XX
 KW Human; probe; ss; gene expression; single exon probe; microarray;
 KW alternative splicing event; genomic alteration.
 XX
 OS Homo sapiens.
 XX
 FN US2003194704-A1.
 XX
 PD 16-OCT-2003.
 XX
 PF 03-APR-2002; 2002US-00029386.
 XX
 PR 03-APR-2002; 2002US-00029386.
 XX
 PA (PENN/) PENN S G.
 PA (RANK/) RANK D R.
 PA (HANK/) HANKEL D K.
 XX
 PI Penn SG, Rank DR, Hanzel DK;
 XX
 DR WPI; 2004-119264/12.
 XX
 PT New human genome-derived single exon nucleic acid probes useful for human
 PT gene expression analysis, for identifying or characterizing alternative
 PT splicing events, for assessing genomic alterations or as tools for
 PT surveying tissues.
 XX
 PS Claim 15; SEQ ID NO 2134; 80pp; English.
 XX
 CC The invention relates to a nucleic acid probe for measuring human gene
 CC expression, comprising any of the 27,400 fully defined nucleotide
 CC sequences in the specification, or their complements or fragments, and
 CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
 CC fully defined in the specification. The probe is a single exon probe that
 CC hybridises under high stringency conditions to a nucleic acid molecule
 CC expressed in human cells or tissues. Also included are a spatially-
 CC addressable set of single exon nucleic acid probes for measuring human
 CC gene expression (comprising a plurality of single exon nucleic acid
 CC probes cited above, where each of the plurality of probes is separately
 CC and addressably isolatable or amplifiable from the plurality), a single
 CC exon microarray for measuring human gene expression, a method of
 CC measuring human gene expression, a vector comprising the single exon
 CC probe cited above, an ORF-encoded peptide comprising at least 8
 CC contiguous amino acids of any of the above-mentioned amino acid
 CC sequences (optionally with conservative amino acid substitutions), an
 CC isolated antibody that binds specifically to a peptide cited above,
 CC a method of selling and/or licensing single exon probes or microarrays to
 CC a customer desiring to measure gene expression, a method of providing
 CC human gene expression data by subscription, and a computer-readable
 CC storage medium which contains a database having a plurality of records
 CC (each record including data on the expression of a single exon probe
 CC cited above). The probe, methods and apparatus are useful in gene
 CC expression analysis. The probes may be used as tools for surveying
 CC tissues to detect the presence of expressed messages that contain their
 CC specific exon, or in constructing genome-derived single exon microarrays.
 CC In addition, the probes are used in identifying and characterising
 CC alternative splicing events, in detecting and characterising gross
 CC alterations in the genomic locus that includes their exon, in assessing
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human

CC single exon probe of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?DocID=20030194704
 XX
 SQ Sequence 589 BP; 148 A; 139 C; 140 G; 162 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 194 Length: 589
 Score: 42.00 Matches: 6
 Percent Similarity: 75.00% Conservative: 0
 Best Local Similarity: 75.00% Mismatches: 2
 Query Match: 79.25% Indels: 0
 DB: 12 Gaps: 0
 US-10-029-756-6 (1-8) x ACH68939 (1-589)
 Qy 1 TrpIleGlyHisAspAlaGlyHis 8
 Db 87 TGGATTGGCACAGCATGGGCCAC 110
 RESULT 34
 AAS05580/c
 ID AAS05580 standard; DNA; 650 BP.
 XX
 AC AAS05580;
 XX
 DT 07-SEP-2001 (first entry)
 XX
 DE Mammalian vestibular system geotactic behaviour modulator gene #180.
 XX
 KW Mammalian vestibular system; invertebrate; geotactic behaviour; vertigo;
 KW graviperceptive disorder; motion sickness; labyrinthitis; sypphilis; ds;
 KW Meniere's disease; acoustic neuroma; multiple sclerosis; epilepsy;
 KW trauma; infection of the middle ear; ototoxic agent exposure.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200140519-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 01-DEC-2000; 2000WO-US032639.
 XX
 PR 02-DEC-1999; 99US-0168579P.
 PR 26-SEP-2000; 2000US-00669751.
 XX
 PA (NEUR-) NEUROSCIENCES RES FOUND INC.
 XX
 PI Greenspan RJ;
 XX
 DR WPI; 2001-356159/37.
 XX
 PT New isolated nucleic acid having mammalian vestibular system-modulating
 PT activity useful in the treatment of disorders such as motion sickness and
 PT vertigo.
 XX
 PS Claim 59; Page 151; 179pp; English.
 XX
 CC The sequences shown in AAS05401-AAS05661 represent DNA with mammalian
 CC vestibular system-modulating activity. The DNA sequences can be used in a
 CC method whereby a first and second strain of an invertebrate is obtained,
 CC and both are subjected to conditions in which the strains exhibit
 CC different geotactic behaviour. Genes that are differentially expressed in
 CC the first strain relative to the second strain are then identified.
 CC Mammalian genes having substantially the same nucleic acid sequence as
 CC these genes are used to decrease the symptoms of graviorperceptive
 CC disorders such as motion sickness, vertigo, labyrinthitis, Meniere's
 CC disease, acoustic neuroma, multiple sclerosis, sypphilis, trauma,
 CC infection of the middle ear, exposure to ototoxic agents and epilepsy
 XX
 SQ Sequence 650 BP; 173 A; 162 C; 131 G; 184 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 216 Length: 650
 Score: 42.00 Matches: 6
 Percent Similarity: 75.00% Conservative: 0
 Best Local Similarity: 75.00% Mismatches: 2
 Query Match: 79.25% Indels: 0
 DB: 5 Gaps: 0

US-10-029-756-6 (1-8) x AAS05580 (1-650)

Qy 1 TtpileGlyHisaspAlaGlyHis 8
 Db 415 TGGTGTGGGCATAGCGCAGGCAC 392

RESULT 35
 AAH05583/C
 ID AAH05583 standard; cDNA; 734 BP.
 XX
 AC AAH05583;
 XX
 DT 26-JUN-2001 (first entry)
 XX
 DE Human cDNA clone (5'-primer) SEQ ID NO:2418.
 XX
 KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 XX
 OS Homo sapiens.
 XX
 PN EPI074617-A2.
 XX
 PD 07-FEB-2001.
 XX
 PF 28-JUL-2000; 2000EP-00116126.
 XX
 PR 29-JUL-1999; 99JP-00248036.
 PR 27-AUG-1999; 99JP-00300253.
 PR 11-JAN-2000; 2000JP-00118776.
 PR 02-MAY-2000; 2000JP-00183767.
 PR 09-JUN-2000; 2000JP-00241899.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX
 DR WPI; 2001-318749/34.
 XX
 XX
 PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
 PS Claim 1; SEQ ID NO 2418; 2537pp + Sequence Listing; English.
 XX
 XX The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-dT primer and an oligonucleotide complementary to the
 CC complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and

CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
 CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 CC present invention
 XX
 SQ Sequence 734 BP; 211 A; 190 C; 153 G; 177 T; 0 U; 3 Other;

Alignment Scores:
 Pred. No.: 246 Length: 734
 Score: 42.00 Matches: 6
 Percent Similarity: 75.00% Conservative: 0
 Best Local Similarity: 75.00% Mismatches: 2
 Query Match: 79.25% Indels: 0
 DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x AAH05583 (1-734)

Qy 1 TtpileGlyHisaspAlaGlyHis 8
 Db 427 TGGATTGGGCACAGCATGGGCCAC 404

RESULT 36
 ABI99493
 ID ABI99493 standard; cDNA; 1514 BP.
 XX
 AC ABI99493;
 XX
 DT 07-MAR-2002 (first entry)
 XX
 DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:463.
 XX
 KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
 XX vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
 XX
 OS Mus musculus.
 XX
 PN WO200188188-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 18-MAY-2001; 2001WO-JP004192.
 XX
 PR 18-MAY-2000; 2000JP-00145977.
 XX
 PA (UYN1-) UNIV NIHON SCHOOL JURIDICAL PERSON.
 XX
 PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
 XX
 DR WPI; 2002-034733/04.
 DR P-PSDB; ABB57191.
 XX
 PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
 PT expression levels of particular genes defined in the specification or by
 PT determining the expression profile of a gene group comprising these
 PT genes.
 PS Claim 2; Page 1289-1290; 2690pp; English.
 XX
 XX The present invention describes a method for examining ischaemic
 CC conditions, comprising measuring the expression levels of particular
 CC genes (I) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (I). The method
 CC is useful for examining the ischaemic condition (e.g. compressive
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
 CC expression levels of particular genes (ABI99202 to ABI99912, encoding the
 CC protein sequences in ABB57020 to ABB57374) or by determining the
 CC expression profile of a gene group comprising these genes. The expression
 CC levels or expression profiles produced by these genes are used as an
 CC indicator when screening for ischaemic condition-improving drugs or
 CC therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR
 CC primers for a mouse ischaemic condition related sequence, which are used
 CC in the exemplification of the present invention
 XX

SQ Sequence 1514 BP; 484 A; 267 C; 350 G; 413 T; 0 U; 0 Other;
Alignment Scores: 539 Length: 1514
Pred. No.: 42.00 Matches: 6
Score: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-6 (1-8) x ABI19493 (1-1514)
QY 1 TtpileGlyHisAspAlaGlyHis 8
DB 400 TGGATTGGCCACCGGGAGGGGCAC 423

RESULT 37
AAQ20695
ID AAQ20695 standard; cDNA; 1542 BP.
AC AAQ20695;
XX
DT 24-APR-1992 (first entry)
XX
DE Mouse OSF.1.
XX
KW MK; calvarial cell; probe; diagnosis; osteoblast; cranial nerve cell; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
CDS 229..735
FT /*tag= a
FT /label= I-I
FT
XX
XX W09200324-A.
XX
XX 09-JAN-1992.
XX
XX 29-JUN-1990; 90JP-00169824.
XX
XX 29-JUN-1990; 90JP-00169824.
XX
XX 28-SEP-1990; 90JP-00256810.
XX
XX (FARH) HOECHST JAPAN LTD.
XX
XX Hashimoto T, Tezuka K, Kumegawa S, Takagi C;
XX
XX WPI; 1992-041516/05.
XX
XX P-PSDB; AAR20238.
XX
XX Protein from mouse calvarial cells - differentiates growth of
XX osteoblast(s) and cranial nerve cells, for treating and diagnosing
XX osteoporosis and dementia.
XX
XX Disclosure; Fig 3(1-5); 43pp; Japanese.
XX
XX A cDNA library was constructed from mouse calvarial cell line MC3T3E1.
XX Differential screening in NIH3T3 cells (ATCC CRL-1658) and cloning, then
XX insertion into vector pUC118 gave plasmid pMC031 which contains the DNA
XX coding for mouse OSF-1 (AAQ20695). This plasmid was used as a probe to
XX clone by plaque hybridisation from a human cDNA library to give a phage
XX clone, HBK1. Insertion into vector pUC118 gave pHBK1 which may be used
XX diagnostically or the OSF-1 cDNA (AAQ20696) incorporated (with poly-A
XX signal sequence and SV40 T-cell antigen promoter) into a vector (such as
XX pHSB-757) for expression (e.g. in CHO cells) of the protein. See also
XX AAQ20695-97
XX
SQ Sequence 1542 BP; 488 A; 277 C; 360 G; 417 T; 0 U; 0 Other;
Alignment Scores: 549 Length: 1542
Pred. No.: 42.00 Matches: 6
Score:

Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-6 (1-8) x AAQ20695 (1-1542)
QY 1 TtpileGlyHisAspAlaGlyHis 8
DB 414 TGGATTGGCCACCGGGAGGGGCAC 437

RESULT 38
AAZ44851
ID AAZ44851 standard; DNA; 1606 BP.
AC AAZ44851;
XX
DT 27-APR-2000 (first entry)
XX
DE Sphingolipid desaturase DNA.
XX
KW Sphingolipid desaturase; sldi; sphingobase; ceramide; capnoid;
KW transgenic plant; crop plant; delta-8-unsaturated long-chain base;
KW tolerance; resistance; soil salinity; ion stress; toxicity; drought;
KW cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
KW pharmaceutical; food; chemical raw material; ds.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
CDS 88..1464
FT /*tag= a
FT /product= "Sphingolipid desaturase"
FT
XX
XX DE19828850-A1.
XX
XX 30-DEC-1999.
XX
XX 27-JUN-1998; 98DE-01028850.
XX
XX 27-JUN-1998; 98DE-01028850.
XX
XX (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
XX
XX Heinz E, Zaehringer U, Schmidt H, Sperling P;
XX
XX WPI; 2000-127549/12.
XX
XX P-PSDB; AAY51348.
XX
XX New sphingolipid desaturase that selectively introduces double bond into
XX sphingolipids and capnoids.
XX
XX Disclosure; Fig 15; 62pp; German.
XX
XX This invention describes a novel sphingolipid desaturase that selectively
XX introduces a double bond into the sphingobase of the ceramide residue of
XX sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
XX desaturase, or a vector containing the DNA sequence, can be used to
XX produce transgenic plants, especially crop plants, with an increased or
XX decreased delta-8-unsaturated long-chain base content or an altered delta
XX -8-unsaturated long-chain base cis/trans ratio, especially to compensate
XX for a delta-8-unsaturated long-chain base deficiency, to exclude
XX production of delta-8-unsaturated bases, to increase tolerance or
XX resistance to soil salinity, ion stress or toxicity, drought, wet
XX conditions, cold or frost and/or phytopathogenic microorganisms, or to
XX alter size growth and flowering time. Cells, transgenic organisms or
XX plants containing the DNA sequence can be used to produce sphingolipids
XX and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
XX can be used in cosmetics, pharmaceuticals and foods and as chemical raw
XX materials. This sequence encodes a sphingolipid desaturase protein
XX described in the method of the invention
XX
XX Sequence 1606 BP; 412 A; 338 C; 370 G; 486 T; 0 U; 0 Other;

CC number or size relative to cells not exposed to the agent. The method
 CC also comprises providing an expression vector and an agent, exposing the
 CC vector to the agent, detecting a change in expression of the gene
 CC relative to expression of the gene in an expression vector not exposed to
 CC the agent, treating a subject with the agent and identifying fat cell
 CC number or size in the subject. The agent comprises an antisense
 CC oligonucleotide. The subject comprises a mammal, preferably a human. The
 CC method also comprises providing a polypeptide and an agent, exposing the
 CC polypeptide to the agent, detecting binding of the agent to the
 CC polypeptide or a change in an activity of the polypeptide, treating a
 CC subject with the agent and identifying fat cell number or size in the
 CC subject. The agent comprises an antibody. A method of regulating fat cell
 CC number or size comprises providing a subject containing fat cells and an
 CC agent that changes the expression of a gene, and treating the subject
 CC with the agent under conditions so that fat cell size or number in the
 CC subject is altered. The method is useful for identifying compounds that
 CC influence fat cell number or size, for preparing a composition for
 CC treating or preventing obesity or diabetes. This sequence represents
 CC human cDNA used in the scope of the invention.

XX
 SQ Sequence 1923 BP; 485 A; 552 C; 449 G; 437 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 697 Length: 1923
 Score: 42.00 Matches: 6
 Percent Similarity: 75.00% Conservative: 0
 Best Local Similarity: 75.00% Mismatches: 2
 Query Match: 79.25% Indels: 0
 DB: 12 Gaps: 0

US-10-029-756-6 (1-8) x ADO07820 (1-1923)

Qy 1 TrrpIleGlyHisAspAlaGlyHis 8
 Db 1527 TGGATAGGCGATCCATTGGCCAC 1504

RESULT 43
 AAS74417/c
 ID AAS74417 standard; cDNA; 1996 BP.

AC AAS74417;
 XX 13-FEB-2002 (first entry)

DT DNA encoding novel human diagnostic protein #10221.

DE Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

OS WO200175067-A2.

PN 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

PF 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR P-PSDB; ABC10230.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX Claim 1; SEQ ID NO 10221; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
 CC coding sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 1996 BP; 762 A; 447 C; 350 G; 437 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 726 Length: 1996
 Score: 42.00 Matches: 6
 Percent Similarity: 75.00% Conservative: 0
 Best Local Similarity: 75.00% Mismatches: 2
 Query Match: 79.25% Indels: 0
 DB: 5 Gaps: 0

US-10-029-756-6 (1-8) x AAS74417 (1-1996)

Qy 1 TrrpIleGlyHisAspAlaGlyHis 8
 Db 1914 TGGATTGGGCACAGCATGGCCAC 1891

RESULT 44
 AAZ42116/c
 ID AAZ42116 standard; cDNA; 2238 BP.

AC AAZ42116;

XX 31-JAN-2000 (first entry)

DT Human endometrium tumour cDNA derived EST 136.

DE Endometrium; human; tumour; cancer; anticancer; cytostatic;
 KW EST; treatment; uterine; gene therapy; expressed sequence tag; ss.

XX Homo sapiens.

OS DE19817948-A1.

PN 21-OCT-1999.

XX 17-APR-1998; 98DE-01017948.

PR 17-APR-1998; 98DE-01017948.

XX (META-) METAGEN GES GENOMFORSCHUNG MBH.

XX Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E;

DR WPI; 1999-591957/51.

XX New nucleic acid sequences expressed in uterine cancer tissues, and
 PT derived polypeptides, for treatment of uterine and endometrial cancer and
 PT identification of therapeutic agents.

XX Claim 3; Page 269-270; 444pp; German.

XX This invention describes novel human nucleic acid (cDNA) sequences (A),
 CC that are highly expressed in uterine tumour tissue and which have
 CC anticancer and cytostatic activity. (A) are used (i) for recombinant
 CC expression of polypeptides (B) and (ii) to isolate complete genes. (B)
 CC are used (i) to identify agents suitable for treatment of uterine or
 CC endometrial cancer; (ii) directly for treating these forms of cancer
 CC (including expression from gene therapy vectors) and (iii) for generation
 CC of specific antibodies. (A) are identified by assembling ESTs (expressed
 CC sequence tags) from a particular tissue type before comparison of
 CC expression patterns. This allows a significantly longer fragment of the
 CC gene to be revealed, so should reduce the number of failures associated
 CC with the fact that ESTs from different libraries may represent different
 CC parts of the same unknown gene, distorting the estimated frequency of
 CC occurrence in a particular tissue. AA241981-242121 represent EST
 CC fragments derived from a human endometrium tumour cDNA library which
 CC encode the protein sequences represented in AAY59941-Y60328
 XX
 SQ Sequence 2238 BP; 602 A; 519 C; 463 G; 653 T; 0 U; 1 Other;
 Alignment Scores:
 Pred. No.: 821 Length: 2238
 Score: 42.00 Matches: 6
 Percent Similarity: 75.00% Conservative: 0
 Best Local Similarity: 75.00% Mismatches: 2
 Query Match: 79.25% Indels: 0
 DB: 2 Gaps: 0
 US-10-029-756-6 (1-8) x AA242116 (1-2238)
 Qy 1 TrpIleGlyHisAspAlaGlyHis 8
 Db 331 TGGATAGGCGCATTCATTGGCCAC 308
 RESULT 45
 ID ABK83895/c
 ID ABK83895 standard; cDNA; 2307 BP.
 XX
 AC ABK83895;
 XX
 DT 14-AUG-2002 (first entry)
 XX
 DE Human cDNA differentially expressed in granulocytic cells #466.
 XX
 KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
 KW viral infection; parasitic infection; protozoal infection;
 KW fungal infection; sterile inflammatory disease; psoriasis;
 KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
 KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
 KW adult respiratory distress syndrome; inflammatory bowel disease;
 KW Crohn's disease; ulcerative colitis; periodontal disease;
 KW granulocyte activation; chronic inflammation; allergy.
 XX
 OS Homo sapiens.
 XX
 PN WO200228999-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 03-OCT-2001; 2001WO-US030821.
 XX
 PR 03-OCT-2000; 2000US-0237189P.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX
 PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
 XX
 DR WPI; 2002-435328/46.
 XX
 PT Detecting granulocyte activation by detecting differential expression of
 PT genes associated with granulocyte activation, which serves as diagnostic
 PT markers that is useful for monitoring disease states and drug toxicity.
 XX

PS Claim 1; SEQ ID NO 466; 114pp; English.
 XX
 CC The invention relates to detecting (M1) granulocyte (GC) activation
 CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
 CC DNA chip analysis as given in the specification, and comparing the
 CC expression level to an expression level in an unactivated GC, where
 CC differential expression of Gs is indicative of GCA. Also included are
 CC modulating (M2) GA by contacting GC with an agent that alters the
 CC expression of at least one gene in Gs; (2) screening (M3) for an agent
 CC capable of modulating GCA or an inflammation (especially chronic) in a
 CC tissue, an allergic response in a subject, exposure of a subject to a
 CC pathogen or sterile inflammatory disease using the gene expression
 CC profile; (3) detecting (M4) an inflammation (especially chronic) in a
 CC tissue, an allergic response in a subject, exposure of a subject to a
 CC pathogen or sterile inflammatory disease, by detecting the level of
 CC expression in a sample of the tissue of gene(s) from Gs, where the level
 CC of expression of the gene is indicative of inflammation; (4) treating
 CC (M5) an inflammation (especially chronic) or in a tissue, an allergic
 CC response in a subject, exposure of a subject to a pathogen or sterile
 CC inflammatory disease, by contacting a tissue having inflammation with an
 CC agent that modulates the expression of gene(s) from Gs in the tissue. M1
 CC is useful for detecting GCA; M2 is useful for modulating GCA; M3 is useful
 CC for screening an agent capable of modulating GCA preferably in an
 CC inflammation in a tissue; M4 is useful for detecting an inflammation
 CC (especially chronic) in a tissue, an allergic response in a subject,
 CC exposure of a subject to a pathogen or sterile inflammatory disease (e.g.
 CC psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,
 CC cardiac reperfusion injury, renal reperfusion injury, ARDS, adult
 CC respiratory distress syndrome, inflammatory bowel disease, Crohn's
 CC disease, ulcerative colitis, periodontal disease; also bacterial
 CC infection, viral infection, parasitic infection, protozoal infection,
 CC fungal infection and M5 is useful for treating one of the above
 CC conditions. The present sequence represents a gene differentially
 CC expressed in granulocytes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 2307 BP; 626 A; 532 C; 488 G; 655 T; 0 U; 6 Other;
 Alignment Scores:
 Pred. No.: 849 Length: 2307
 Score: 42.00 Matches: 6
 Percent Similarity: 75.00% Conservative: 0
 Best Local Similarity: 75.00% Mismatches: 2
 Query Match: 79.25% Indels: 0
 DB: 6 Gaps: 0
 US-10-029-756-6 (1-8) x ABK83895 (1-2307)
 Qy 1 TrpIleGlyHisAspAlaGlyHis 8
 Db 550 TGGATAGGCGCATTCATTGGCCAC 527
 RESULT 46
 ADD12700/c
 ID ADD12700 standard; cDNA; 2458 BP.
 XX
 AC ADD12700;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Human cDNA expressed during adipocyte differentiation #46.
 XX
 KW ss; gene; human; adipocyte differentiation; obesity; type II diabetes;
 KW lipodystrophy; hyperinsulinaemia.
 XX
 OS Homo sapiens.
 XX
 PN US2003113720-A1.
 XX
 PD 19-JUN-2003.
 XX

PF 30-JUL-2001; 2001US-00918624.
 XX
 PR 28-JUL-2000; 2000US-0222470P.
 XX
 PA (SCHE/) SCHEBYE X M.
 PA (SORN/) SORNASSE T.
 XX
 PI Schebye XM, Sornasse T;
 XX
 DR WPI; 2003-810888/76.
 XX
 PT Novel isolated cDNAs expressed in adipocyte differentiation useful for
 PT treating subject with disorder such as obesity, type II diabetes,
 PT lipodystrophy or hyperinsulinemia.
 XX
 XX Claim 1; SEQ ID NO 46; 105pp; English.
 PS
 CC The invention relates to an isolated cDNA expressed during adipocyte
 CC differentiation. The cDNA is useful for treating a subject with a
 CC disorder such as obesity, type II diabetes, lipodystrophy or
 CC hyperinsulinemia. The nucleic acid is useful for a high throughput
 CC method of using a cDNA to screen several molecules or compounds to
 CC identify a ligand which specifically binds the cDNA which involves
 CC combining the nucleic acid with several molecules or compounds under
 CC conditions to allow specific binding, and detecting specific binding
 CC between each cDNA and at least one molecule or compound, thus identifying
 CC a ligand that specifically binds to each cDNA. The several molecules or
 CC compounds are chosen from DNA molecules, RNA molecules, peptide nucleic
 CC acid molecules, mimetics, peptides, transcription factors, repressors and
 CC regulatory proteins. The present sequence represents a human cDNA
 CC expressed during adipocyte differentiation.
 XX
 SQ Sequence 2458 BP; 679 A; 543 C; 537 G; 699 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 909 Length: 2458
 Score: 42.00 Matches: 6
 Percent Similarity: 75.00% Conservative: 0
 Best Local Similarity: 75.00% Mismatches: 2
 Query Match: 79.25% Indels: 0
 DB: 10 Gaps: 0
 US-10-029-756-6 (1-8) x ADD12700 (1-2458)
 Qy 1 TrrpGlyHisAspAlaGlyHis 8
 Db 991 TGGATTGGGCACGACGATGGCCAC 968
 RESULT 47
 ADB63204/c
 ID ADB63204 standard; cDNA; 2486 BP.
 XX
 AC ADB63204;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Human cDNA encoding clone SPLEN20138600.
 XX
 KW Human; ss; gene; pharmaceutical; diagnostic; gene therapy;
 KW tissue regeneration; cell regeneration; membrane protein;
 KW signal transduction-related protein; transcription-related protein;
 KW osteoporosis; neurological disease; cancer; tumour.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1166..1582
 FT /*tag= a
 FT /product= "Clone SPLEN20138600 protein"
 XX
 PN EPI308459-A2.
 XX
 PD 07-MAY-2003.

XX 28-MAR-2002; 2002EP-00007401.
 XX
 PR 05-NOV-2001; 2001JP-00379298.
 PR 25-JAN-2002; 2002US-00350978.
 XX
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
 XX
 DR WPI; 2003-450961/43.
 DR P-PSDB; ADB65174.
 XX
 PT New polynucleotides and polypeptides, useful for developing a diagnostic
 PT marker or medicines for regulation of their expression and activity, or
 PT as targets of gene therapy.
 XX
 XX Claim 1; Page: 222pp; English.
 PS
 CC The invention discloses a polynucleotide comprising a sequence selected
 CC from 1970 fully defined nucleotide sequences which encode novel
 CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
 CC or its partial peptide, an antibody binding to the polypeptide or peptide
 CC of the polynucleotide, immunologically assaying the polypeptide or
 CC peptide of the polynucleotide by contacting the polypeptide or peptide
 CC with the antibody of the encoded protein, and observing the binding
 CC between the two, a transformant carrying the polynucleotide in an
 CC expressible manner and an antisense polynucleotide. The oligonucleotide
 CC is useful as a primer for synthesising the polynucleotide, or as a probe
 CC for detecting the polynucleotide. The polynucleotides and encoded
 CC proteins are useful as pharmaceutical agents and many disease-related
 CC genes may be included in them for developing a diagnostic marker or
 CC medicines for regulation of their expression and activity, or as targets
 CC of gene therapy. The genes are involved in tissue and/or cell
 CC regeneration. Membrane proteins, signal transduction-related proteins,
 CC transcription-related proteins, disease-related proteins and genes
 CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
 CC neurological diseases, cancer, tumours. The cDNA may be used to regulate
 CC the activity or expression of the encoded protein to treat diseases. The
 CC sequence presented is a cDNA of the invention. Note: Some of the sequence
 CC data for this patent is not represented in the printed specification, but
 CC is based on sequence information supplied by the European Patent Office.
 XX
 SQ Sequence 2486 BP; 679 A; 594 C; 532 G; 681 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 920 Length: 2486
 Score: 42.00 Matches: 6
 Percent Similarity: 75.00% Conservative: 0
 Best Local Similarity: 75.00% Mismatches: 2
 Query Match: 79.25% Indels: 0
 DB: 10 Gaps: 0
 US-10-029-756-6 (1-8) x ADB63204 (1-2486)
 Qy 1 TrrpGlyHisAspAlaGlyHis 8
 Db 1272 TGGATAGGGCATTCATTGGCCAC 1249
 RESULT 48
 ABV25875/c
 ID ABV25875 standard; cDNA; 2702 BP.
 XX
 AC ABV25875;
 XX
 DT 16-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 25866.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

KW pharmacogenomic marker; gene; ss.
OS Homo sapiens.
XX WO200160860-A2.
XX 23-AUG-2001.
XX 20-FEB-2001; 2001WO-US005171.
XX 17-FEB-2000; 2000US-0183319P.
XX 16-MAR-2000; 2000US-0189862P.
XX 25-MAY-2000; 2000US-0207454P.
XX 09-JUN-2000; 2000US-0211314P.
XX 18-JUL-2000; 2000US-0219007P.
XX 13-DEC-2000; 2000US-0255281P.
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX Schlegel R, Endege WO, Monahan JE;
XX WPI; 2001-662795/76.
XX Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
XX Claim 1; Page 5224; 11750pp; English.
XX The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) is also useful as a pharmacodynamic or pharmacogenomic marker
SQ Sequence 2702 BP; 714 A; 615 C; 568 G; 788 T; 0 U; 17 Other;

Alignment Scores:
Pred. No.: 1.01e+03 Length: 2702
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 5 Gaps: 0

US-10-029-756-6 (1-8) x ABV25875 (1-2702)
Qy 1 TtpIleGlyHisAspAlaGlyHis 8
Db 710 TGGATAGGCGCATTCATTGGCCAC 687

RESULT 49
ABL22487/c
ID ABL22487 standard; DNA; 2741 BP.
XX ABL22487;
XX 26-MAR-2002 (first entry)
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 18934.
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 18934.
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; da.
XX Drosophila melanogaster.
XX

PN WO200171042-A2.
XX 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US009231.
XX 23-MAR-2000; 2000US-0191637P.
XX 11-JUL-2000; 2000US-00614150.
XX (PEKE) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
XX Claim 1; SEQ ID NO 18934; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABBS72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 2741 BP; 643 A; 763 C; 777 G; 558 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.02e+03 Length: 2741
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x ABL22487 (1-2741)
Qy 1 TtpIleGlyHisAspAlaGlyHis 8
Db 93 TGGTGTGGCATAGCGAGGCGAC 70

RESULT 50
AAC77708/c
ID AAC77708 standard; cDNA; 2804 BP.
XX AAC77708;
XX 08-FEB-2001 (first entry)
XX Human cancer associated gene sequence SEQ ID NO:102.
XX Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antiinflammatory; antithyroid; antiallergic; antibacterial; cardiac; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; angiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening; ss.
XX Homo sapiens.
XX WO200055350-A1.
XX

PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US005882.
XX
XX 12-MAR-1999; 99US-0124270P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
FA
XX Rosen CA, Ruben SM;
XX
XX WPI: 2000-587533/55.
XX
XX P-PSDB; AAB43499.
XX
XX
XX Novel isolated nucleic acids comprising sequences encoding peptides
XX useful for treating or diagnosing e.g. cancer.
XX
XX Claim 1; Page 692-693; 2352pp; English.
XX
XX AAC77607 to AAC78448 encode the human cancer associated proteins given in
XX AAB43398 to AAB44239. The proteins can have activities based on the
XX tissues and cells the genes are expressed in. Example of activities
XX include: cytostatic; proliferative; vulnerary; immunomodulator;
XX antidiabetic; antiaethmatic; antirheumatic; antiarthritic;
XX antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
XX dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
XX nootropic; vasotropic; antipsoriatic and antiangiogenic. The
XX polynucleotides and polypeptides can be used for preventing, treating or
XX ameliorating medical conditions and diagnosing pathological conditions.
XX Polynucleotides, polypeptides, antibodies, agonists and antagonists from
XX the present invention may be used to treat immune disorders by activating
XX or inhibiting the proliferation, differentiation or mobilisation of
XX immune cells, to treat disorders of haematopoietic cells, autoimmune
XX disorders, allergic reactions, graft versus host disease and organ
XX rejection, modulate haemostatic or thrombolytic activity, modulate
XX inflammation, cancers, cardiovascular disorders, neurological disease and
XX bacterial or viral infections. The peptides, nucleotides, antibodies,
XX agonists and antagonists may be also be used in drug screens. AAC78449 to
XX AAC78457 and AAB44240 represent sequences used in the exemplification of
XX the present invention
XX
SQ Sequence 2804 BP; 764 A; 682 C; 596 G; 758 T; 0 U; 4 Other;

Alignment Scores:
Pred. No.: 1.05e+03 Length: 2804
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-6 (1-8) x AAC77708 (1-2804)

Qy 1 TptlleglyHisAepAlaGlyHis 8
|||
Db 979 TGGATAGGGCATTCATTGGCCAC 956
|||
RESULT 51
AAS61862/c
ID AAS61862 standard; CDNA; 2846 BP.
XX
XX AAS61862;
XX
XX 29-JAN-2002 (first entry)
XX
XX Lung small cell carcinoma antigen, CDNA #403.
XX
XX Human; cytostatic; antitumour; lung small cell cancer antigen; tumour;
XX lung cancer; ss.
XX
XX Homo sapiens.
XX
XX WO200177168-A2.
XX
XX

PD 18-OCT-2001.
XX
PF 11-APR-2001; 2001WO-US011859.
XX
XX 11-APR-2000; 2000US-0196780P.
XX 21-JUN-2000; 2000US-0213361P.
XX 01-SEP-2000; 2000US-0229783P.
XX 05-SEP-2000; 2000US-0230629P.
XX 14-SEP-2000; 2000US-0232565P.
XX 19-DEC-2000; 2000US-0257037P.
XX 08-JAN-2001; 2001US-0260796P.
XX
XX (CORI-) CORIXA CORP.
FA
XX Lodes MJ, Wang T, Mohamath R, Indirias CY;
XX
XX WPI: 2002-010896/01.
XX P-PSDB; RAU69422.
XX
XX Lung tumor polynucleotide and polypeptides useful in therapy and
XX diagnosis of cancer especially lung cancer.
XX
XX Claim 1; Page 273-274; 295pp; English.
XX
XX The invention relates to novel isolated lung small cell cancer antigen
XX polynucleotides (I) and polypeptides (II) used in a method of detecting
XX cancer in a patient. The method is optionally performed by utilising
XX oligonucleotides (III), where the biological sample from the patient is
XX contacted with (III), detecting the amount of polynucleotide hybridised
XX to (III) in the sample and comparing the amount of polynucleotide to a
XX predetermined cut-off value and thereby determining cancer in a patient.
XX (I), (II) or antigen-presenting cells expressing (II) is useful for
XX stimulating and/or expanding T cells specific for a tumour protein. The
XX method comprises contacting T cells with one of the components under
XX conditions to permit the stimulation and/or expansion of the cells. A
XX composition comprising (I) is useful for stimulating an immune response
XX in a patient and for inhibiting the development of a cancer especially
XX lung cancer in a patient. An isolated T cell population is useful for
XX removing tumour cells from the biological sample and for inhibiting the
XX development of cancer in a patient. AAS61460-AAS61874 represent novel
XX human lung small cell cancer antigen coding sequences of the invention
XX
SQ Sequence 2846 BP; 818 A; 614 C; 633 G; 781 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.05e+03 Length: 2846
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-6 (1-8) x AAS61862 (1-2846)

Qy 1 TptlleglyHisAepAlaGlyHis 8
|||
Db 1351 TGGATTGGGCACAGCATGGGCCAC 1328
|||
RESULT 52
ADE56172/c
ID ADE56172 standard; DNA; 2893 BP.
XX
XX ADE56172;
XX
XX 29-JAN-2004 (first entry)
XX
XX Rat gene D38492, SEQ ID NO 2021.
XX
XX Rat; ds; gene; pain; neuronal tissue; gene therapy;
XX spinal segmental nerve injury; chronic constriction injury;CCI;
XX spared nerve injury; SNI; Chung.
XX
XX Rattus norvegicus.
XX
XX

XX WO2003016475-A2.
 XX
 XX 27-FEB-2003.
 XX
 XX 14-AUG-2002; 2002WO-US025765.
 XX
 XX 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 XX (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 XX Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 DR GENBANK; D38492.
 DR
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 XX Claim 1; Page: 101pp; English.
 PS
 XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derived or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat DNA (shown in Table 2 of the
 CC specification) which encodes one of the polypeptides of the invention
 CC which is differentially expressed during pain. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 2893 BP; 824 A; 726 C; 702 G; 641 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.08e+03 Length: 2893
 Score: 42.00 Matches: 6
 Percent Similarity: 75.00% Conservative: 0
 Best Local Similarity: 75.00% Mismatches: 2
 Query Match: 79.25% Indels: 0
 DB: 10 Gaps: 0

US-10-029-756-6 (1-8) x ADE56172 (1-2893)

Oy 1 TrpIleGlyHisAspAlaGlyHis 8
 |||||
 Db 2644 TGGATAGGCCACGACAGATCCAC 2621
 |||||

RESULT 53
 ABQ54696/c
 ID ABQ54696 standard; cDNA; 2984 BP.
 XX

AC ABQ54696;
 XX 22-AUG-2002 (first entry)
 XX Human ovarian antigen HLYDC86 cDNA, SEQ ID NO:576.
 XX
 XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive; chromosome 14q24.3; gene;
 KW ss.
 XX
 XX Homo sapiens.
 OS
 XX W0200200677-A1.
 PN
 XX 03-JAN-2002.
 PD
 XX 07-JUN-2001; 2001WO-US018569.
 XX
 XX 07-JUN-2000; 2000US-0209467P.
 PR
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Birse CE, Rosen CA;
 PI
 XX WPI; 2002-147878/19.
 XX
 XX P-PSDB; ABP41619.
 DR
 XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 PT cancer), immune disorders, cardiovascular disorders and neurological
 PT diseases.
 XX
 XX Claim 1; SEQ ID NO 576; 2922pp; English.
 PS
 XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovary and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents cDNA encoding a human ovarian antigen of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 2984 BP; 821 A; 720 C; 646 G; 792 T; 0 U; 5 Other;

Alignment Scores:
Pred. No.: 1.12e+03 Length: 2984
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: Gaps: 0

US-10-029-756-6 (1-8) x ABQ54696 (1-2984)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
|||||
Db 1177 TGGATAGGCATTCATTGGCCAC 1154

RESULT 54
AAV70355/c
ID AAV70355 standard; cDNA; 2995 BP.

XX AAV70355;

DT 08-FEB-1999 (first entry)

DE Human h-NUMB encoding cDNA.

XX Human; cytoplasmic protein; EH-containing protein; epa15; epa15R;
KW epa15 homology; intracellular interaction; EH domain binding specificity;
KW signal transducer; NPF motif; h-NUMB; h-RAB-R; h-RAB; h-RAB-R; ehb3;
KW ehb10; ehb21; cell proliferation; diagnosis; detection; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
FH 279. .2090
FT CDS /*tag= a

XX WO9846744-A1.

XX 22-OCT-1998.

XX 06-APR-1998; 98WO-IT000077.

XX 15-APR-1997; 97IT-MI000868.

XX (EUON-) IST EURO DI ONCOLOGIA SRL.

PI Salcini AB, Doria M, Pellicci PG, Di Fiore PP;

XX WPI; 1998-594574/50.

XX P-PSDB; AAW83214.

XX New isolated EH domain binding proteins and peptide(s) - obtained using
PT signal transducers epa15 and epa15R containing EH domains by detecting
PT specific binding activity.

XX Claim 3; Page 45-47; 90pp; English.

XX The present invention describes a new intracellular interactor and novel
CC protein:protein interaction (EH) domain binding protein having (parts of)
CC one of the following human derived sequences designated: (I) h-NUMB; (II)
CC h-NUMB-R; (III) h-RAB-R; (IV) ehb3; (V) ehb10; or (VI) ehb21. The present
CC invention also describes peptides containing at least one NPF (Asp-Pro-
CC Phe) motif, able to bind to a protein with at least one EH domain. The
CC proteins with a NPF-containing peptide or the peptides themselves can be
CC used to identify and purify EH containing proteins. Antisense RNA,
CC complementary to mRNA encoding h-NUMB, h-NUMB-R, ehb3, ehb10, or
CC ehb21, can be used for diagnostic and therapeutic uses. Products from the
CC present invention can also be used to develop agents for use in control
CC of cell proliferation. The present sequence encodes human h-NUMB

XX Sequence 2995 BP; 837 A; 733 C; 696 G; 729 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.13e+03 Length: 2995
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: Gaps: 0

US-10-029-756-6 (1-8) x AAV70355 (1-2995)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
|||||
Db 1694 TGGATAGGCATTCATTGGCCAC 1671

RESULT 55

ADR25565/c

ID ADR25565 standard; DNA; 3050 BP.

XX ADR25565;

DT 21-OCT-2004 (first entry)

DE Breast cancer prognosis marker #1426.

KW ds; breast cancer; prognosis; gene expression; diagnosis.

XX Homo sapiens.

XX WO2004065545-A2.

XX 05-AUG-2004.

XX 15-JAN-2004; 2004WO-US001100.

XX 15-JAN-2003; 2003US-00342887.

XX (ROSE-) ROSETTA INPHARMATICS LLC.
XX (NECA-) NETHERLANDS CANCER INST.

XX Van't Veer LJ, He Y;

XX WPI; 2004-593473/57.

XX Classifying a breast cancer patient according to prognosis comprises
PT determining the similarity between the level of expression of each of
PT five genes in a cell sample taken from patient, to control levels.

XX Disclosure; SEQ ID NO 1426; 226pp; English.

XX The invention relates to a method of classifying a breast cancer patient
CC according to prognosis by determining the similarity between the level of
CC expression of each of five genes for which markers are listed in the
CC specification, in a cell sample taken from the breast cancer patient, to
CC control levels of expression for each respective five genes to obtain a
CC patient similarity value. The methods are useful for classifying a breast
CC cancer patient according to prognosis. Kits and computer program products
CC are useful for data analysis using the diagnostic, prognostic and
CC statistical methods of the invention. This sequence corresponds to a
CC marker used in the method of the invention.

XX Sequence 3050 BP; 850 A; 651 C; 713 G; 836 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.15e+03 Length: 3050
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: Gaps: 0

US-10-029-756-6 (1-8) x ADR25565 (1-3050)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
|||||

Db 1606 TGGATTGGGCACGATGGGCCAC 1583

RESULT 56

AA561859/c

ID AAS61859 standard; cDNA; 3079 BP.

XX AC AAS61859;

XX 29-JAN-2002 (first entry)

XX DT

XX DE Lung small cell carcinoma antigen, cDNA #400.

XX KW Human; cytostatic; antitumour; lung small cell cancer antigen; tumour;

XX KW lung cancer; ss.

XX OS Homo sapiens.

XX FN WO200177168-A2.

XX PD 18-OCT-2001.

XX PF 11-APR-2001; 2001WO-US011859.

XX PR 11-APR-2000; 2000US-0196780P.

XX PR 21-JUN-2000; 2000US-0213361P.

XX PR 01-SEP-2000; 2000US-0229763P.

XX PR 05-SEP-2000; 2000US-0230629P.

XX PR 14-SEP-2000; 2000US-0232565P.

XX PR 19-DEC-2000; 2000US-0257037P.

XX PR 08-JAN-2001; 2001US-0260796P.

XX PA (CORI-) CORIXA CORP.

XX PI Lodes MJ, Wang T, Mohamath R, Indirias CY;

XX DR WPI; 2002-010896/01.

XX DR P-PSDB; RAU69419.

XX PT Lung tumor polynucleotide and polypeptides useful in therapy and diagnosis of cancer especially lung cancer.

XX PS Claim 1; Page 269-270; 295pp; English.

XX CC The invention relates to novel isolated lung small cell cancer antigen polynucleotides (I) and polypeptides (II) used in a method of detecting cancer in a patient. The method is optionally performed by utilising oligonucleotides (III), where the biological sample from the patient is contacted with (III), detecting the amount of polynucleotide hybridised to (III) in the sample and comparing the amount of polynucleotide to a predetermined cut-off value and thereby determining cancer in a patient. (I), (II) or antigen-presenting cells expressing (II) is useful for stimulating and/or expanding T cells specific for a tumour protein. The method comprises contacting T cells with one of the components under conditions to permit the stimulation and/or expansion of the cells. A composition comprising (I) is useful for stimulating an immune response in a patient and for inhibiting the development of a cancer especially lung cancer in a patient. An isolated T cell population is useful for removing tumour cells from the biological sample and for inhibiting the development of cancer in a patient. AAS61460-AAS61874 represent novel human lung small cell cancer antigen coding sequences of the invention

XX SQ Sequence 3079 BP; 865 A; 652 C; 719 G; 843 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.16e+03 Length: 3079

Score: 42.00 Matches: 6

Percent Similarity: 75.00% Conservative: 0

Best Local Similarity: 75.00% Mismatches: 2

Query Match: 79.25% Indels: 0

DB: 6 Gaps: 0

US-10-029-756-6 (1-8) x AAS61859 (1-3079)

Qy 1 TTPileGlyHisaspAlaGlyHis 8

Db 1613 TGGATTGGGCACGATGGGCCAC 1590

RESULT 57

AAI59203/c

ID AAI59203 standard; cDNA; 3144 BP.

XX AC AAI59203;

XX 22-OCT-2001 (first entry)

XX DT

XX DE Human polynucleotide SEQ ID NO 1406.

XX KW Human; nototropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia; ss.

XX OS Homo sapiens.

XX FN WO200153312-A1.

XX PD 26-JUL-2001.

XX PF 26-DEC-2000; 2000WO-US034263.

XX PR 23-DEC-1999; 99US-00471275.

XX PR 21-JAN-2000; 2000US-00488725.

XX PR 25-APR-2000; 2000US-00552317.

XX PR 20-JUN-2000; 2000US-00598042.

XX PR 19-JUL-2000; 2000US-00620312.

XX PR 03-AUG-2000; 2000US-00653450.

XX PR 14-SEP-2000; 2000US-00662191.

XX PR 19-OCT-2000; 2000US-00693036.

XX PR 29-NOV-2000; 2000US-00727344.

XX PA (HYSE-) HYSEQ INC.

XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D; Zhou J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA; Zhou P, Goodrich R, Drmanac RT;

XX DR WPI; 2001-442253/47.

XX DR P-PSDB; AAM40047.

XX PT Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.

XX PS Claim 1; SEQ ID NO 1406; 10078pp; English.

XX CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification

XX SQ Sequence 3144 BP; 879 A; 671 C; 742 G; 852 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.19e+03 Length: 3144


```

ABLI13718/c
ID  ABL13718 standard; cDNA; 3155 BP.
AC  ABL13718;
XX
XX  26-MAR-2002 (first entry)
XX
XX  Drosophila melanogaster expressed polynucleotide SEQ ID NO 35636.
XX
XX  Drosophila; developmental biology; cell signalling; insecticide;
KW  pharmaceutical; gene; ss.
XX
XX  Drosophila melanogaster.
OS
XX  WO200171042-A2.
XX
XX  27-SEP-2001.
XX
XX  23-MAR-2001; 2001WO-US009231.
XX
XX  23-MAR-2000; 2000US-0191637P.
PR
XX  11-JUL-2000; 2000US-00614150.
XX
XX  (PEKE ) PE CORP NY.
XX
XX  Venter JC, Adams M, Li PWD, Myers EW;
PI
XX  WPI; 2001-656860/75.
DR
XX  P-PSDB; ABB69615.
XX
XX  New isolated nucleic acid detection reagent for detecting 1000 or more
PT  genes from Drosophila and for elucidating cell signaling and cell-cell
PT  interactions.
XX
XX  Claim 1; SEQ ID NO 35636; 21bp + Sequence Listing; English.
XX
XX  The invention relates to an isolated nucleic acid detection reagent
CC  capable of detecting 1000 or more genes from Drosophila. The invention is
CC  useful in developmental biology and in elucidating cell signalling and
CC  cell-cell interactions in higher eukaryotes for the development of
CC  insecticides, therapeutics and pharmaceutical drugs. The invention
CC  discloses genomic DNA sequences (ABLI16176-ABLI30511), expressed DNA
CC  sequences (ABLI01840-ABLI16175) and the encoded proteins (ABB57737-
CC  ABB572072). The sequence data for this patent did not form part of the
CC  printed specification, but was obtained in electronic format directly
CC  from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX  Sequence 3155 BP; 868 A; 759 C; 728 G; 800 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.19e+03 Length: 3155
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x ABL13718 (1-3155)
Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 2611 TGGGTGGGCATAGCGAGGGCCAC 2588
RESULT 61
ABX71357/c
ID ABX71357 standard; cDNA; 3237 BP.
XX
XX  ABX71357;
AC
XX
XX  14-APR-2003 (first entry)
DT
XX  Human signal transduction-associated cDNA from clone DKFZphtes3_lcl.
DE
XX
XX

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KW  Human; gene; gene therapy; vaccine; disease treatment; detection; ss.
XX
XX  Homo sapiens.
OS
XX  WO200112659-A2.
XX
XX  22-FEB-2001.
XX
XX  18-AUG-2000; 2000WO-IB001496.
XX
XX  18-AUG-1999; 99US-0149499P.
PR
XX  28-SEP-1999; 99US-0156503P.
XX
XX  (GEHU-) GERMAN HUMAN GENOME PROJECT.
XX
XX  Wiemann S;
PI
XX  WPI; 2001-327840/34.
XX
XX  P-PSDB; ABUS3065.
XX
XX  Nucleic acids having the sequences of clones isolated from libraries of
PT  different human tissues, useful in recombinant DNA methodologies.
XX
XX  Claim 1; Page 658-659; 1095pp; English.
XX
XX  This invention describes novel polynucleotides and polypeptides isolated
CC  from human cDNA libraries which can be used for gene therapy or in
CC  vaccines. The polynucleotides of the invention and antibodies encoded by
CC  them may be used in the prevention, diagnosis and treatment of diseases
CC  associated with inappropriate polypeptide expression. The products of the
CC  invention may also be used to identify modulators of expression and
CC  activity and to down regulate expression and activity. The antibodies of
CC  the invention may also be used as diagnostic agents for detecting the
CC  presence of polypeptides in samples. This sequence encodes a polypeptide
CC  described in the disclosure of the invention
XX
XX  Sequence 3237 BP; 938 A; 668 C; 749 G; 882 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.22e+03 Length: 3237
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 5 Gaps: 0

US-10-029-756-6 (1-8) x ABX71357 (1-3237)
Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 1760 TGGATTGGGCACAGCATGGGCCAC 1737
RESULT 62
ADP64967/c
ID ADP64967 standard; DNA; 3237 BP.
XX
XX  ADP64967;
AC
XX
XX  12-AUG-2004 (first entry)
DT
XX
XX  Human Rac GTPase activating protein 1 (RACGAP1) DNA sequence.
XX
XX  autoimmune disease; arthritis; gene expression analysis;
KW  rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
KW  antiarthritic; osteopathic; antigout; antinflammatory; dermatological;
KW  immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;
KW  fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
KW  immune; ds; human.
XX
XX  Homo sapiens.
OS
XX  WO2003072827-A1.
XX
XX

```


PD 04-SEP-2003.
 XX 31-OCT-2002; 2002WO-US035433.
 XX 31-OCT-2001; 2001US-0336220P.
 XX (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 XX Hirsch R, Thorton SL;
 DR WPI; 2003-712740/67.
 DR GENBANK; NM_013277.
 XX
 PT Diagnosing and analyzing autoimmune disease using gene expression
 PT profiles and microarray technology, useful for diagnosing and treating
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
 PT gout.
 XX
 PS Disclosure; Page; 56pp; English.
 XX
 CC The invention relates to a novel method for diagnosing and analysing
 CC autoimmune disease or arthritides. The method comprises obtaining a
 CC patient sample containing mRNA, analysing gene expression using the mRNA
 CC that results in a gene expression signature of the mRNA, and using that
 CC gene expression signature to diagnose or analyse the autoimmune disease
 CC or arthritides in the patient, where gene expression of at least 60% of
 CC the genes correlates with that of the gene signature. The invention
 CC further comprises: a treatment of rheumatoid arthritis; identification of
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
 CC analyses of autoimmune disease or rheumatoid arthritis; screening the
 CC efficacy of a candidate drug in vitro for the treatment of collagen-
 CC induced arthritis; and reducing the symptoms associated with collagen-
 CC induced arthritis. The compositions of the invention have the following
 CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
 CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
 CC methods and compositions of the present invention are useful for
 CC diagnosing and treating autoimmune disease or arthritides, such as
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
 CC immune disease caused by an infectious agent. This polynucleotide
 CC represents a DNA sequence relating to the genes used in the analysis and
 CC treatment of autoimmune diseases or arthritides. Note: This sequence is
 CC not shown in the specification. It has been supplied in an electronic
 CC format from WIPO.
 XX
 SQ Sequence 3237 BP; 938 A; 668 C; 749 G; 882 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.22e+03 Length: 3237
 Score: 42.00 Matches: 6
 Percent Similarity: 75.00% Conservative: 0
 Best Local Similarity: 75.00% Mismatches: 2
 Query Match: 79.25% Indels: 0
 DB: 11 Gaps: 0
 US-10-029-756-6 (1-8) x ADP64967 (1-3237)
 Qy 1 TptleGlyHisAepAlaGlyHis 8
 Db 1760 TGGATTGGGCACGATGGGCCAC 1737
 RESULT 63
 ADP65420/C
 ID ADP65420 standard; DNA; 3237 BP.
 AC
 XX ADP65420;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Human mRNA, cDNA DKFZp34C011 (from clone DKFZp34C011), DNA.
 XX

KW autoimmune disease; arthritis; gene expression analysis;
 KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
 KW antiarthritic; osteopathic; antigout; antiinflammatory; dermatological;
 KW immunomodulatory; lupus; ankylosing spondylitis; fibrositis;
 KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
 KW immune; ds; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003072827-A1.
 XX
 PD 04-SEP-2003.
 XX
 PF 31-OCT-2002; 2002WO-US035433.
 XX
 PR 31-OCT-2001; 2001US-0336220P.
 XX
 PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
 XX
 PI Hirsch R, Thorton SL;
 XX
 DR WPI; 2003-712740/67.
 DR GENBANK; AL136794.
 XX
 PT Diagnosing and analyzing autoimmune disease using gene expression
 PT profiles and microarray technology, useful for diagnosing and treating
 PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
 PT gout.
 XX
 PS Disclosure; Page; 56pp; English.
 XX
 CC The invention relates to a novel method for diagnosing and analysing
 CC autoimmune disease or arthritides. The method comprises obtaining a
 CC patient sample containing mRNA, analysing gene expression using the mRNA
 CC that results in a gene expression signature of the mRNA, and using that
 CC gene expression signature to diagnose or analyse the autoimmune disease
 CC or arthritides in the patient, where gene expression of at least 60% of
 CC the genes correlates with that of the gene signature. The invention
 CC further comprises: a treatment of rheumatoid arthritis; identification of
 CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
 CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
 CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
 CC analyses of autoimmune disease or rheumatoid arthritis; screening the
 CC efficacy of a candidate drug in vitro for the treatment of collagen-
 CC induced arthritis; and reducing the symptoms associated with collagen-
 CC induced arthritis. The compositions of the invention have the following
 CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
 CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
 CC methods and compositions of the present invention are useful for
 CC diagnosing and treating autoimmune disease or arthritides, such as
 CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
 CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
 CC immune disease caused by an infectious agent. This polynucleotide
 CC represents a DNA sequence relating to the genes used in the analysis and
 CC treatment of autoimmune diseases or arthritides. Note: This sequence is
 CC not shown in the specification. It has been supplied in an electronic
 CC format from WIPO.
 XX
 SQ Sequence 3237 BP; 938 A; 668 C; 749 G; 882 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.22e+03 Length: 3237
 Score: 42.00 Matches: 6
 Percent Similarity: 75.00% Conservative: 0
 Best Local Similarity: 75.00% Mismatches: 2
 Query Match: 79.25% Indels: 0
 DB: 11 Gaps: 0
 US-10-029-756-6 (1-8) x ADP65420 (1-3237)
 Qy 1 TptleGlyHisAepAlaGlyHis 8
 Db 1760 TGGATTGGGCACGATGGGCCAC 1737

RESULT 64
ADO20213/c
ID ADO20213 standard; cDNA; 3237 BP.
XX AC ADO20213;
XX DT 12-AUG-2004 (first entry)
XX DE Human PRO polynucleotide #559.
XX KW Human; PRO; gene; ss; immune related disorder;
KW systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis;
KW juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome;
KW vasculitis; sarcoidosis; autoimmune haemolytic anaemia;
KW autoimmune thrombocytopenia; thyroiditis; diabetes mellitus;
KW renal disease; demyelinating disease; central nervous system;
KW peripheral nervous system; demyelinating polyneuropathy;
KW Guillain-Barre syndrome;
KW chronic inflammatory demyelinating polyneuropathy.
XX OS Homo sapiens.
XX PN WO2004043361-A2.
XX PD 27-MAY-2004.
XX PF 06-NOV-2003; 2003WO-US035268.
XX PR 08-NOV-2002; 2002US-0425235P.
XX PA (GETH) GENENTECH INC.
XX PI Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
PI Wood WT, Wu TD;
XX DR WPI; 2004-420067/39.
XX DR P-PSDB; ADO20214.
XX PT Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
PT treating an immune related disorder such as systemic lupus erythematosus,
PT rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
PT spondyloarthropathy.
XX PS Claim 1; SEQ ID NO 1182; 1731pp; English.
XX CC The invention relates to human PRO polypeptides and the polynucleotides
CC encoding them. The polypeptides and polynucleotides are useful for
CC treating and diagnosing immune related disorders in mammals. The immune
CC related disorders include systemic lupus erythematosus, rheumatoid
CC arthritis, osteoarthritis, juvenile chronic arthritis, systemic
CC sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
CC haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
CC mellitus, immune-mediated renal disease, demyelinating diseases of the
CC central or peripheral nervous system, demyelinating polyneuropathy,
CC Guillain-Barre syndrome and chronic inflammatory demyelinating
CC polyneuropathy. This sequence represents a human PRO polynucleotide of
CC the invention.
SQ Sequence 3237 BP; 938 A; 668 C; 749 G; 882 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.22e+03 Length: 3237
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
Gaps: 0
DB: 12

US-10-029-756-6 (1-8) x ADO20213 (1-3237)
QY 1 TrpIleGlyHisAspAlaGlyHis 8
|||||

Db 1760 TGGATTGGCAGCAGCATGGGCCAC 1737
RESULT 65
ACN39430/c
ID ACN39430 standard; cDNA; 3237 BP.
XX AC ACN39430;
XX DT 18-NOV-2004 (first entry)
XX DE Tumour-associated antigenic target (TAT) CDNA DNA325648, SEQ ID NO:3566.
XX KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic; gene; ss.
XX OS Homo sapiens.
XX PN WO2004030615-A2.
XX PD 15-APR-2004.
XX PF 29-SEP-2003; 2003WO-US028547.
XX PR 02-OCT-2002; 2002US-0414971P.
XX PA (GETH) GENENTECH INC.
XX PI Wu TD, Zhang Z, Zhou Y;
XX DR WPI; 2004-347921/32.
XX DR P-PSDB; ABM81380.
XX PT New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX PS Claim 1; SEQ ID NO 3566; 7273pp; English.
XX CC The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT nucleic acid of the invention
XX SQ Sequence 3237 BP; 938 A; 668 C; 749 G; 882 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.22e+03 Length: 3237
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0

DB: 13 Gaps: 0

US-10-029-756-6 (1-8) x ACN39430 (1-3237)

QY 1 TtpIlleGlyHisAspAlaGlyHis 8

Db 1760 TGGATTGGGCACAGCATGGCCAC 1737

RESULT 66

ID AAS84091/c

AC AAS84091;

DT 13-FEB-2002 (first entry)

DE DNA encoding novel human diagnostic protein #19895.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX Homo sapiens.

XX WO200175067-A2.

PN 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US008631.

XX 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR P-PSDB; ABG19904.

XX New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensic, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity.

XX Claim 1; SEQ ID NO 19895; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)

CC sequences. (I) is useful as hybridisation probes, polymerase chain

CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

CC and in recombinant production of (II). The polynucleotides are also used

CC in diagnostics as expressed sequence tags for identifying expressed

CC genes. (I) is useful in gene therapy techniques to restore normal

CC activity of (II) or to treat disease states involving (II). (II) is

CC useful for generating antibodies against it, detecting or quantitating a

CC polypeptide in tissue, as molecular weight markers and as a food

CC supplement. (II) and its binding partners are useful in medical imaging

CC of sites expressing (II). (I) and (II) are useful for treating disorders

CC involving aberrant protein expression or biological activity. The

CC polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic

CC coding sequences of the invention. Note: The sequence data for this

CC patent did not appear in the printed specification, but was obtained in

CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 3259 BP; 1296 A; 701 C; 604 G; 658 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.23e+03 Length: 3259

Score: 42.00 Matches: 6

Percent Similarity: 75.00% Conservative: 0

Best Local Similarity: 75.00% Mismatches: 2

Query Match: 79.25% Indels: 0

DB: 5 Gaps: 0

US-10-029-756-6 (1-8) x AAS84091 (1-3259)

QY 1 TtpIlleGlyHisAspAlaGlyHis 8

Db 3177 TGGATTGGGCACAGCATGGCCAC 3154

RESULT 67

ABL11165/c

ID ABL11165 standard; cDNA; 3336 BP.

XX ABL11165;

XX 26-MAR-2002 (first entry)

DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 27977.

XX Drosophila; developmental biology; cell signalling; insecticide;

KW pharmaceutical; gene; ss.

XX Drosophila melanogaster.

OS WO200171042-A2.

PN 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

PR 23-MAR-2000; 2000US-0191637P.

PR 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

PI WPI; 2001-656860/75.

DR P-PSDB; ABB67062.

XX New isolated nucleic acid detection reagent for detecting 1000 or more

PT genes from Drosophila and for elucidating cell signalling and cell-cell

PT interactions.

XX Claim 1; SEQ ID NO 27977; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent

CC capable of detecting 1000 or more genes from Drosophila. The invention is

CC useful in developmental biology and in elucidating cell signalling and

CC cell-cell interactions in higher eukaryotes for the development of

CC insecticides, therapeutics and pharmaceutical drugs. The invention

CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA

CC sequences (ABU01840-ABU16175) and the encoded proteins (ABB57737-

CC ABB72072). The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly

CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 3336 BP; 887 A; 919 C; 823 G; 707 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.26e+03 Length: 3336

Score: 42.00 Matches: 7

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 79.25% Indels: 0

DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x ABL11165 (1-3336)

QY 2 IleGlyHisAspAlaGlyHis 8

Db 1197 ATAGTCACGATGCTGGACAT 1177

RESULT 68
ABK35882/c
ID ABK35882 standard; cDNA; 3355 BP.
XX AC ABK35882;
XX DT 08-MAY-2002 (first entry)
XX DE cDNA sequence #273 encoding novel human secreted protein.
XX KW Human secreted protein; hyperproliferative disorder; autoimmune disorder;
XX KW immune deficiency disorder; blood disorder; inflammatory disorder;
XX KW infectious disorder; allergic condition; neurodegenerative disorder;
XX KW liver fibrosis; coagulation disorder; gene therapy; antimicrobial;
XX KW tumour; cancer; hepatotropic; immunosuppressive; antirheumatic; gene; ss.
XX OS Homo sapiens.
XX PN WO200177289-A2.
XX PD 18-OCT-2001.
XX PF 29-MAR-2001; 2001WO-US010232.
XX PR 06-APR-2000; 2000US-0195605P.
XX PA (GEMY) GENETICS INST INC.
XX PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
XX PI Merberg D, Treacy M, Agostino MJ, Bowman MR, Spaulding V, Wong GG;
XX PI Clark HP, Fichtel K, Howes SH, Resnick RJ, Gulukota K, Graham JR;
XX DR WPI; 2002-179322/23.
XX PT Six hundred and twenty three polynucleotides derived from a variety of
XX PT human tissue sources which encode secreted proteins, useful for treating
XX PT immune deficiencies and disorders such as autoimmune disorders.
XX FS Claim 1; Page 240-241; 393pp; English.
XX CC The present invention relates to the isolation of novel cDNA sequences
XX CC which encode human secreted proteins. The cDNA sequences have been
XX CC derived from a variety of human tissues. The invention also provides a
XX CC method for producing proteins from these polynucleotide sequences. The
XX CC proteins are useful for identifying compounds that modulate their
XX CC activity and production. The sequences of the invention are useful for
XX CC treating diseases such as hyperproliferative disorders (e.g. cancer),
XX CC immune deficiency disorders (e.g. severe combined immunodeficiency
XX CC (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders
XX CC (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis),
XX CC infectious disorders (e.g. hepatitis), allergic conditions (e.g. asthma),
XX CC neurodegenerative disorders (e.g. Alzheimer's disease), liver fibrosis,
XX CC coagulation disorders (e.g. haemophilia), and tumours. The polynucleotide
XX CC sequences of the invention are also useful in gene therapy. ABK35810-
XX CC ABK36232 represent the cDNA sequences of the invention that encode for
XX CC novel human secreted proteins

SQ Sequence 3355 BP; 828 A; 711 C; 712 G; 1103 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 1.27e+03 Length: 3355
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-6 (1-8) x ABK35882 (1-3355)
Oy 1 TrpIleGlyHisAspAlaGlyHis 8
|||||

Db 2940 TGGATTGGGCACGACATGGGCCAC 2917

RESULT 69
AAS94909/c
ID AAS94909 standard; DNA; 3370 BP.
XX AC AAS94909;
XX DT 14-FEB-2002 (first entry)
XX DE Human DNA sequence #164 expressed during foam cell differentiation.
XX KW Human; foam cell differentiation; atherosclerosis; cerebral stroke;
XX KW cardiovascular disorder; coronary artery disease; gene therapy; ds.
XX OS Homo sapiens.
XX PN WO200177389-A2.
XX PD 18-OCT-2001.
XX PF 04-APR-2001; 2001WO-US011128.
XX PR 05-APR-2000; 2000US-0195106P.
XX PA (INCY-) INCYTE GENOMICS INC.
XX PI Shiffman D, Somogyi R, Lawn R, Seilhamer JJ, Porter GJ, Mikita T;
XX PI Tai J;
XX DR WPI; 2002-010925/01.
XX PT Composition useful for diagnosis of conditions, disorders or diseases
XX PT associated with atherosclerosis, comprises several polynucleotides that
XX PT are differentially expressed in foam cell development.
XX FS Claim 1; Page 219-220; 315pp; English.
XX CC The present invention relates to the isolation of human polynucleotide
XX CC sequences that are differentially expressed during foam cell
XX CC differentiation. The polynucleotide sequences of the invention or a
XX CC composition comprising these polynucleotides are useful as a high
XX CC throughput method for detecting altered expression of one or more
XX CC polynucleotides in a sample. The polynucleotides can be used in the
XX CC diagnosis of disorders associated with foam cell development such as
XX CC atherosclerosis, cerebral stroke, and cardiovascular disorders such as
XX CC coronary artery disease. The polynucleotide sequences can also be used as
XX CC PCR primers and probes. The polynucleotides of the invention are also
XX CC useful in gene therapy. AAS94746-AAS95021 represent the human
XX CC polynucleotide sequences of the invention which are differentially
XX CC expressed during foam cell differentiation

SQ Sequence 3370 BP; 936 A; 791 C; 762 G; 881 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.28e+03 Length: 3370
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-6 (1-8) x AAS94909 (1-3370)
Oy 1 TrpIleGlyHisAspAlaGlyHis 8
|||||

Db 1598 TGGATAGGGCATCCATTGGCCAC 1575

RESULT 70
AAS78145/c
ID AAS78145 standard; cDNA; 3419 BP.
XX AC AAS78145;

XX 13-FEB-2002 (first entry)
XX DNA encoding novel human diagnostic protein #13949.
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX Homo sapiens.
XX WO200175067-A2.
XX PD 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US008631.
XX 31-MAR-2000; 2000US-00540217.
XX 23-AUG-2000; 2000US-00649167.
XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX P-PSDB; ASG13958.
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX Claim 1; SEQ ID NO 13949; 103pp; English.
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (I) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activity. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
XX coding sequences of the invention. Note: The sequence data for this
XX patent did not appear in the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 3419 BP; 1383 A; 751 C; 593 G; 692 T; 0 U; 0 Other;
Alignment Scores:
Pred No.: 1.3e+03 Length: 3419
Score: 42.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 79.25% Indels: 0
DB: 5 Gaps: 0
US-10-029-756-6 (1-8) x AAS78145 (1-3419)
Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 3337 TGGATTGGGCACGACGATGGCCAC 3314
RESULT 71
ACC46735/c

ID ACC46735 standard; cDNA; 3470 BP.
XX AC ACC46735;
XX DT 02-JUN-2003 (first entry)
XX DE Human dithp growth/development-associated protein-encoding cDNA.
XX Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;
XX cancer; cell proliferative disorder; autoimmune disorder;
XX inflammatory disorder; infection; hormonal disorder; metabolic disorder;
XX neurological disorder; gastrointestinal disorder; transport disorder;
XX connective tissue disorder; drug screening; proteome analysis;
XX gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
XX disease model; toxicological testing; transcript imaging; growth;
XX development; gene; ss.
XX Homo sapiens.
XX WO200297031-A2.
XX PD 05-DEC-2002.
XX PF 27-MAR-2002; 2002WO-US010056.
XX 28-MAR-2001; 2001US-0279619P.
XX 29-MAR-2001; 2001US-0280067P.
XX 29-MAR-2001; 2001US-0280068P.
XX 16-MAY-2001; 2001US-0291280P.
XX 17-MAY-2001; 2001US-0291829P.
XX 17-MAY-2001; 2001US-0291849P.
XX 19-JUN-2001; 2001US-0299428P.
XX 20-JUN-2001; 2001US-0299776P.
XX 20-JUN-2001; 2001US-0300001P.
XX (INCY-) INCYTE GENOMICS INC.
XX Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
XX Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Ameshey SR;
XX Daugherty SC, Dam TC, Liu TP, Nguyen DA, Kleefeld Y, Gerstin EH;
XX Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
XX Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
XX WPI; 2003-129518/12.
XX P-PSDB; ABR41798.
XX Novel human diagnostic and therapeutic polypeptide useful for identifying
XX test compound which specifically binds to a polypeptide encoded by human
XX diagnostic and therapeutic polynucleotide, and to induce antibodies.
XX Claim 2; SEQ ID NO 656; 591pp; English.
XX The invention relates to novel human diagnostic and therapeutic
XX polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded
XX proteins (DITHP; ABR41136-ABR41812). The invention also relates to
XX polynucleotide sequences at least 90% identical to the dithp cDNA
XX sequences of the invention; recombinant vectors, host cells and
XX transgenic organisms comprising a dithp nucleic acid sequence; the
XX recombinant production of DITHP proteins; antibodies specific for DITHP
XX proteins; microarrays comprising dithp nucleic acid sequences; methods of
XX detecting dithp nucleotide and protein sequences; methods of screening
XX for compounds which specifically bind a DITHP protein; and methods of
XX assessing the toxicity of test compounds using a dithp hybridisation
XX probe. Dithp nucleic acid sequences and DITHP proteins may be used in the
XX diagnosis of a wide variety of conditions including cancer and other cell
XX proliferative disorders; autoimmune or inflammatory disorders; bacterial,
XX viral, fungal or parasitic infections; hormonal disorders; metabolic
XX disorders; neurological disorders; gastrointestinal disorders; transport
XX disorders; and connective tissue disorders. They may also be used to
XX screen for modulators of protein activity or gene expression. DITHP
XX proteins can additionally be used in analysis of the proteome of a tissue
XX or cell type and to induce antibodies. The dithp nucleic acids are
XX additionally useful in somatic or germline gene therapy of the disorders

CC mentioned above, as a source of antisense sequences, as a source of
 CC probes and primers, in genotyping and identification of individuals, in
 CC the generation of transgenic animal models of human disease or knock in
 CC humanised animals, in toxicological testing, and in transcript imaging.
 CC The present sequence represents a dithp cDNA encoding a DITHP protein
 CC which is associated with growth and development. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 CC
 XX SQ Sequence 3470 BP; 965 A; 812 C; 791 G; 902 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1.32e+03 Length: 3470
 Score: 42.00 Matches: 6
 Percent Similarity: 75.00% Conservative: 0
 Best Local Similarity: 75.00% Mismatches: 2
 Query Match: 79.25% Indels: 0
 DB: 8 Gaps: 0

US-10-029-756-6 (1-8) x ACC46735 (1-3470)

Oy 1 TptileGlyHisAspAlaGlyHis 8

Db 1720 TGGATAGGCGATTCATTGGCCAC 1697

RESULT 72

ADE31423/C

ID ADE31423 standard; DNA; 4023 BP.

XX AC ADE31423;

XX DT 29-JAN-2004 (first entry)

XX DE Human diagnostic and therapeutic polynucleotide (dithp), SEQ ID No 178.
 XX KW diagnostic and therapeutic polynucleotide: dithp; antiarteriosclerotic;
 KW antiinflammatory; cerebroprotective; antilipaeamic; antidiabetic;
 KW immunosuppressive; neuroprotective; nootropic; neuroleptic; tranquilizer;
 KW osteopathic; antiarthritic; antirheumatic; cytostatic; hepatotropic;
 KW virucide; haemostatic; anti-HIV; antithyroid; thyromimetic;
 KW dermatological; antibacterial; fungicide; antiparasitic; anticonvulsant;
 KW thrombolytic; anticoagulant; anorectic; vasotropic; antiulcer;
 KW gene therapy; protein replacement therapy; human; gene; ds.

XX OS Homo sapiens.

XX XX WO2003062376-A2.

XX PN 31-JUL-2003.

XX PD 13-JAN-2003; 2003WO-US001096.

XX PF 16-JAN-2002; 2002US-0349384P.

XX PR 17-JAN-2002; 2002US-0349413P.

XX PR 17-JAN-2002; 2002US-0349946P.

XX XX (INCY-) INCYTE GENOMICS INC.

XX PI Jones AL, Dahl CR, Gietzen D, Chinn J, Dufour GE, Jackson JL;
 PI Yu JY, Tuason O, Yap PE, Anshey SR, Dam TC, Gerstein EH;
 PI Peralta CH, Lewis SA, Chen A, Marwaha R, Lan RY, Urashka ME;
 PI Krishnam SR, Kolluru V, Panesar IS;
 XX DR WPI; 2003-636732/60.
 XX DR P-PSDB; ADE31234.

XX XX New human diagnostic and therapeutic polynucleotides and polypeptides,
 PT useful for diagnosing, treating or preventing e.g. leukemia, brain
 PT cancer, atherosclerosis, AIDS, thyroiditis, infections, obesity, stroke
 PT or Alzheimer's.
 XX XX Claim 1; SEQ ID NO 178; 634pp; English.

XX CC The invention relates to a novel isolated human diagnostic and
 CC therapeutic polynucleotide (designated dithp). The novel dithp
 CC polynucleotide comprises: any of 188 DNA sequences consisting of 195-7798
 CC base pairs fully defined in the specification; a polynucleotide
 CC comprising a naturally occurring polynucleotide sequence at least 90%
 CC identical to the dithp polynucleotide; a polynucleotide complementary to
 CC the dithp polynucleotide or its polynucleotide which is at least 90%
 CC identical; or an RNA equivalent of any of the polynucleotides mentioned
 CC above. The dithp polynucleotides have the following activities:
 CC antiarteriosclerotic, antiinflammatory, cerebroprotective, antilipaeamic,
 CC antidiabetic, immunosuppressive, neuroprotective, nootropic, neuroleptic,
 CC tranquilizer, osteopathic, antiarthritic, antirheumatic, cytostatic,
 CC hepatotropic, virucide, haemostatic, anti-HIV, antithyroid, thyromimetic,
 CC dermatological, antibacterial, fungicide, antiparasitic, anticonvulsant,
 CC thrombolytic, anticoagulant, anorectic, vasotropic, and antiulcer. The
 CC novel DITHP polynucleotides polypeptide can be used in gene therapy and
 CC protein replacement therapy. The dithp polynucleotides or DITHP
 CC polypeptides are useful for diagnosing, preventing or treating diseases
 CC associated with the expression of human molecules. In particular, these
 CC diseases include cancers (e.g. adenocarcinoma, leukaemia, melanoma, brain
 CC cancer, breast cancer, cervix cancer, bone cancer, liver cancer, lung
 CC cancer) or other cell proliferative disorders (e.g. arteriosclerosis,
 CC atherosclerosis, cirrhosis, hepatitis, polycythemia vera, primary
 CC thrombocytopenia), autoimmune/inflammatory disorders (e.g. AIDS,
 CC Addison's disease, thyroiditis, Crohn's disease, Graves' disease,
 CC Hashimoto's thyroiditis, multiple sclerosis, osteoarthritis, rheumatoid
 CC arthritis, scleroderma, systemic lupus erythematosus), infections (e.g.
 CC viral, bacterial, fungal or parasitic infection), developmental disorders
 CC (e.g. Cushing's syndrome or epilepsy), endocrine disorders (e.g.
 CC thrombosis, hypopituitarism, hypogonadism, gigantism, goiter) metabolic
 CC disorders (e.g. hypercholesterolaemia, hypoglycaemia, diabetes,
 CC hyperlipidaemia, obesity), neurological disorders (e.g. ischaemic
 CC cerebrovascular disease, stroke, Alzheimer's disease, Pick's disease,
 CC Huntington's disease, Parkinson's disease, Creutzfeldt-Jakob disease,
 CC anxiety, schizophrenia), gastrointestinal disorders (e.g. ulcers),
 CC transport disorders (e.g. akinesia or multidrug resistance), or
 CC connective tissue disorders (e.g. Paget's disease or rickets). This
 CC polynucleotide sequence represents one of the human dithp DNA sequences
 CC of the invention.

XX SQ Sequence 4023 BP; 1082 A; 923 C; 833 G; 1185 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.55e+03 Length: 4023
 Score: 42.00 Matches: 6
 Percent Similarity: 75.00% Conservative: 0
 Best Local Similarity: 75.00% Mismatches: 2
 Query Match: 79.25% Indels: 0
 DB: 10 Gaps: 0

US-10-029-756-6 (1-8) x ADE31423 (1-4023)

Oy 1 TptileGlyHisAspAlaGlyHis 8

Db 612 TGGATAGGCGATTCATTGGCCAC 589

RESULT 73

ABL22485/C

ID ABL22486 standard; DNA; 4741 BP.

XX AC ABL22486;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 18931.
 XX KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ds.
 XX OS Drosophila melanogaster.
 XX PN WO200171042-A2.

XX PD 27-SEP-2001.
 XX PF 23-MAR-2001; 2001WO-US009231.
 XX PR 23-MAR-2000; 2000US-0191637P.
 XX PR 11-JUL-2000; 2000US-00614150.
 XX PA (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX WPI; 2001-656860/75.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
 XX Claim 1; SEQ ID NO 18931; 21pp + Sequence Listing; English.
 XX The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 4741 BP; 1269 A; 1141 C; 1132 G; 1199 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1.85e+03 Length: 4741
 Score: 42.00 Matches: 6
 Percent Similarity: 75.00% Conservative: 0
 Best Local Similarity: 75.00% Mismatches: 2
 Query Match: 79.25% Indels: 0
 DB: 4 Gaps: 0
 US-10-029-756-6 (1-8) x ABL22486 (1-4741)
 QY 1 TrpIleGlyHisAspAlaGlyHis 8
 ID ABL11164 standard; cDNA; 6005 BP.
 XX ABL11164;
 XX DT 26-MAR-2002 (first entry)
 XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 27974.
 XX Drosophila; developmental biology; cell signalling; insecticide;
 XX pharmaceutical; gene; ss.
 XX Drosophila melanogaster.
 XX WO200171042-A2.
 XX 27-SEP-2001.
 XX 23-MAR-2001; 2001WO-US009231.
 XX 23-MAR-2000; 2000US-0191637P.
 XX 11-JUL-2000; 2000US-00614150.
 XX PA (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li PWD, Myers EW;
 XX WPI; 2001-656860/75.
 XX P-PSDB; ABB67061.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
 XX Claim 1; SEQ ID NO 27974; 21pp + Sequence Listing; English.
 XX The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 6005 BP; 1693 A; 1451 C; 1343 G; 1518 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 2.39e+03 Length: 6005
 Score: 42.00 Matches: 7
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 79.25% Indels: 0
 DB: 4 Gaps: 0
 US-10-029-756-6 (1-8) x ABL11164 (1-6005)
 QY 2 IleGlyHisAspAlaGlyHis 8
 ID ABL11164 standard; cDNA; 8335 BP.
 XX AAS78974/c
 XX AAS78974;
 XX DT 13-FEB-2002 (first entry)
 XX DNA encoding novel human diagnostic protein #14778.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX Homo sapiens.
 XX WO200175067-A2.
 XX 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US008631.
 XX 31-MAR-2000; 2000US-00540217.
 XX 23-AUG-2000; 2000US-00649167.
 XX (HYSE-) HYSEQ INC.
 XX Drmanac RT, Liu C, Tang YT;
 XX WPI; 2001-639362/73.
 XX P-PSDB; ABG14787.
 XX New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.

XX PS Claim 1; SEQ ID NO 14778; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, CC and in recombinant production of (II). The polynucleotides are also used CC in diagnostics as expressed sequence tags for identifying expressed CC genes. (II) is useful in gene therapy techniques to restore normal CC activity of (II) or to treat disease states involving (II). (II) is CC useful for generating antibodies against it, detecting or quantitating a CC polypeptide in tissue, as molecular weight markers and as a food CC supplement. (II) and its binding partners are useful in medical imaging CC of sites expressing (II). (I) and (II) are useful for treating disorders CC involving aberrant protein expression or biological activity. The CC polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity CC and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic CC coding sequences of the invention. Note: The sequence data for this CC patent did not appear in the printed specification, but was obtained in CC electronic format directly from WIPO at CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 8335 BP; 3298 A; 1823 C; 1564 G; 1650 T; 0 U; 0 Other;

Alignment Scores:

| | | | |
|------------------------|---------|---------------|------|
| Pred. No.: | 3.4e+03 | Length: | 8335 |
| Score: | 42.00 | Matches: | 6 |
| Percent Similarity: | 75.00% | Conservative: | 0 |
| Best Local Similarity: | 75.00% | Mismatches: | 2 |
| Query Match: | 79.25% | Indels: | 0 |
| DB: | 5 | Gaps: | 0 |

US-10-029-756-6 (1-8) x AAS78974 (1-8335)

Qy 1 TrrileGlyHisAspAlaGlyHis 8
|||||

Db 8253 TGGATTGGGCACAGCATGGGCCAC 8230

RESULT 76

| | | | |
|--|----------|---------------|--------|
| ADQ59518 | 5.02e+04 | Length: | 100762 |
| ID ADQ59518 standard; DNA; 100762 BP. | 42.00 | Matches: | 6 |
| XX AC ADQ59518; | 87.50% | Conservative: | 1 |
| XX DT 07-OCT-2004 (first entry) | 75.00% | Mismatches: | 1 |
| XX DE Human cancer-associated (CA) gene sequence SEQ ID NO:154. | 79.25% | Indels: | 0 |
| XX KW human; cancer-associated gene; cancer-associated protein; cytostatic; gene therapy; vaccine; tyrosine kinase antagonist; | 12 | Gaps: | 0 |
| XX KW G-protein coupled receptor antagonist; cancer; lymphoma; gene; ds. | | | |
| XX OS Homo sapiens. | | | |
| XX FN WO2004058288-A1. | | | |
| XX PD 15-JUL-2004. | | | |
| XX PF 15-DEC-2003; 2003WO-US040082. | | | |
| XX PR 17-DEC-2002; 2002US-00322696. | | | |
| XX PA (SAGR-) SAGRES DISCOVERY INC. | | | |
| XX PI Morris DW, Malandro MS; | | | |
| XX DR WPI; 2004-543349/52. | | | |
| XX DR P-PSDB; ADQ59520. | | | |
| XX PT New cancer-associated nucleic acid for diagnosing, preventing or treating | | | |

cancer (e.g. lymphoma) or for screening agents that may be used for treating or preventing cancer.

Claim 16; SEQ ID NO 154; 143pp; English.

The present invention describes human cancer-associated (CA) nucleotide sequences (I). Also described: (1) an expression vector comprising (I); (2) a host cell comprising (I) or the expression vector; (3) a microarray for detecting a CA nucleic acid; (4) an isolated polypeptide encoded within an open reading frame of a CA sequence; (5) an isolated antibody, or its antigen binding fragment, that binds to the above polypeptide; (6) a hybridoma that produces the monoclonal antibody described above; (7) a pharmaceutical composition comprising the antibody and a pharmaceutical excipient; (8) a kit for detecting or diagnosing cancer cells, comprising the above (monoclonal) antibody or polynucleotide that selectively hybridises to any of the polynucleotide sequences mentioned above; (9) methods for diagnosing cancer or for detecting the presence or absence of cancer cells in an individual; (10) a method for inhibiting growth of cancer cells in an individual; (11) a method for delivering a therapeutic agent to cancer cells in an individual; (12) an electronic library comprising the polynucleotide or polypeptide, or their fragments, mentioned above; (13) a method of screening for anticancer activity; (14) methods for detecting cancer associated with expression of a polypeptide or the presence of the antibody in a test cell or serum sample; (15) a method for screening for a bioactive agent capable of modulating the activity of a CA protein encoded by the above nucleic acid molecule; and (16) a method for treating cancers. (I) has cytostatic activity, and can be used in gene therapy, in vaccines, as a tyrosine kinase antagonist, and as a G-protein coupled receptor antagonist. The compositions and methods of the present invention can be used for diagnosing, preventing and treating cancer, especially lymphomas. They may also be used in screening for agents that may be used for treating or preventing cancer. The present sequence represents a human CA gene sequence, which is given in the exemplification of the present invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 100762 BP; 23383 A; 25739 C; 25440 G; 26180 T; 0 U; 20 Other;

Alignment Scores:

| | | | |
|------------------------|----------|---------------|--------|
| Pred. No.: | 5.02e+04 | Length: | 100762 |
| Score: | 42.00 | Matches: | 6 |
| Percent Similarity: | 87.50% | Conservative: | 1 |
| Best Local Similarity: | 75.00% | Mismatches: | 1 |
| Query Match: | 79.25% | Indels: | 0 |
| DB: | 12 | Gaps: | 0 |

US-10-029-756-6 (1-8) x ADQ59518 (1-100762)

Qy 1 TrrileGlyHisAspAlaGlyHis 8
|||||

Db 66464 TGGCTAGTCAATTGTGCTGCTCAC 66487

RESULT 77

| | | | |
|---|----------|---------------|--------|
| ACH20392/C | 5.02e+04 | Length: | 100762 |
| ID ACH20392 standard; cDNA; 418 BP. | 42.00 | Matches: | 6 |
| XX AC ACH20392; | 87.50% | Conservative: | 1 |
| XX DT 13-OCT-2003 (first entry) | 75.00% | Mismatches: | 1 |
| XX DE Human adult liver cDNA #4. | 79.25% | Indels: | 0 |
| XX KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder. | 12 | Gaps: | 0 |
| XX OS Homo sapiens. | | | |
| XX FN US2003073623-A1. | | | |
| XX PD 17-APR-2003. | | | |


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PF 30-JUL-2001; 2001US-00918995.
XX
PR 30-JUL-2001; 2001US-00918995.
XX
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX
PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX
DR WPI; 2003-615964/58.
XX
PT New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX
PS Claim 1; SEQ ID NO 7604; 44pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversity, or in identifying mutations
CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
SQ Sequence 418 BP; 109 A; 124 C; 101 G; 84 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 204 Length: 418
Score: 41.00 Matches: 5
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 71.43% Mismatches: 0
Query Match: 77.36% Indels: 0
DB: 9 Gaps: 0

US-10-029-756-6 (1-8) x ACH20392 (1-418)
Oy 1 TrrileGlyHisAspAlaGly 7
Db 310 TGGGTGGGTCATGATTCGGG 290

RESULT 78
ABL93274
ID ABL93274 standard; cDNA; 476 BP.
XX
AC ABL93274;
XX
DT 10-JUN-2002 (first entry)
XX
DE Arabidopsis thaliana nucleic acid sequence Ref:2027039 SEQ ID NO:39.
XX
KW Arabidopsis thaliana; insecticide; fungicide; plant; mapping; diagnosis;
KW Genetic modification; gene; ss.
XX
OS Arabidopsis thaliana.
XX
FN US2002023280-A1.
XX
PD 21-FEB-2002.

26-JAN-2001; 2001US-00770444.
27-JAN-2000; 2000US-0178502P.
(GORL/) GORLACH J.
(ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUY/) YU Y.
PA (RAME/) RAMEKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
XX
Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
Rameka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
Hurban P;
WPI; 2002-267486/31.
XX
New Arabidopsis thaliana nucleic acid, for identifying homologous genes,
PT producing compositions that modulate the expression or function of its
PT encoded protein, and mapping functional regions of a protein.
XX
Claim 1; SEQ ID NO 39; 44pp; English.
XX
The present invention describes an Arabidopsis thaliana nucleic acid (1)
comprising a sequence capable of hybridising under stringent conditions
to a sequence (S1) selected from any one of the 999 sequences given in
ABL93236 to ABL94234. (1) have insecticide and fungicide activities, and
they can be used as protein expression modulators. (1) can be used in
identifying homologous or related genes, in producing compositions that
modulate the expression or function of their encoded proteins, mapping
functional regions of the proteins, and in studying associated
physiological pathways. (1) can also be used: (1) for the genetic
manipulation of cells, particularly plant cells; (2) in screening assays
of various plant strains to determine the strains that are best capable
of withstanding a particular disease or environmental stress; (3) for
enhancing or inhibiting production of a biosynthetic product in a plant;
(4) as probes in mapping and in diagnosis, in genetic modification and
for screening purposes, to generate additional copies of the nucleic
acids, to generate ribozymes or antisense oligonucleotides, and as single
-stranded DNA probes or as triple-stand forming oligonucleotides; and (5)
for generating genetically modified transgenic organisms. Note: The
sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from the
USPTO web site
XX
SQ Sequence 476 BP; 98 A; 145 C; 95 G; 136 T; 0 U; 2 Other;

Alignment Scores:
Pred. No.: 234 Length: 476
Score: 41.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 75.00% Mismatches: 0
Query Match: 77.36% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-6 (1-8) x ABL93274 (1-476)
Oy 1 TrrileGlyHisAspAlaGlyHis 8

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::||| ||| ||| ||| ::||| |||
 TACATAGGTCACGATTCGGTCAT 359

CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC sedata.uspto.gov/sequence.html?DocID=20030194704

RESULT 79
ACH78188/c
ID ACH78188 standard; DNA: 514 BP.

ACH78188;

DT 29-JUL-2004 (first entry)

DE Human genome derived single exon probe #11383.

Human; probe; ss; gene expression; single exon probe; microarray; KW alternative splicing event; genomic alteration.

XX
OS
Homo sapiens.

US2003194704-A1.

16-OCT-2003.

03-APR-2002: 2002US-00029386.

PR 03-APR-2002: 2002US-00029386.

PA (PENN/) PENN S G.

PA (KANR/) KANR D K.
PA (HANZ/) HANZEL D K.

Penn SG, Rank DR,

DR WPI; 2004-119264/12.

PT New human genome-derived

PT surviving tissues.

PS Claim 15; SEQ ID NO 11383; 80pp; English.

The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a vector comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above-mentioned amino acid sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, a method of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing human gene expression data by subcription, and a computer-readable storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising alternative splicing events, in detecting and characterising gross alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this

CC variations as indicated in (S1, SEQ ID NO:1 to 168) of the PA gene locus
 CC of the subject and where the single nucleotide polymorphism (SNP) class
 CC of the SNP is a cardiovascular disease (CVD) as described in PA SNPs, SNP
 CC classes and putative PA genes listing table given in the specification,
 CC where a risk genotype has a risk ratio of greater than 1 as described in
 CC the correlation table of genotypes of PA SNPs to relative risk as given
 CC in the specification; (11) determining (M4) a patient's individual
 CC response to statin therapy, including drug efficacy and adverse drug
 CC reactions, involves determining the identity of nucleotide variation in
 CC sequences of (S1) of the PA gene locus of the subject and where the SNP
 CC class of the SNP is adverse drug response (ADR), drug efficacy (EPF), or
 CC both as described in PA SNPs, SNP classes and putative PA genes listing
 CC table given in the specification, where the probability for such response
 CC can as described in the correlation table of genotypes of PA SNPs to
 CC relative risk as given in the specification; (12) use of (M4) for
 CC preparation of medicament tailored to suit a patient's response to statin
 CC therapy; and (13) a kit (V1) for assessing cardiovascular status or
 CC statin response. (M2) is useful for screening for agents which regulate
 CC the activity of PA gene. (M3) is useful for determining whether a human
 CC subject has, or is at the risk of developing a cardiovascular disease.
 CC (M4) is useful for determining a patient's individual response to statin
 CC therapy. (M4) is useful for preparation of medicament tailored to suit a
 CC patient's response to statin therapy.

SQ Sequence 544 BP; 137 A; 143 C; 150 G; 113 T; 0 U; 1 Other;

Alignment Scores:

| | | | |
|------------------------|---------|---------------|-----|
| Pred. No.: | 271 | Length: | 544 |
| Score: | 41.00 | Matches: | 5 |
| Percent Similarity: | 100.00% | Conservative: | 2 |
| Best Local Similarity: | 71.43% | Mismatches: | 0 |
| Query Match: | 77.36% | Indels: | 0 |
| DB: | 12 | Gaps: | 0 |

US-10-029-756-6 (1-8) x ADJ84393 (1-544)

Qy 1 TrpIleGlyHisAspAlaGly 7

Db 485 TGGGTGGTCATGATTCGGG 505

RESULT 81

AAK63843/C

ID AAK63843 standard; cDNA; 564 BP.

XX AAK63843;

XX 06-NOV-2001 (first entry)

DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:8903.

XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;

XX cytostatic; gene therapy; vaccine; metastasis; ss.

OS Homo sapiens.

XX WO200157182-A2.

XX 09-AUG-2001.

FF 17-JAN-2001; 2001WO-US001354.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225266P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.

PR 18-AUG-2000; 2000US-0225759P.

PR 22-AUG-2000; 2000US-0226279P.

PR 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0226868P.

PR 23-AUG-2000; 2000US-0227182P.

PR 30-AUG-2000; 2000US-0227009P.

PR 01-SEP-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0229287P.

PR 01-SEP-2000; 2000US-0229343P.

PR 01-SEP-2000; 2000US-0229344P.

PR 05-SEP-2000; 2000US-0229345P.

PR 05-SEP-2000; 2000US-0229509P.

PR 06-SEP-2000; 2000US-0229513P.

PR 06-SEP-2000; 2000US-0230437P.

PR 08-SEP-2000; 2000US-0230438P.

PR 08-SEP-2000; 2000US-0231242P.

PR 08-SEP-2000; 2000US-0231243P.

PR 08-SEP-2000; 2000US-0231244P.

PR 08-SEP-2000; 2000US-0231413P.

PR 08-SEP-2000; 2000US-0231414P.

PR 08-SEP-2000; 2000US-0232080P.

PR 12-SEP-2000; 2000US-0232081P.

PR 14-SEP-2000; 2000US-0231968P.

PR 14-SEP-2000; 2000US-0232397P.

PR 14-SEP-2000; 2000US-0232398P.

PR 14-SEP-2000; 2000US-0232399P.

PR 14-SEP-2000; 2000US-0232400P.

PR 14-SEP-2000; 2000US-0232401P.

PR 14-SEP-2000; 2000US-0233063P.

PR 14-SEP-2000; 2000US-0233064P.

PR 14-SEP-2000; 2000US-0233065P.

PR 21-SEP-2000; 2000US-0234274P.

PR 21-SEP-2000; 2000US-0234275P.

PR 25-SEP-2000; 2000US-0234997P.

PR 25-SEP-2000; 2000US-0234998P.

PR 26-SEP-2000; 2000US-0235484P.

PR 27-SEP-2000; 2000US-0235834P.

PR 27-SEP-2000; 2000US-0235836P.

PR 29-SEP-2000; 2000US-0236367P.

PR 29-SEP-2000; 2000US-0236368P.

PR 29-SEP-2000; 2000US-0236369P.

PR 29-SEP-2000; 2000US-0236370P.

PR 02-OCT-2000; 2000US-0236802P.

PR 02-OCT-2000; 2000US-0237037P.

PR 02-OCT-2000; 2000US-0237038P.

PR 02-OCT-2000; 2000US-0237039P.

PR 13-OCT-2000; 2000US-0237040P.

PR 13-OCT-2000; 2000US-0239935P.

PR 13-OCT-2000; 2000US-0239937P.

PR 20-OCT-2000; 2000US-0240960P.

PR 20-OCT-2000; 2000US-0241221P.

PR 20-OCT-2000; 2000US-0241785P.

PR 20-OCT-2000; 2000US-0241786P.

PR 20-OCT-2000; 2000US-0241877P.

PR 20-OCT-2000; 2000US-0241808P.

PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249254P.
PR 17-NOV-2000; 2000US-0249255P.
PR 17-NOV-2000; 2000US-0249256P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-483426/52.
XX P-ESDB; AAM91062.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and metastasis.
XX
XX Claim 1; SEQ ID NO 8903; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
XX amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patients own production of (I). Additionally, (I)

CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention
XX
XX Sequence 564 BP; 76 A; 165 C; 121 G; 198 T; 0 U; 4 Other;
SQ
Alignment Scores:
Pred. No.: 281 Length: 564
Score: 41.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 77.36% Indels: 0
DB: 4 Gaps: 0
US-10-029-756-6 (1-8) x AAK63843 (1-564)
Oy 1 TrrlleGlyHisaspAlaGlyHis 8
Db 223 TGGATTGGACATCGAGGAGGTCA 200
RESULT 82
ADS60395/c
ID ADS60395 standard; cDNA; 656 BP.
XX AC ADS60395;
XX 02-DEC-2004 (first entry)
XX Bacterial polynucleotide #12382.
XX Recombinant DNA construct; transformed plant; improved plant property;
XX cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
XX pathogen tolerance; pest tolerance; plant disease resistance;
XX cell cycle pathway modification; plant growth regulator;
XX homologous recombination; seed oil yield; protein yield; carbohydrate;
XX nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
XX bacterial polynucleotide; gene; ss.
XX Bacteria.
XX OS US2003233675-A1.
XX PN 18-DEC-2003.
XX PD 20-FEB-2003; 2003US-00369493.
XX PF 21-FEB-2002; 2002US-0360039P.
XX PR (CAOY/) CAO Y.
XX PA (HINK/) HINKLE G J.
XX PA (SLAT/) SLATER S C.
XX PA (CHEN/) CHEN X.
XX PA (GOLD/) GOLDMAN B S.
XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX New recombinant DNA construct comprising a promoter positioned to provide
XX for expression of a polynucleotide encoding a polypeptide from a
XX microbial source, useful for producing plants with improved properties.
XX Claim 1; SEQ ID NO 36069; 122pp; English.
XX The invention relates to a recombinant DNA construct comprising a
XX promoter functional in a plant cell, where the promoter is positioned to
XX provide for expression of a polynucleotide encoding a polypeptide from a
XX microbial source. The invention also relates to a transformed plant


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XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
PI WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
XX for expression of a polynucleotide encoding a polypeptide from a
XX microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 30806; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
XX promoter functional in a plant cell, where the promoter is positioned to
XX provide for expression of a polynucleotide encoding a polypeptide from a
XX microbial source. The invention also relates to a transformed plant
XX comprising the recombinant DNA construct and a method of producing a
XX transformed plant having an improved property. The plant is a crop plant
XX such as maize or soybean. The method of producing a transformed plant
XX having an improved property comprises transforming a plant with the
XX recombinant DNA construct and growing the transformed plant, where the
XX polynucleotide or polypeptide is useful for improving plant properties.
XX The recombinant DNA construct is useful for producing plants with
XX improved plant properties, e.g. improved cold, heat or drought tolerance,
XX tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
XX increased resistance to plant disease, better growth rate by modification
XX of the cell cycle pathway with plant growth regulators, increased rate of
XX homologous recombination, modified seed oil or protein yield and/or
XX content, improved yield by modification of carbohydrate, nitrogen or
XX phosphorus use and/or uptake, by modification of photosynthesis or by
XX providing improved plant growth and development under at least one stress
XX condition, improved lignin production or improved galactomannan
XX production. This sequence represents a bacterial polynucleotide used in
XX the scope of the invention. Note: The sequence data for this patent did
XX not form part of the printed specification but was obtained in electronic
XX format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX SQ Sequence 780 BP; 125 A; 238 C; 264 G; 153 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 399 Length: 780
Score: 41.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 77.36% Indels: 0
DB: 13 Gaps: 0

US-10-029-756-6 (1-8) x ADS55132 (1-780)

QY 1 TrpIleGlyHisAspAlaGlyHis 8
Db 691 TGGCGAGGTCAGACATCGGCCAC 658

RESULT 87
AAF82258
ID AAF82258 standard; DNA; 816 BP.
XX
XX AAF82258;
XX
XX 21-JUN-2001 (first entry)
XX
XX Bacillus subtilis IFO 3336 DNA sequence.
XX
XX Bacterial; poly-gamma-L-glutamic acid; L-PGA;
XX poly-gamma-D,L-glutamic acid; PGA; glutamate racemase; ds.
XX
XX Bacillus subtilis.
XX
XX Key Location/Qualifiers
XX CDS 1..816
XX /*tag= a
XX /transl_except= (pos:1..3,aa:Met)
XX
XX JP2001017182-A.
PT
```

```
XX 23-JAN-2001.
XX
XX 09-JUL-1999; 99JP-00196335.
XX
XX 09-JUL-1999; 99JP-00196335.
XX (NAGS ) NAGASE SANGYO KK.
XX
XX WPI; 2001-285408/30.
XX P-PSDB; AAB74027.
XX
XX New nucleic acid encoding a glutamate racemase enzyme useful for the
XX preparation of poly-gamma-glutamic acid.
XX
XX Disclosure; page 15-16; 17pp; Japanese.
XX
XX The present sequence is one of four open reading frames of a region of
XX DNA from Bacillus subtilis that encodes an enzyme which is useful in the
XX production of poly-gamma-L-glutamic acid (L-PGA) or poly-gamma-D,L-
XX glutamic acid (PGA). A plasmid comprising DNA encoding the enzyme may be
XX used to transform Escherichia coli. The transformants express the enzyme
XX and PGA is produced in the culture
XX
XX SQ Sequence 816 BP; 240 A; 180 C; 203 G; 193 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 419 Length: 816
Score: 41.00 Matches: 5
Percent Similarity: 75.00% Conservative: 1
Best Local Similarity: 62.50% Mismatches: 2
Query Match: 77.36% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x AAF82258 (1-816)

QY 1 TrpIleGlyHisAspAlaGlyHis 8
Db 754 TGGTTGGCCATGAAGTCGGGCAT 777

RESULT 88
ADE81200
ID ADE81200 standard; DNA; 921 BP.
XX
XX ADE81200;
XX
XX 29-JAN-2004 (first entry)
XX
XX Orf14 coding sequence, SEQ ID 28.
XX
XX ML-236B; HMG-CoA reducing enzyme; ds; Orf14.
XX
XX Penicillium citrinum.
XX
XX Key Location/Qualifiers
XX CDS 1..921
XX /*tag= a
XX /product= "Orf14"
XX
XX JP2003116567-A.
XX
XX 22-APR-2003.
XX
XX 15-OCT-2001; 2001JP-00316578.
XX
XX 15-OCT-2001; 2001JP-00316578.
XX (SANYO ) SANKYO CO LTD.
XX
XX WPI; 2003-817677/77.
XX P-PSDB; ADE81201.
XX
XX Novel DNA associated with synthesis of ML-236B, useful for improving ML-
```



```

PT 236B production in ML-236B producing microbe.
XX
PS Example 8; SEQ ID NO 28; 142pp; Japanese.
XX
CC The present invention relates to a DNA sequence (I, ADE81173), which is
CC associated with ML-236B synthesis. (I) is useful for improving ML-236B
CC production in a HMG-CoA reducing-enzyme-inhibitor ML-236B producing
CC microbe. The present sequence was used to illustrate the invention.
XX
SQ Sequence 921 BP; 232 A; 237 C; 246 G; 206 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 478 Length: 921
Score: 41.00 Matches: 6
Percent Similarity: 75.00% Conservatives: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 77.36% Indels: 0
DB: 10 Gaps: 0

US-10-029-756-6 (1-8) x ADE81200 (1-921)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 744 TGGCAAGGACACGACAGAGTGCAT 767

RESULT 89
AAFW1706
ID AAF71706 standard; DNA; 955 BP.
XX
AC AAF71706;
XX
DT 30-APR-2001 (first entry)
XX
DE Corynebacterium glutamicum SMP protein nucleotide sequence SEQ ID NO:693.
XX
KW Corynebacterium glutamicum; carbon metabolism and energy production;
KW SMP protein; sugar metabolism and oxidative phosphorylation protein;
KW fine chemical production; organic acid; proteinogenic amino acid;
KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleoside;
KW nucleotide; lipid; saturated fatty acid; unsaturated fatty acid; diol;
KW carbohydrate; aromatic compound; vitamin; cofactor; polypeptide; enzyme;
KW diagnosis; Corynebacterium diphtheriae; evolutionary study; ds.
XX
OS Corynebacterium glutamicum.
XX
FN WO200100844-A2.
XX
PD 04-JAN-2001.
XX
PF 23-JUN-2000; 2000WO-IB000943.
XX
PR 25-JUN-1999; 99US-0141031P.
PR 08-JUL-1999; 99DE-01031412.
PR 08-JUL-1999; 99DE-01031413.
PR 08-JUL-1999; 99DE-01031419.
PR 08-JUL-1999; 99DE-01031420.
PR 08-JUL-1999; 99DE-01031424.
PR 08-JUL-1999; 99DE-01031428.
PR 08-JUL-1999; 99DE-01031431.
PR 08-JUL-1999; 99DE-01031433.
PR 08-JUL-1999; 99DE-01031434.
PR 08-JUL-1999; 99DE-01031510.
PR 08-JUL-1999; 99DE-01031562.
PR 08-JUL-1999; 99DE-01031634.
PR 09-JUL-1999; 99DE-01032180.
PR 09-JUL-1999; 99DE-01032227.
PR 09-JUL-1999; 99DE-01032230.
PR 09-JUL-1999; 99US-0143208P.
PR 14-JUL-1999; 99DE-01032924.
PR 14-JUL-1999; 99DE-01032973.
PR 14-JUL-1999; 99DE-01033005.
PR 27-AUG-1999; 99DE-01040765.
PR 31-AUG-1999; 99US-0151572P.

105 03-SEP-1999; 99DE-01042076.
106 03-SEP-1999; 99DE-01042079.
107 03-SEP-1999; 99DE-01042086.
108 03-SEP-1999; 99DE-01042087.
109 03-SEP-1999; 99DE-01042088.
110 03-SEP-1999; 99DE-01042095.
111 03-SEP-1999; 99DE-01042123.
112 03-SEP-1999; 99DE-01042125.
XX
FA (BADI ) BASF AG.
XX
PI Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G;
XX
WPI; 2001-061975/07.
XX
P-PSDB; AAB79589.
XX
New isolated Corynebacterium glutamicum nucleic acid encoding a sugar
metabolism and oxidative phosphorylation protein for production or
modulation of production of fine chemicals e.g. amino acids,
carbohydrates or enzymes.
XX
Claim 3; Page 1128-1129; 1246pp; English.
XX
AAFW1360 to AAF71750 encode the Corynebacterium glutamicum sugar
metabolism and oxidative phosphorylation (SMP) proteins given in AAB79243
to AAB 79633 which are involved in carbon metabolism and energy
production. The C. glutamicum SMP gene can be used in vectors (II) for
expression in host cells and production or modulation of production of
fine chemicals, such as, an organic acid, a proteinogenic or
nonproteinogenic amino acid (preferred), a purine or pyrimidine base, a
nucleoside, a nucleotide, a lipid, a saturated or unsaturated fatty acid,
a diol, a carbohydrate, an aromatic compound, a vitamin, a cofactor, a
polypeptide, or an enzyme. The presence of (I) or SMP proteins (III)
encoded by them are used for diagnosing the presence or activity of
Corynebacterium diphtheriae in a subject. (I), (II), (III) or host cells
containing them are used to map genomes of organisms related to C.
glutamicum, identify and localise C. glutamicum sequences of interest, in
evolutionary studies, in determining SMP protein regions required for
function, in modulating SMP protein activity, in modulating the
metabolism of sugars, and in modulating high-energy molecule production
in a cell (i.e. ATP, NADPH)
XX
SQ Sequence 955 BP; 151 A; 272 C; 256 G; 276 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 497 Length: 955
Score: 41.00 Matches: 6
Percent Similarity: 75.00% Conservatives: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 77.36% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x AAF71706 (1-955)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 613 TGGATTGGCCATGCTGCTGGGCAT 636

RESULT 90
ADA69970/c
ID ADA69970 standard; DNA; 1143 BP.
XX
AC ADA69970;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice gene, SEQ ID 3293.
XX
KW Plant; bacterial infection; fungal infection; viral infection; rice;
KW gene; ds.
XX
OS Oryza sativa.
XX

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PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249272P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 06-DEC-2000; 2000US-0251719P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0251990P.
PR 05-JAN-2001; 2001US-0259678P.
PR (HUMA-) HUMAN GENOME SCI INC.
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and metastasis.
XX Disclosure; SEQ ID NO 40858; 3071pp + Sequence Listing; English.
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)

CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 1161 BP; 234 A; 330 C; 268 G; 328 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.: 614 Length: 1161
Score: 41.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 77.36% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x AAK86046 (1-1161)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
| | | | | | | | | | | | | | | | | | | | | |
Db 816 TGGATTGGACATCGAGGAGGTCC 793

RESULT 92
AAZ96369
ID AAZ96369 standard; DNA; 1311 BP.
XX
AC AAZ96369;
XX
DT 10-APR-2000 (first entry)
XX
DE S. pneumoniae derived DNA from ORF #197.
XX
KW Treatment; prevention; disease; diagnosis; gene therapy; screening;
KW bacterial; antimicrobial; antibiotic; pathogenesis; infection; ss.
XX
OS Streptococcus pneumoniae.
XX
PN WO9806734-A1.
XX
PD 19-FEB-1998.
XX
XX 15-AUG-1997; 97WO-US014436.
PF
XX 16-AUG-1996; 96US-0024022P.
PR
XX (SMIK) SMITHKLINE BEECHAM CORP.
PA
XX Black MT, Hodgson JE, Knowles DJC, Lonetto MA, Nicholas RO;
PI Stodola RK;
XX
XX WPI; 1998-159452/14.
DR P-PSDB; AAY86038.
XX
XX Streptococcus pneumoniae proteins and related DNA - useful for screening
PT compounds for antibacterial activity.
XX
XX Claim 4; Page 228-229; 640pp; English.
PS
XX This invention describes novel isolated Streptococcus pneumoniae
XX polynucleotides (see AAZ96173-296494) and their encoded proteins (see
CC AAY8792-Y86182). The DNA, vectors and host cells described in the method
XX of the invention are useful for the recombinant expression of the

CC polypeptides. The polypeptides are useful for treatment or prevention of
CC disease, or diagnosis of disease related to expression or activity of
CC such a polypeptide. They can also be used to screen for compounds which
CC interact with and inhibit or activate such a polypeptide. The
CC polypeptides (or DNA encoding them, via gene therapy) are also useful for
CC inducing an immunological response in a mammal. The antagonists are
CC useful to inhibit such bacterial polypeptides. The polypeptides are
CC particularly useful to identify antimicrobial compounds and antibiotics.
CC They are also useful to determine their role in pathogenesis of
CC infection, dysfunction and disease
XX
SQ Sequence 1311 BP; 363 A; 249 C; 296 G; 403 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 700 Length: 1311
Score: 41.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 77.36% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-6 (1-8) x AAZ96369 (1-1311)

Qy 1 TrrileGlyHisAspAlaGlyHis 8
Db 365 TGGATTGGCGATGATGATATCAT 388

RESULT 93

ABZ12753
ID ABZ12753 standard; DNA; 1350 BP.

XX AC ABZ12753;

XX DT 21-JAN-2003 (first entry)

XX DE Arabidopsis thaliana stress regulated gene SEQ ID NO 558.

XX KW Arabidopsis thaliana; plant; gene; stress; transgenic; db.

XX OS Arabidopsis thaliana.

XX PN W0200216655-A2.

XX PD 28-FEB-2002.

XX PF 24-AUG-2001; 2001WO-US026685.

XX PR 24-AUG-2000; 2000US-0227866P.

XX PR 26-JAN-2001; 2001US-0264647P.

XX PR 22-JUN-2001; 2001US-0300111P.

XX (SCRI) SCRIPPS RES INST.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX PI Harper JF, Kreps J, Wang X, Zhu T;

XX WPI; 2002-304127/34.

XX Identifying a stress condition to which a plant cell has been exposed and
XX producing plants with increased tolerance to these abiotic stresses.

XX Claim 6; SEQ ID NO 558; 577pp + Sequence Listing; English.

XX The invention relates to identifying a stress condition to which a plant
XX cell has been exposed, comprising: (a) contacting nucleic acid
XX representative of expressed polynucleotides in the plant cell with an
XX array or probes representative of the plant cell genome; and (b)
XX detecting a profile of expressed polynucleotides in the plant cell
XX characteristic of a stress response. The method is useful in the
XX production of transgenic plants, cells and seeds and in producing plants
XX with increased tolerance to abiotic stress. The present sequence is that
XX of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
XX in methods of the invention. Note: The sequence data for this patent is

CC not represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office
XX
SQ Sequence 1350 BP; 325 A; 359 C; 274 G; 392 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 722 Length: 1350
Score: 41.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 75.00% Mismatches: 0
Query Match: 77.36% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-6 (1-8) x ABZ12753 (1-1350)

Qy 1 TrrileGlyHisAspAlaGlyHis 8

Db 469 TACATAGGTACGATTCGTGTCAT 492

RESULT 94

ABA01201/c

ID ABA01201 standard; DNA; 1461 BP.

XX AC ABA01201;

XX DT 25-JAN-2002 (first entry)

XX DE Aldehyde-dehydrogenase coding sequence.

XX KW Aldehyde-dehydrogenase; enzyme; phenanthrene; anthracene; ds.

XX OS Nocardioides sp. KP7.

XX FH Key Location/Qualifiers

XX CDS 1..1461

XX FT /*tag= a

XX FT /product= "Aldehyde-dehydrogenase"

XX PN JP2001245662-A.

XX PD 11-SEP-2001.

XX PF 03-MAR-2000; 2000JP-00059523.

XX PR 03-MAR-2000; 2000JP-00059523.

XX (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.

XX WPI; 2002-002935/01.

XX DR P-ESDB; AAMS2347.

XX Genes and proteins involved in the upstream of the pathway of degradation
XX of a polycyclic aromatic compound.

XX Example 4; Page 18-20; 47pp; Japanese.

XX The present sequence is the coding sequence for aldehyde-dehydrogenase.
XX The enzyme is useful as a reagent for converting the metabolite
XX intermediates of polycyclic aromatic compounds such as phenanthrene and
XX anthracene

XX SQ Sequence 1461 BP; 244 A; 505 C; 505 G; 207 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 787 Length: 1461
Score: 41.00 Matches: 6
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 85.71% Mismatches: 0
Query Match: 77.36% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-6 (1-8) x ABA01201 (1-1461)

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Alignment Scores:
Pred. No.: 897
Score: 41.00
Percent Similarity: 100.00%
Best Local Similarity: 75.00%
Query Match: 77.36%
DB: 3
Length: 1650
Matches: 6
Conservative: 2
Mismatches: 0
Indels: 0
Gaps: 0

US-10-029-756-6 (1-8) x AAC51462 (1-1650)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
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Db 675 TACATAGTCACGATTCTGGTCAT 698
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AAC33846
ID AAC33846 standard; DNA; 1650 BP.
XX
AC AAC33846;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 4526.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
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| Pred. No.: | 897 | Length: | 1650 |
| Score: | 41.00 | Matches: | 6 |
| Percent Similarity: | 100.00% | Conservative: | 2 |
| Best Local Similarity: | 75.00% | Mismatches: | 0 |
| Query Match: | 77.36% | Indels: | 0 |
| DB: | 3 | Gaps: | 0 |

US-10-029-756-6 (1-8) x AAC33846 (1-1650)

| | | | |
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| Qy | 1 | TrpIleClyHisAspAlaGlyHis | 8 |
| Db | 673 | TACATAGGTCACGATTCTGGTCAT | 696 |

RESULT 97
AAZ44833
ID AAZ44833 standard; DNA; 1678 BP.
XX AC AAZ44833;
XX DT 27-APR-2000 (first entry)
XX DE A. thaliana sld1 DNA.
XX KW Spingolipid desaturase; sld1; sphingobase; ceramide; capnoid;
KW transgenic plant; crop plant; delta-8-unsaturated long-chain base;
KW tolerance; resistance; soil salinity; ion stress; toxicity; drought;
KW cold; frost; phytopathogenic microorganism; flowering time; cosmetic;
KW pharmaceutical; food; chemical raw material; ds.
XX OS Arabidopsis thaliana.
XX FH Key
FT CDS Location/Qualifiers
FT 172..1521
FT /*tag= a
FT /product= "sphingolipid desaturase"
XX DE19828850-A1.
XX PD 30-DEC-1999.
XX PF 27-JUN-1998; 98DE-01028850.
XX PR 27-JUN-1998; 98DE-01028850.
XX PA (GVSE-) GVS GES ERWERB & VERW LANDWIRTSCHAFTLICH.
XX PI Heinz E, Zaehrer U, Schmidt H, Sperling P;
XX WPI; 2000-127549/12.
XX DR P-PSDB; AAY51334.
XX PT New sphingolipid desaturase that selectively introduces double bond into
sphingolipids and capnoids.
XX PS Claim 11; Fig 3; 62pp; German.
XX CC This invention describes a novel sphingolipid desaturase that selectively
introduces a double bond into the sphingobase of the ceramide residue of
sphingolipids and capnoids. A DNA sequence encoding the sphingolipid
desaturase, or a vector containing the DNA sequence, can be used to
produce transgenic plants, especially crop plants, with an increased or
decreased delta-8-unsaturated long-chain base content or an altered delta
-8-unsaturated long-chain base cis/trans ratio, especially to compensate
for a delta-8-unsaturated long-chain base deficiency, to exclude
production of delta-8-unsaturated bases, to increase tolerance or
resistance to soil salinity, ion stress or toxicity, drought, wet
conditions, cold or frost and/or phytopathogenic microorganisms, or to
alter size growth and flowering time. Cells, transgenic organisms or
plants containing the DNA sequence can be used to produce sphingolipids
and capnoids with unsaturated sphingobases. The sphingolipids or capnoids
can be used in cosmetics, pharmaceuticals and foods and as chemical raw
materials. This sequence encodes the Arabidopsis thaliana sphingolipid
desaturase sld1 protein described in the method of the invention
XX SQ Sequence 1678 BP; 416 A; 408 C; 339 G; 515 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 914 Length: 1678
Score: 41.00 Matches: 6
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 75.00% Mismatches: 0
Query Match: 77.36% Indels: 0
DB: 3 Gaps: 0
US-10-029-756-6 (1-8) x AAZ44833 (1-1678)

QY 1 TrpIleGlyHisAspAlaGlyHis 8
Db 640 TACATAGTGCACGATTCGTGCAT 663
RESULT 98
AAK86044/c
ID AAK86044 standard; DNA; 1756 BP.
XX AC AAK86044;
XX DT 07-NOV-2001 (first entry)
XX DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40856.
XX KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX OS Homo sapiens.
XX FN WO200157182-A2.
XX PD 09-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US001354.
XX PR 31-JAN-2000; 2000US-0179065P.
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PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.

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PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/haematopoietic antigen polypeptides,
XX useful for preventing, diagnosing and/or treating cancers and metastasis.
XX Disclosure; SEQ ID NO 40856; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
XX amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
XX activity, and can be used in gene therapy and vaccine production. (I)
XX proteins and polynucleotides may be used in the prevention, diagnosis and
XX treatment of diseases associated with inappropriate (I) expression. For
XX example, they may be used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of (I) by expressing inactive proteins or to
XX supplement the patient's own production of (I). Additionally, (I)
XX polynucleotides may be used to produce the secreted (I), by inserting the
XX nucleic acids into a host cell and culturing the cell to express the
XX protein. (I) proteins and polynucleotides may be used to prevent,
XX diagnose and treat immune/haematopoietic-related diseases, especially
XX cancers and cancer metastases of haematopoietic-derived cells. AAK64703
XX to AAK87694 represent human immune/haematopoietic antigen genomic
XX sequences from the present invention. AAK54942 to AAK54950 and AAK82169
XX represent sequences used in the exemplification of the present invention
XX
XX SQ Sequence 1756 BP; 368 A; 460 C; 418 G; 510 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 960 Length: 1756
Score: 41.00 Matches: 6
Percent Similarity: 75.00% Conservative: 0
Best Local Similarity: 75.00% Mismatches: 2
Query Match: 77.36% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-6 (1-8) x AAK86044 (1-1756)

Qy 1 TrpIleGlyHisAspAlaGlyHis 8
Db 844 TGGATTGGACATCGAGGAGGTCC 821

RESULT 99
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XX 07-NOV-2001 (first entry)
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XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40857.
XX
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.
KW
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| XX PD | 09-AUG-2001. | PR 27-SEP-2000; 2000US-0235836P. |
| XX PF | 17-JAN-2001; 2001WO-US001354. | PR 29-SEP-2000; 2000US-0236327P. |
| XX PR | 31-JAN-2000; 2000US-0179065P. | PR 29-SEP-2000; 2000US-0236367P. |
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| PR | 25-SEP-2000; 2000US-0234998P. | |

XX

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 8, 2005, 09:39:06 ; Search time 1030.26 Seconds
(without alignments)
235.159 Million cell updates/sec

Title: US-10-029-756-12

Perfect score: 34
Sequence: 1 HNAHH 5

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Command line parameters:

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-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| C 96 | 34 | 100.0 | 993 | 6 | BD235645 | BD235645 GRIP and | C 169 | 34 | 100.0 | 1554 | 6 | AX618808 | AX618808 Sequence |
| C 97 | 34 | 100.0 | 993 | 9 | AF236120 | AF236120 Homo sapi | C 170 | 34 | 100.0 | 1558 | 9 | AY069959 | AY069959 Homo sapi |
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| C 99 | 34 | 100.0 | 1026 | 6 | AX925633 | AX925633 Sequence | C 172 | 34 | 100.0 | 1572 | 6 | BD179626 | BD179626 Highly th |
| C 100 | 34 | 100.0 | 1027 | 5 | AF034693 | AF034693 Coturnix | C 173 | 34 | 100.0 | 1574 | 6 | AX402400 | AX402400 Sequence |
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| C 108 | 34 | 100.0 | 1161 | 8 | AF308454 | AF308454 Medicago | C 181 | 34 | 100.0 | 1611 | 9 | BC026002 | BC026002 Homo sapi |
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| C 110 | 34 | 100.0 | 1206 | 6 | BD061976 | BD061976 Antigenic | C 183 | 34 | 100.0 | 1614 | 1 | ECOHPA2 | ECOHPA2 |
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| C 112 | 34 | 100.0 | 1209 | 6 | CQ734784 | CQ734784 Sequence | C 185 | 34 | 100.0 | 1618 | 8 | AF234127 | AF234127 Primula v |
| C 113 | 34 | 100.0 | 1214 | 14 | AY208085 | AY208085 Human cox | C 186 | 34 | 100.0 | 1633 | 8 | AF001394 | AF001394 Arabidops |
| C 114 | 34 | 100.0 | 1236 | 6 | AF110794 | AF110794 Volvox ca | C 187 | 34 | 100.0 | 1637 | 3 | ECGTUB2 | ECGTUB2 |
| C 115 | 34 | 100.0 | 1241 | 6 | CQ730418 | CQ730418 Sequence | C 188 | 34 | 100.0 | 1652 | 6 | AR217930 | AR217930 Sequence |
| C 116 | 34 | 100.0 | 1255 | 9 | AF102694 | AF102694 Homo sapi | C 189 | 34 | 100.0 | 1661 | 6 | AR217930 | AR217930 Sequence |
| C 117 | 34 | 100.0 | 1258 | 9 | AF129476 | AF129476 Homo sapi | C 190 | 34 | 100.0 | 1661 | 6 | BD057812 | BD057812 Growth fa |
| C 118 | 34 | 100.0 | 1266 | 6 | CQ831420 | CQ831420 Sequence | C 191 | 34 | 100.0 | 1665 | 6 | AX0402408 | AX0402408 Sequence |
| C 119 | 34 | 100.0 | 1275 | 6 | BD242779 | BD242779 Desaturas | C 192 | 34 | 100.0 | 1678 | 6 | AX007241 | AX007241 Sequence |
| C 120 | 34 | 100.0 | 1275 | 8 | AF139720 | AF139720 Euglena g | C 193 | 34 | 100.0 | 1681 | 8 | AY234124 | AY234124 Primula f |
| C 121 | 34 | 100.0 | 1293 | 6 | AR450683 | AR450683 Sequence | C 194 | 34 | 100.0 | 1684 | 6 | AR076814 | AR076814 Sequence |
| C 122 | 34 | 100.0 | 1298 | 6 | A04377 | A04377 E.coli phoE | C 195 | 34 | 100.0 | 1684 | 6 | AR084177 | AR084177 Sequence |
| C 123 | 34 | 100.0 | 1303 | 9 | HS4011736 | AJ011736 Homo sapi | C 196 | 34 | 100.0 | 1684 | 6 | BD062571 | BD062571 A sunflow |
| C 124 | 34 | 100.0 | 1311 | 9 | AF121002 | AF121002 Homo sapi | C 197 | 34 | 100.0 | 1684 | 6 | BD070919 | BD070919 An oleosi |
| C 125 | 34 | 100.0 | 1322 | 9 | AF090456 | AF090456 Homo sapi | C 198 | 34 | 100.0 | 1685 | 6 | AR020904 | AR020904 Sequence |
| C 126 | 34 | 100.0 | 1323 | 6 | AR545311 | AR545311 Sequence | C 199 | 34 | 100.0 | 1685 | 6 | I38430 | I38430 Sequence |
| C 127 | 34 | 100.0 | 1328 | 3 | DROSH2P | M95199 Drosophila | C 200 | 34 | 100.0 | 1685 | 6 | AR200408 | AR200408 Sequence |
| C 128 | 34 | 100.0 | 1340 | 6 | AX653094 | AX653094 Sequence | C 201 | 34 | 100.0 | 1685 | 6 | AR455421 | AR455421 Sequence |
| C 129 | 34 | 100.0 | 1341 | 8 | AF406816 | AF406816 Aquilegia | C 202 | 34 | 100.0 | 1685 | 8 | AF007561 | AF007561 Borago of |
| C 130 | 34 | 100.0 | 1341 | 8 | AF536525 | AF536525 Anemone l | C 203 | 34 | 100.0 | 1687 | 6 | AX951561 | AX951561 Sequence |
| C 131 | 34 | 100.0 | 1347 | 8 | AY131238 | AY131238 Argania s | C 204 | 34 | 100.0 | 1689 | 8 | BOU79010 | BOU79010 Borago offi |
| C 132 | 34 | 100.0 | 1350 | 6 | AX505863 | AX505863 Sequence | C 205 | 34 | 100.0 | 1689 | 8 | ATU19537 | ATU19537 Arabidopsis |
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| C 134 | 34 | 100.0 | 1362 | 6 | AX824971 | AX824971 Sequence | C 207 | 34 | 100.0 | 1702 | 6 | AR455422 | AR455422 Sequence |
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| C 136 | 34 | 100.0 | 1363 | 6 | CQ497201 | CQ497201 Sequence | C 209 | 34 | 100.0 | 1704 | 8 | AF428420 | AF428420 Arabidops |
| C 137 | 34 | 100.0 | 1385 | 8 | AY234126 | AY234126 Primula v | C 210 | 34 | 100.0 | 1705 | 8 | AF428420 | AF428420 Arabidops |
| C 138 | 34 | 100.0 | 1410 | 8 | AY234125 | AY234125 Primula f | C 211 | 34 | 100.0 | 1708 | 8 | AK064680 | AK064680 Oryza sat |
| C 139 | 34 | 100.0 | 1419 | 6 | CQ608955 | CQ608955 Sequence | C 212 | 34 | 100.0 | 1715 | 6 | AX402398 | AX402398 Sequence |
| C 140 | 34 | 100.0 | 1419 | 6 | AX058721 | AX058721 Sequence | C 213 | 34 | 100.0 | 1716 | 6 | AX402392 | AX402392 Sequence |
| C 141 | 34 | 100.0 | 1420 | 6 | CQ600930 | CQ600930 Sequence | C 214 | 34 | 100.0 | 1716 | 10 | BC050752 | BC050752 Mus muscu |
| C 142 | 34 | 100.0 | 1421 | 1 | ECOGADB | M84024 E. coli glu | C 215 | 34 | 100.0 | 1727 | 1 | HHISH26 | HHISH26 |
| C 143 | 34 | 100.0 | 1421 | 1 | ECOGADB | M84025 E. coli glu | C 216 | 34 | 100.0 | 1737 | 8 | AX617772 | AX617772 Sequence |
| C 144 | 34 | 100.0 | 1425 | 6 | AR451014 | AR451014 Sequence | C 217 | 34 | 100.0 | 1743 | 8 | BT000442 | BT000442 Arabidops |
| C 145 | 34 | 100.0 | 1428 | 9 | BT007152 | BT007152 Homo sapi | C 218 | 34 | 100.0 | 1748 | 8 | AK103193 | AK103193 Oryza sat |
| C 146 | 34 | 100.0 | 1428 | 9 | CR457409 | CR457409 Homo sapi | C 219 | 34 | 100.0 | 1757 | 6 | AX402399 | AX402399 Sequence |
| C 147 | 34 | 100.0 | 1428 | 12 | BT008195 | BT008195 Synthetic | C 220 | 34 | 100.0 | 1757 | 6 | AX402405 | AX402405 Sequence |
| C 148 | 34 | 100.0 | 1434 | 9 | AF208540 | AF208540 Homo sapi | C 221 | 34 | 100.0 | 1758 | 6 | AX402390 | AX402390 Sequence |
| C 149 | 34 | 100.0 | 1439 | 3 | ECGAMTUB2 | Y09551 E. crassus m | C 222 | 34 | 100.0 | 1765 | 6 | AX402401 | AX402401 Sequence |
| C 150 | 34 | 100.0 | 1445 | 3 | ECGAMTUB2 | Y09551 E. crassus m | C 223 | 34 | 100.0 | 1766 | 6 | AX402389 | AX402389 Sequence |
| C 151 | 34 | 100.0 | 1445 | 3 | ECGAMTUB2 | Y09551 E. crassus m | C 224 | 34 | 100.0 | 1766 | 6 | AX402394 | AX402394 Sequence |

| | | | | | | | | | | | | | |
|-------|----|-------|------|----|----------|-----------|-------|----|-------|------|----|-----------|--------------------|
| 224 | 34 | 100.0 | 1767 | 6 | AX402393 | Sequence | 297 | 34 | 100.0 | 2000 | 6 | AX831670 | Sequence |
| 225 | 34 | 100.0 | 1767 | 6 | AX402402 | Sequence | 298 | 34 | 100.0 | 2000 | 6 | AX831836 | Sequence |
| 226 | 34 | 100.0 | 1767 | 6 | AX402403 | Sequence | 299 | 34 | 100.0 | 2000 | 6 | AX832184 | Sequence |
| 227 | 34 | 100.0 | 1767 | 6 | AX402404 | Sequence | 300 | 34 | 100.0 | 2000 | 6 | AX832320 | Sequence |
| 228 | 34 | 100.0 | 1767 | 6 | AX402405 | Sequence | 301 | 34 | 100.0 | 2000 | 6 | AX832324 | Sequence |
| 229 | 34 | 100.0 | 1767 | 6 | AX402409 | Sequence | 302 | 34 | 100.0 | 2000 | 6 | AX832452 | Sequence |
| c 230 | 34 | 100.0 | 1770 | 6 | AX098422 | Sequence | c 303 | 34 | 100.0 | 2029 | 3 | AX116692 | Ciona int |
| c 231 | 34 | 100.0 | 1800 | 6 | AX389150 | Sequence | c 304 | 34 | 100.0 | 2060 | 6 | CQ593385 | CQ593385 |
| c 232 | 34 | 100.0 | 1825 | 10 | BC019606 | Mus muscu | c 305 | 34 | 100.0 | 2065 | 3 | AY058347 | AY058347 Drosophil |
| c 233 | 34 | 100.0 | 1867 | 3 | AF045786 | Drosophil | c 306 | 34 | 100.0 | 2083 | 11 | BV177634 | BV177634 sqm95874 |
| c 234 | 34 | 100.0 | 1869 | 8 | AF133728 | Borago of | c 307 | 34 | 100.0 | 2110 | 8 | AF428316 | AF428316 Arabidops |
| c 235 | 34 | 100.0 | 1875 | 6 | AX505999 | Sequence | c 308 | 34 | 100.0 | 2111 | 9 | BC008481 | BC008481 Homo sapi |
| c 236 | 34 | 100.0 | 1875 | 6 | AX651697 | Sequence | c 309 | 34 | 100.0 | 2118 | 3 | AX113085 | AX113085 Ciona int |
| c 237 | 34 | 100.0 | 1879 | 10 | BC005803 | Mus muscu | c 310 | 34 | 100.0 | 2122 | 8 | AY098893 | AY098893 Citrus hy |
| c 238 | 34 | 100.0 | 1903 | 10 | BC057937 | Mus muscu | c 311 | 34 | 100.0 | 2124 | 8 | AK099028 | AK099028 Oryza sat |
| c 239 | 34 | 100.0 | 1909 | 3 | AF139008 | Speleonec | c 312 | 34 | 100.0 | 2125 | 9 | BC019877 | BC019877 Homo sapi |
| c 240 | 34 | 100.0 | 1915 | 5 | BC075928 | Danio rer | c 313 | 34 | 100.0 | 2146 | 5 | AF034570 | AF034570 Gallus ga |
| c 241 | 34 | 100.0 | 1934 | 6 | CQ715584 | Sequence | c 314 | 34 | 100.0 | 2151 | 8 | AX045903 | AX045903 Arabidops |
| c 242 | 34 | 100.0 | 1958 | 6 | CQ052068 | Sequence | c 315 | 34 | 100.0 | 2170 | 6 | AX451705 | AX451705 Sequence |
| c 243 | 34 | 100.0 | 1958 | 6 | CQ067112 | Sequence | c 316 | 34 | 100.0 | 2176 | 14 | NPHF74X | NPHF74X |
| c 244 | 34 | 100.0 | 1958 | 6 | CQ171531 | Sequence | c 317 | 34 | 100.0 | 2181 | 8 | ATANTMR | ATANTMR |
| c 245 | 34 | 100.0 | 1958 | 6 | CQ216159 | Sequence | c 318 | 34 | 100.0 | 2191 | 3 | AF045790 | AF045790 Drosophil |
| c 246 | 34 | 100.0 | 1958 | 6 | CQ254724 | Sequence | c 319 | 34 | 100.0 | 2196 | 3 | AF045791 | AF045791 Drosophil |
| c 247 | 34 | 100.0 | 1958 | 6 | CQ328864 | Sequence | c 320 | 34 | 100.0 | 2197 | 3 | AF045788 | AF045788 Drosophil |
| c 248 | 34 | 100.0 | 1975 | 8 | AY155462 | Physcomit | c 321 | 34 | 100.0 | 2199 | 3 | AF045792 | AF045792 Drosophil |
| c 249 | 34 | 100.0 | 1980 | 1 | ECPHOE | ECPHOE | c 322 | 34 | 100.0 | 2202 | 3 | AF045793 | AF045793 Drosophil |
| c 250 | 34 | 100.0 | 1980 | 6 | BD157976 | Primer fo | c 323 | 34 | 100.0 | 2205 | 3 | AF045789 | AF045789 Drosophil |
| c 251 | 34 | 100.0 | 1985 | 6 | AX879700 | Sequence | c 324 | 34 | 100.0 | 2209 | 3 | AF045795 | AF045795 Drosophil |
| c 252 | 34 | 100.0 | 1985 | 9 | AK022735 | Homo sapi | c 325 | 34 | 100.0 | 2210 | 9 | AK096193 | AK096193 Homo sapi |
| c 253 | 34 | 100.0 | 2000 | 6 | AX509561 | Sequence | c 326 | 34 | 100.0 | 2212 | 9 | BC013963 | BC013963 Homo sapi |
| c 254 | 34 | 100.0 | 2000 | 6 | AX509847 | Sequence | c 327 | 34 | 100.0 | 2214 | 3 | AY044166 | AY044166 Drosophil |
| c 255 | 34 | 100.0 | 2000 | 6 | AX594424 | Sequence | c 328 | 34 | 100.0 | 2220 | 3 | AF045787 | AF045787 Drosophil |
| c 256 | 34 | 100.0 | 2000 | 6 | AX594700 | Sequence | c 329 | 34 | 100.0 | 2230 | 3 | AF045794 | AF045794 Drosophil |
| c 257 | 34 | 100.0 | 2000 | 6 | AX595136 | Sequence | c 330 | 34 | 100.0 | 2231 | 3 | AF045796 | AF045796 Drosophil |
| c 258 | 34 | 100.0 | 2000 | 6 | AX595184 | Sequence | c 331 | 34 | 100.0 | 2234 | 6 | CQ611507 | CQ611507 Sequence |
| c 259 | 34 | 100.0 | 2000 | 6 | AX595462 | Sequence | c 332 | 34 | 100.0 | 2285 | 3 | AY061538 | AY061538 Drosophil |
| c 260 | 34 | 100.0 | 2000 | 6 | AX595786 | Sequence | c 333 | 34 | 100.0 | 2288 | 5 | CR760497 | CR760497 Xenopus t |
| c 261 | 34 | 100.0 | 2000 | 6 | AX596038 | Sequence | c 334 | 34 | 100.0 | 2342 | 6 | AX833224 | AX833224 Sequence |
| c 262 | 34 | 100.0 | 2000 | 6 | AX596344 | Sequence | c 335 | 34 | 100.0 | 2342 | 9 | AK094797 | AK094797 Homo sapi |
| c 263 | 34 | 100.0 | 2000 | 6 | AX596348 | Sequence | c 336 | 34 | 100.0 | 2344 | 9 | AK098211 | AK098211 Homo sapi |
| c 264 | 34 | 100.0 | 2000 | 6 | AX596572 | Sequence | c 337 | 34 | 100.0 | 2358 | 5 | BC045402 | BC045402 Danio rer |
| c 265 | 34 | 100.0 | 2000 | 6 | AX596760 | Sequence | c 338 | 34 | 100.0 | 2361 | 14 | HSSWIEP | HSSWIEP |
| c 266 | 34 | 100.0 | 2000 | 6 | AX596862 | Sequence | c 339 | 34 | 100.0 | 2373 | 6 | AX528299 | AX528299 Sequence |
| c 267 | 34 | 100.0 | 2000 | 6 | AX596866 | Sequence | c 340 | 34 | 100.0 | 2384 | 3 | AY061234 | AY061234 Drosophil |
| c 268 | 34 | 100.0 | 2000 | 6 | AX596980 | Sequence | c 341 | 34 | 100.0 | 2417 | 8 | KLDNAMIG1 | 250017 K.lactis DN |
| c 269 | 34 | 100.0 | 2000 | 6 | AX596980 | Sequence | c 342 | 34 | 100.0 | 2422 | 6 | CQ595866 | CQ595866 Sequence |
| c 270 | 34 | 100.0 | 2000 | 6 | AX655607 | Sequence | c 343 | 34 | 100.0 | 2453 | 8 | AK065590 | AK065590 Oryza sat |
| c 271 | 34 | 100.0 | 2000 | 6 | AX656340 | Sequence | c 344 | 34 | 100.0 | 2528 | 10 | BC005472 | BC005472 Mus muscu |
| c 272 | 34 | 100.0 | 2000 | 6 | AX818546 | Sequence | c 345 | 34 | 100.0 | 2543 | 10 | BC005446 | BC005446 Mus muscu |
| c 273 | 34 | 100.0 | 2000 | 6 | AX819140 | Sequence | c 346 | 34 | 100.0 | 2550 | 3 | PLINTB | AX128889 Mus muscu |
| c 274 | 34 | 100.0 | 2000 | 6 | AX819196 | Sequence | c 347 | 34 | 100.0 | 2551 | 6 | AR380455 | AR380455 Sequence |
| c 275 | 34 | 100.0 | 2000 | 6 | AX819580 | Sequence | c 348 | 34 | 100.0 | 2591 | 6 | AX775123 | AX775123 Sequence |
| c 276 | 34 | 100.0 | 2000 | 6 | AX819946 | Sequence | c 349 | 34 | 100.0 | 2591 | 9 | HUMADCY | L12168 Homo sapien |
| c 277 | 34 | 100.0 | 2000 | 6 | AX819982 | Sequence | c 350 | 34 | 100.0 | 2614 | 6 | CQ800917 | CQ800917 Sequence |
| c 278 | 34 | 100.0 | 2000 | 6 | AX820296 | Sequence | c 351 | 34 | 100.0 | 2614 | 6 | AX779813 | AX779813 Sequence |
| c 279 | 34 | 100.0 | 2000 | 6 | AX820472 | Sequence | c 352 | 34 | 100.0 | 2664 | 6 | CQ583305 | CQ583305 Sequence |
| c 280 | 34 | 100.0 | 2000 | 6 | AX820636 | Sequence | c 353 | 34 | 100.0 | 2669 | 8 | SCU73805 | U73805 Saccharomyc |
| c 281 | 34 | 100.0 | 2000 | 6 | AX820640 | Sequence | c 354 | 34 | 100.0 | 2683 | 5 | BC076869 | BC076869 Xenopus l |
| c 282 | 34 | 100.0 | 2000 | 6 | AX820806 | Sequence | c 355 | 34 | 100.0 | 2683 | 5 | BC076869 | BC076869 Xenopus l |
| c 283 | 34 | 100.0 | 2000 | 6 | AX821154 | Sequence | c 356 | 34 | 100.0 | 2694 | 10 | AK172943 | AK172943 Mus muscu |
| c 284 | 34 | 100.0 | 2000 | 6 | AX821290 | Sequence | c 357 | 34 | 100.0 | 2724 | 6 | CQ654002 | CQ654002 Sequence |
| c 285 | 34 | 100.0 | 2000 | 6 | AX821294 | Sequence | c 358 | 34 | 100.0 | 2731 | 8 | AX110399 | AX110399 Oryza sat |
| c 286 | 34 | 100.0 | 2000 | 6 | AX821422 | Sequence | c 359 | 34 | 100.0 | 2781 | 6 | CQ646530 | CQ646530 Sequence |
| c 287 | 34 | 100.0 | 2000 | 6 | AX829576 | Sequence | c 360 | 34 | 100.0 | 2784 | 1 | AY050492 | AY050492 Streptoco |
| c 288 | 34 | 100.0 | 2000 | 6 | AX830170 | Sequence | c 361 | 34 | 100.0 | 2784 | 6 | AX608470 | AX608470 Sequence |
| c 289 | 34 | 100.0 | 2000 | 6 | AX830226 | Sequence | c 362 | 34 | 100.0 | 2786 | 3 | S57693 | S57693 fat body pr |
| c 290 | 34 | 100.0 | 2000 | 6 | AX830232 | Sequence | c 363 | 34 | 100.0 | 2800 | 8 | AF107116 | AF107116 Candida g |
| c 291 | 34 | 100.0 | 2000 | 6 | AX830610 | Sequence | c 364 | 34 | 100.0 | 2814 | 8 | AB126946 | AB126946 Colacium |
| c 292 | 34 | 100.0 | 2000 | 6 | AX830976 | Sequence | c 365 | 34 | 100.0 | 2818 | 10 | AF202994 | AF202994 Mus muscu |
| c 293 | 34 | 100.0 | 2000 | 6 | AX831012 | Sequence | c 366 | 34 | 100.0 | 2888 | 10 | MMU19860 | U19860 Mus muscu |
| c 294 | 34 | 100.0 | 2000 | 6 | AX831326 | Sequence | c 367 | 34 | 100.0 | 2970 | 6 | AR449553 | AR449553 Sequence |
| c 295 | 34 | 100.0 | 2000 | 6 | AX831502 | Sequence | c 368 | 34 | 100.0 | 3025 | 3 | BT015203 | BT015203 Drosophil |
| c 296 | 34 | 100.0 | 2000 | 6 | AX831666 | Sequence | c 369 | 34 | 100.0 | 3041 | 1 | ECPROAB | X00786 E. coli gen |

| | | | | | | | | | | | | | |
|-----|----|-------|------|----|------------|---------------------|-------|----|-------|------|----|-----------|--------------------|
| 370 | 34 | 100.0 | 3051 | 6 | CQ604893 | CQ604893 Sequence | 443 | 34 | 100.0 | 4328 | 6 | AR137192 | AR137192 Sequence |
| 371 | 34 | 100.0 | 3079 | 8 | AK100579 | AK100579 Oryza sat | 444 | 34 | 100.0 | 4328 | 6 | AR158346 | AR158346 Sequence |
| 372 | 34 | 100.0 | 3095 | 6 | BC030156 | BC030156 Homo sapi | 445 | 34 | 100.0 | 4328 | 6 | AR241208 | AR241208 Sequence |
| 373 | 34 | 100.0 | 3106 | 6 | CQ608461 | CQ608461 Sequence | 446 | 34 | 100.0 | 4328 | 6 | AR338179 | AR338179 Sequence |
| 374 | 34 | 100.0 | 3108 | 8 | SCYD1239C | SCYD1239C Sequence | 447 | 34 | 100.0 | 4328 | 6 | AR340481 | AR340481 Sequence |
| 375 | 34 | 100.0 | 3109 | 9 | BC007671 | BC007671 Homo sapi | c 448 | 34 | 100.0 | 4336 | 6 | AR354428 | AR354428 Sequence |
| 376 | 34 | 100.0 | 3162 | 9 | AB060844 | AB060844 Macaca fa | c 449 | 34 | 100.0 | 4336 | 6 | AR535984 | AR535984 Sequence |
| 377 | 34 | 100.0 | 3168 | 3 | THO278945 | THO278945 Trachiple | c 450 | 34 | 100.0 | 4346 | 5 | BC077819 | BC077819 Xenopus 1 |
| 378 | 34 | 100.0 | 3176 | 3 | DRONCX | L39835 Drosophila | c 451 | 34 | 100.0 | 4357 | 8 | AY072188 | AY072188 Arabidops |
| 379 | 34 | 100.0 | 3194 | 5 | AF134320 | AF134320 Drosophil | c 452 | 34 | 100.0 | 4380 | 6 | CQ721015 | CQ721015 Sequence |
| 380 | 34 | 100.0 | 3247 | 6 | CQ610127 | CQ610127 Sequence | c 453 | 34 | 100.0 | 4395 | 6 | CQ606464 | CQ606464 Sequence |
| 381 | 34 | 100.0 | 3258 | 14 | PVU09508 | U09508 Potato viru | c 454 | 34 | 100.0 | 4523 | 8 | AY346360 | AY346360 Rhizopus |
| 382 | 34 | 100.0 | 3269 | 6 | CQ608907 | CQ608907 Sequence | c 455 | 34 | 100.0 | 4546 | 6 | CQ584196 | CQ584196 Sequence |
| 383 | 34 | 100.0 | 3278 | 6 | CQ610625 | CQ610625 Sequence | c 456 | 34 | 100.0 | 4575 | 6 | AX801769 | AX801769 Sequence |
| 384 | 34 | 100.0 | 3291 | 6 | CQ804192 | CQ804192 Sequence | c 457 | 34 | 100.0 | 4622 | 6 | AX299128 | AX299128 Sequence |
| 385 | 34 | 100.0 | 3304 | 6 | CQ579476 | CQ579476 Sequence | c 458 | 34 | 100.0 | 4666 | 1 | ECOFOLBDA | ECOFOLBDA |
| 386 | 34 | 100.0 | 3304 | 6 | AR447355 | AR447355 Sequence | c 459 | 34 | 100.0 | 4755 | 6 | AX801767 | AX801767 Sequence |
| 387 | 34 | 100.0 | 3331 | 6 | CQ607811 | CQ607811 Sequence | c 460 | 34 | 100.0 | 4779 | 6 | AX809955 | AX809955 Sequence |
| 388 | 34 | 100.0 | 3391 | 1 | SAAJ3164 | AJ003164 Streptoco | c 461 | 34 | 100.0 | 4818 | 6 | A92668 | A92668 Sequence 4 |
| 389 | 34 | 100.0 | 3391 | 1 | TPALAS | X95571 T. ferrooxid | c 462 | 34 | 100.0 | 4818 | 6 | AR158348 | AR158348 Sequence |
| 390 | 34 | 100.0 | 3391 | 1 | AY429663 | AY429663 Streptoco | c 463 | 34 | 100.0 | 4818 | 6 | AR241210 | AR241210 Sequence |
| 391 | 34 | 100.0 | 3395 | 1 | SAG251493 | AJ251493 Streptoco | c 464 | 34 | 100.0 | 4828 | 6 | CQ608954 | CQ608954 Sequence |
| 392 | 34 | 100.0 | 3395 | 1 | SAG251494 | AJ251494 Streptoco | c 465 | 34 | 100.0 | 4912 | 6 | BD271227 | BD271227 Nucleic a |
| 393 | 34 | 100.0 | 3408 | 1 | SAG251495 | AJ251495 Streptoco | c 466 | 34 | 100.0 | 4912 | 6 | BD081935 | BD081935 Nucleic a |
| 394 | 34 | 100.0 | 3408 | 1 | SAG251496 | AJ251496 Streptoco | c 467 | 34 | 100.0 | 4928 | 6 | AR141727 | AR141727 Sequence |
| 395 | 34 | 100.0 | 3408 | 1 | SAG251497 | AJ251497 Streptoco | c 468 | 34 | 100.0 | 4928 | 6 | CQ870784 | CQ870784 Sequence |
| 396 | 34 | 100.0 | 3408 | 1 | SAG251498 | AJ251498 Streptoco | c 469 | 34 | 100.0 | 4928 | 6 | I49890 | I49890 Sequence 1 |
| 397 | 34 | 100.0 | 3409 | 1 | SAG251499 | AJ251499 Streptoco | c 470 | 34 | 100.0 | 4928 | 6 | AR212221 | AR212221 Sequence |
| 398 | 34 | 100.0 | 3419 | 5 | AB100021 | AB100021 Leionath | c 471 | 34 | 100.0 | 4949 | 8 | AF135863 | AF135863 Neurospor |
| 399 | 34 | 100.0 | 3438 | 6 | AX416597 | AX416597 Sequence | c 472 | 34 | 100.0 | 5089 | 6 | AX776820 | AX776820 Sequence |
| 400 | 34 | 100.0 | 3469 | 10 | AK129370 | AK129370 Mus muscu | c 473 | 34 | 100.0 | 5089 | 6 | AX776823 | AX776823 Sequence |
| 401 | 34 | 100.0 | 3483 | 6 | CQ585131 | CQ585131 Sequence | c 474 | 34 | 100.0 | 5107 | 6 | A92667 | A92667 Sequence 3 |
| 402 | 34 | 100.0 | 3514 | 6 | CQ849717 | CQ849717 Sequence | c 475 | 34 | 100.0 | 5107 | 6 | AR158347 | AR158347 Sequence |
| 403 | 34 | 100.0 | 3514 | 9 | AK126758 | AK126758 Homo sapi | c 476 | 34 | 100.0 | 5107 | 6 | CQ607805 | CQ607805 Sequence |
| 404 | 34 | 100.0 | 3539 | 9 | AK096417 | AK096417 Homo sapi | c 477 | 34 | 100.0 | 5107 | 6 | AR241209 | AR241209 Sequence |
| 405 | 34 | 100.0 | 3580 | 4 | CFU55029 | U55029 Canis fami | c 478 | 34 | 100.0 | 5108 | 6 | AR562804 | AR562804 Sequence |
| 406 | 34 | 100.0 | 3581 | 6 | CQ851210 | CQ851210 Sequence | c 479 | 34 | 100.0 | 5108 | 6 | AR562805 | AR562805 Sequence |
| 407 | 34 | 100.0 | 3581 | 9 | AK128436 | AK128436 Homo sapi | c 480 | 34 | 100.0 | 5108 | 6 | AX138932 | AX138932 Sequence |
| 408 | 34 | 100.0 | 3602 | 8 | AK110173 | AK110173 Oryza sat | c 481 | 34 | 100.0 | 5108 | 6 | AX138933 | AX138933 Sequence |
| 409 | 34 | 100.0 | 3701 | 6 | AX327334 | AX327334 Sequence | c 482 | 34 | 100.0 | 5108 | 6 | BD000697 | BD000697 Growth ho |
| 410 | 34 | 100.0 | 3726 | 10 | AY274810 | AY274810 Rattus no | c 483 | 34 | 100.0 | 5108 | 6 | BD000698 | BD000698 Growth ho |
| 411 | 34 | 100.0 | 3743 | 3 | AY118680 | AY118680 Drosophil | c 484 | 34 | 100.0 | 5111 | 6 | AR562808 | AR562808 Sequence |
| 412 | 34 | 100.0 | 3747 | 3 | BT011420 | BT011420 Drosophil | c 485 | 34 | 100.0 | 5111 | 6 | AX138936 | AX138936 Sequence |
| 413 | 34 | 100.0 | 3785 | 8 | AF411833 | AF411833 Arabidops | c 486 | 34 | 100.0 | 5111 | 6 | BD000701 | BD000701 Growth ho |
| 414 | 34 | 100.0 | 3797 | 6 | CQ591686 | CQ591686 Sequence | c 487 | 34 | 100.0 | 5128 | 6 | AX154497 | AX154497 Sequence |
| 415 | 34 | 100.0 | 3874 | 6 | CQ612372 | CQ612372 Sequence | c 488 | 34 | 100.0 | 5130 | 12 | AF286076 | AF286076 Expressio |
| 416 | 34 | 100.0 | 3875 | 9 | HSPGTER2G1 | AF134201 Homo sapi | c 489 | 34 | 100.0 | 5185 | 6 | AR562800 | AR562800 Sequence |
| 417 | 34 | 100.0 | 3879 | 1 | ECOMPP | X74278 E.coli ompf | c 490 | 34 | 100.0 | 5185 | 6 | AX138928 | AX138928 Sequence |
| 418 | 34 | 100.0 | 3884 | 6 | BD159728 | BD159728 Primer fo | c 491 | 34 | 100.0 | 5185 | 6 | BD000693 | BD000693 Growth ho |
| 419 | 34 | 100.0 | 3884 | 6 | AX882444 | AX882444 Sequence | c 492 | 34 | 100.0 | 5188 | 6 | AR562812 | AR562812 Sequence |
| 420 | 34 | 100.0 | 3884 | 9 | AK022953 | AK022953 Homo sapi | c 493 | 34 | 100.0 | 5188 | 6 | AX138940 | AX138940 Sequence |
| 421 | 34 | 100.0 | 3886 | 3 | DMU07595 | U07595 Drosophila | c 494 | 34 | 100.0 | 5188 | 6 | BD000705 | BD000705 Growth ho |
| 422 | 34 | 100.0 | 3893 | 12 | AF425299 | AF425299 Expressio | c 495 | 34 | 100.0 | 5215 | 6 | AR231278 | AR231278 Sequence |
| 423 | 34 | 100.0 | 3898 | 12 | AF425297 | AF425297 Expressio | c 496 | 34 | 100.0 | 5215 | 6 | BD008823 | BD008823 Compositi |
| 424 | 34 | 100.0 | 3934 | 10 | AF323987 | AF323987 Mus muscu | c 497 | 34 | 100.0 | 5254 | 6 | AR562813 | AR562813 Sequence |
| 425 | 34 | 100.0 | 3948 | 4 | AB121737 | AB121737 Bos tauru | c 498 | 34 | 100.0 | 5254 | 6 | AX138941 | AX138941 Sequence |
| 426 | 34 | 100.0 | 3960 | 9 | BC043258 | BC043258 Homo sapi | c 499 | 34 | 100.0 | 5254 | 6 | BD000706 | BD000706 Growth ho |
| 427 | 34 | 100.0 | 3974 | 5 | XU373733 | U373733 Xenopus lae | c 500 | 34 | 100.0 | 5254 | 8 | AK120962 | AK120962 Oryza sat |
| 428 | 34 | 100.0 | 3989 | 6 | AX354698 | AX354698 Sequence | c 501 | 34 | 100.0 | 5259 | 6 | CQ847548 | CQ847548 Sequence |
| 429 | 34 | 100.0 | 3989 | 6 | AR536254 | AR536254 Sequence | c 502 | 34 | 100.0 | 5259 | 6 | BD086100 | BD086100 Cytokine- |
| 430 | 34 | 100.0 | 4039 | 5 | AY152408 | AY152408 Gallus ga | c 503 | 34 | 100.0 | 5259 | 6 | BD086104 | BD086104 Cytokine- |
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| 432 | 34 | 100.0 | 4051 | 1 | HU26665 | U26665 Haemophilus | c 505 | 34 | 100.0 | 5287 | 6 | E03599 | E03599 E.coli polB |
| 433 | 34 | 100.0 | 4060 | 6 | CQ593384 | CQ593384 Sequence | c 506 | 34 | 100.0 | 5303 | 6 | CQ583304 | CQ583304 Sequence |
| 434 | 34 | 100.0 | 4081 | 1 | ECFOUB | X54847 E. coli pol | c 507 | 34 | 100.0 | 5310 | 6 | AX080989 | AX080989 Sequence |
| 435 | 34 | 100.0 | 4152 | 8 | AY133875 | AY133875 Arabidops | c 508 | 34 | 100.0 | 5322 | 6 | CQ847550 | CQ847550 Sequence |
| 436 | 34 | 100.0 | 4156 | 9 | AK092387 | AK092387 Homo sapi | c 509 | 34 | 100.0 | 5322 | 6 | AX080956 | AX080956 Sequence |
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| 438 | 34 | 100.0 | 4247 | 10 | BC023757 | BC023757 Mus muscu | c 511 | 34 | 100.0 | 5325 | 8 | AY583466 | AY583466 Marchanti |
| 439 | 34 | 100.0 | 4276 | 6 | AX154496 | AX154496 Sequence | c 512 | 34 | 100.0 | 5386 | 6 | AX743953 | AX743953 Sequence |
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|-----|----|-------|------|----|-----------|---------------------|-----|----|-------|------|---|----------|----------|
| 516 | 34 | 100.0 | 5422 | 6 | BD086103 | BD086103 Cytokine- | 589 | 34 | 100.0 | 6610 | 6 | AX427828 | Sequence |
| 517 | 34 | 100.0 | 5428 | 6 | CQ847547 | CQ847547 Cytokine- | 590 | 34 | 100.0 | 6610 | 6 | AX427829 | Sequence |
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| 662 | 34 | 100.0 | 6790 | 6 | AX427914 | Sequence | AX427914 | Sequence | 735 | 34 | 100.0 | 9620 | 6 | AX164581 | Sequence | AX164581 | Sequence |
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| 678 | 34 | 100.0 | 7003 | 6 | AX427835 | Sequence | AX427835 | Sequence | c 751 | 34 | 100.0 | 10150 | 1 | AE005393 | Escherich | AE005393 | Escherich |
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| c 695 | 34 | 100.0 | 7403 | 6 | CO579467 | Sequence | CO579467 | Sequence | c 768 | 34 | 100.0 | 12272 | 10 | F255566S22 | Mus muscu | F255566S22 | Mus muscu |
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| 701 | 34 | 100.0 | 7552 | 6 | AX427849 | Sequence | AX427849 | Sequence | c 774 | 34 | 100.0 | 12563 | 1 | AE001346 | Chlamydia | AE001346 | Chlamydia |
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| 703 | 34 | 100.0 | 7807 | 6 | CO855141 | Sequence | CO855141 | Sequence | c 776 | 34 | 100.0 | 12641 | 1 | AE014731 | Bifidobac | AE014731 | Bifidobac |
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| 708 | 34 | 100.0 | 8001 | 6 | CO855137 | Sequence | CO855137 | Sequence | c 781 | 34 | 100.0 | 13464 | 6 | CO855143 | Sequence | CO855143 | Sequence |
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ALIGNMENTS

RESULT 1
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DEFINITION AX273053
ACCESSION AX273053
VERSION AX273053.1 GI:16545790
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 622 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
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ORGANISM Homo sapiens
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REFERENCE 1
AUTHORS Jarvis,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and Ellis,J.H.
TITLE Method and reagent for the inhibition of grid
JOURNAL Patent: WO 0162911-A 845 30-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB)
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ACCESSION AR503335
VERSION AR503335.1 GI:52438810
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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 82)
AUTHORS Homburger,S.A., Ebens,A.J. Jr., Erickson,C.S., Francis-Lang,H.L., Margolis,J.S., Reddy,B.P., Ruddy,D.A. and Buchman,A.R.
TITLE Drosophila sequences
JOURNAL Patent: US 6703491-A 8295 09-MAR-2004;
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR503335 (1-82)

QY 1 HisAenAlaHisHis 5
Db 2 CACAACGCCACAC 16

RESULT 4
AR518617
LOCUS AR518617 82 bp DNA linear PAT 22-SEP-2004
DEFINITION Sequence 23577 from patent US 6703491.
ACCESSION AR518617
VERSION AR518617.1 GI:52454092
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 82)
AUTHORS Homburger,S.A., Ebene,A.J. Jr., Erickson,C.S., Francis-Lang,H.L.,
Margolis,J.S., Reddy,B.P., Ruddy,D.A. and Buchman,A.R.
TITLE Drosophila sequences
JOURNAL Patent: US 6703491-A 23577 09-MAR-2004;
FEATURES
source
1..82
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 239 Length: 82
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR518617 (1-82)

QY 1 HisAenAlaHisHis 5
Db 2 CACAACGCCACAC 16

RESULT 5
AR523914
LOCUS AR523914 206 bp DNA linear PAT 22-SEP-2004
DEFINITION Sequence 28874 from patent US 6703491.
ACCESSION AR523914
VERSION AR523914.1 GI:52459389
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 206)
AUTHORS Homburger,S.A., Ebene,A.J. Jr., Erickson,C.S., Francis-Lang,H.L.,
Margolis,J.S., Reddy,B.P., Ruddy,D.A. and Buchman,A.R.
TITLE Drosophila sequences
JOURNAL Patent: US 6703491-A 28874 09-MAR-2004;
FEATURES
source
1..206
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:

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Pred. No.: 565 Length: 206
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR523914 (1-206)

QY 1 HisAenAlaHisHis 5
Db 183 CACAATGCCACCAT 197

RESULT 6
HSA555925/c
LOCUS HSA555925 224 bp DNA linear PRI 16-APR-2003
DEFINITION Homo sapiens rearranged immunoglobulin gene DNA, isolate case 1,
cell 40.
ACCESSION AJ555925
VERSION AJ555925.1 GI:29836815
KEYWORDS immunoglobulin.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Brauning,A., Spieker,T., Mottok,A., Baur,A., Koppers,R. and
Hanemann,M.L.
TITLE Epstein Barr virus (EBV)-positive lymphoproliferations in
posttransplant patients show immunoglobulin V gene mutation
patterns suggesting interference of EBV with normal B cell
differentiation processes
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 224)
AUTHORS Brauning,A.
TITLE Direct Submission
JOURNAL Submitted (08-APR-2003) Brauning,A., Pathology, University of
Frankfurt, Theodor Stern Kai 7, 60590, GERMANY
FEATURES
source
1..224
/organism="Homo sapiens"
/mol_type="genomic DNA"
/isolate="case 1, cell 40"
/db_xref="taxon:9606"
/tissue type="posttransplantation lymphoproliferative
disease"
/rearranged

ORIGIN
Alignment Scores:
Pred. No.: 611 Length: 224
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-029-756-12 (1-5) x HSA555925 (1-224)

QY 1 HisAenAlaHisHis 5
Db 216 CATATGCTCATCAC 202

RESULT 7
CQ611508
LOCUS CQ611508 234 bp DNA linear PAT 02-FEB-2004
DEFINITION Sequence 39286 from Patent WO0171042.
ACCESSION CQ611508
VERSION CQ611508.1 GI:41662985
KEYWORDS
SOURCE Drosophila sp.
ORGANISM Drosophila sp.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1
REFERENCE
AUTHORS Venter, J.C., Adams, M., Li, P.W. and Myers, E.W.
TITLE Detection kits, such as nucleic acid arrays, for detecting the
JOURNAL expression of 10,000 or more Drosophila genes and uses thereof
Patent: WO 0171042-A 3266 27-SEP-2001;
PE Corporation (NY) (US)
FEATURES
source Location/Qualifiers
1..234
/organism="Drosophila sp."
/mol_type="unassigned DNA"
/db_xref="taxon:7242"
ORIGIN
Alignment Scores:
Pred. No.: 636 Length: 234
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-029-756-12 (1-5) x CQ611508 (1-234)
Qy 1 HisAenAlaHisHis 5
Db 90 CATRACGGCCACCAC 104
RESULT 8
AF171953/240 bp DNA linear PLN 01-MAY-2000
LOCUS Lindheimera texana internal transcribed spacer 1, complete
DEFINITION
sequence.
ACCESSION AF171953
VERSION AF171953.1 GI:7673204
KEYWORDS Lindheimera texana
ORGANISM Lindheimera texana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Lindheimera.
REFERENCE
1 (bases 1 to 240)
Clevinger, J.A. and Panero, J.L.
Phylogenetic analysis of Silphium and subtribe Engelmanniinae
(Asteraceae: Heliantheae) based on ITS and ETS sequence data
Am. J. Bot. 87 (4), 565-572 (2000)
JOURNAL 10766728
PUBMED
REFERENCE
2 (bases 1 to 240)
Clevinger, J.A. and Panero, J.L.
Direct Submission
TITLE Submitted (26-JUL-1999) Biology, James Madison University, MSC
JOURNAL 7801, Harrisonburg, Virginia 22807, USA
LOCATION/Qualifiers
FEATURES
source
1..240
/organism="Lindheimera texana"
/mol_type="genomic DNA"
/isolate="Saunders-3500"
/db_xref="taxon:53585"
misc_RNA 1..240
/product="internal transcribed spacer 1"
ORIGIN
Alignment Scores:
Pred. No.: 651 Length: 240
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0
US-10-029-756-12 (1-5) x AF171953 (1-240)

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Qy 1 HisAenAlaHisHis 5
Db 222 CACAATGGCCACCAC 208
RESULT 9
AF479986
LOCUS Saccharomyces cerevisiae YAL068W-A gene, complete cds.
DEFINITION
ACCESSION AF479986
VERSION AF479986.1 GI:18767167
KEYWORDS Saccharomyces cerevisiae (baker's yeast)
SOURCE Saccharomyces cerevisiae
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
REFERENCE
1 (bases 1 to 255)
Kumar, A., Harrison, P.M., Cheung, K.H., Lan, N., Echols, N.,
Bertone, P., Miller, P., Gerstein, M.B. and Snyder, M.
TITLE An integrated approach for finding overlooked genes in yeast
JOURNAL Nat. Biotechnol. 20 (1), 58-63 (2002)
MEDLINE 21624570
PUBMED 11753363
REFERENCE
2 (bases 1 to 255)
Kumar, A., Paul, H.M., Cheung, K.H., Lan, N., Echols, N., Bertone, P.,
Miller, P., Gerstein, M.B. and Snyder, M.
Direct Submission
TITLE Submitted (01-FEB-2002) MCD Biology, Yale University, P.O. Box
JOURNAL 208103, New Haven, CT 06520-8103, USA
LOCATION/Qualifiers
FEATURES
source
1..255
/organism="Saccharomyces cerevisiae"
/mol_type="genomic DNA"
/db_xref="taxon:4932"
<1..>255
/gene="YAL068W-A"
<1..>255
/gene="YAL068W-A"
<1..>255
/product="unknown"
1..255
/gene="YAL068W-A"
/codon_start=1
/product="unknown"
/db_xref="GI:18767168"
/translation="MHGTCLSGLYPVPFTNAHHYHFDIYISFGPKYCITALNTYY
IPLHLHLITTPFIYTYVYNITEKSPQKSPKHNILLFNNT"
ORIGIN
Alignment Scores:
Pred. No.: 689 Length: 255
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0
US-10-029-756-12 (1-5) x AF479986 (1-255)
Qy 1 HisAenAlaHisHis 5
Db 46 CATRACGGCCACCAC 60
RESULT 10
AF688473S1/c
LOCUS Balduina uniflora clone BuITS1 internal transcribed spacer 1,
DEFINITION partial sequence.
ACCESSION AY688473
VERSION AY688473.1 GI:51039204
KEYWORDS Balduina uniflora
SEGMENT 1 of 2
SOURCE Balduina uniflora

```

ORGANISM Balduina uniflora
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Helenieae; Balduina.
REFERENCE 1 (bases 1 to 261)
AUTHORS Simurda,M.C., Marshall,D.C. and Knox,J.S.
TITLE Phylogeography of the narrow endemic, *Helenium virginicum*
(Asteraceae), based upon ITS sequence comparisons
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 261)
AUTHORS Simurda,M.C., Marshall,D.C. and Knox,J.S.
TITLE Direct Submission
JOURNAL Submitted (15-JUL-2004) Biology, Washington and Lee University,
Lexington, VA 24450-0303, USA
FEATURES
source
1..261
/organism="Balduina uniflora"
/mol_type="genomic DNA"
/db_xref="taxon:128714"
/clone="BuITS1"
misc_RNA
<1..>261
/product="internal transcribed spacer 1"
ORIGIN
Alignment Scores:
Pred. No.: 705 Length: 261
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0
US-10-029-756-12 (1-5) x AY688473S1 (1-261)
Qy 1 HisAenAlaHisHie 5
Db 142 CACAATGCCCATCAT 128
RESULT 11
LOCUS AX801775 311 bp DNA linear PAT 24-NOV-2003
DEFINITION Sequence 9 from Patent WO03057867.
ACCESSION AX801775
VERSION AX801775.1 GI:38500699
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Xiao,Y.
TITLE Regulation of human fatty acid CoA ligase-like AMP-binding enzyme
JOURNAL Patent: WO 03057867-A 9 17-JUL-2003;
Bayer Aktiengesellschaft (DE)
FEATURES
source
1..311
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 830 Length: 311
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-029-756-12 (1-5) x AX801775 (1-311)
Qy 1 HisAenAlaHisHie 5

Db 264 CACAATGCCCATCAT 250
RESULT 12
LOCUS AY208086 313 bp RNA linear VRL 19-APR-2003
DEFINITION Human coxsackievirus A16 strain C6292-115/99 VPI gene, partial cds.
ACCESSION AY208086
VERSION AY208086.1 GI:30025149
KEYWORDS
SOURCE Human coxsackievirus A16
ORGANISM Human coxsackievirus A16
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 313)
AUTHORS Norder,H., Bjerregaard,L., Magnus,L.O., Lina,B., Aymard,M. and
Chomel,J.J.
TITLE Sequencing of 'untypable' enteroviruses reveals two new types,
EV-77 and EV-78, within human enterovirus type B and substitutions
in the BC loop of the VPI protein for known types
JOURNAL J. Gen. Virol. 84 (Pt 4), 827-836 (2003)
MEDLINE 22541853
PUBMED 12655083
REFERENCE 2 (bases 1 to 313)
AUTHORS Norder,H., Bjerregaard,L., Magnus,L.O., Lina,B., Aymard,M. and
Chomel,J.J.
TITLE Direct Submission
JOURNAL Submitted (27-DEC-2002) Virological Department, Swedish Institute
for Infectious Disease Control, Hepatitis Section, Solna SE- 171
82, Sweden
FEATURES
source
1..313
/organism="Human coxsackievirus A16"
/mol_type="genomic RNA"
/strain="C6292-115/99"
/db_xref="taxon:31704"
CDS
<1..>313
/codon_start=1
/product="VP1"
/protein_id="AAP04537.1"
/db_xref="GI:30025150"
/translation="SSNASDKNLIETRCVLNHHSTQETAIGNPFSRAGLVSLITMPTT
GTQNTDGVNWDIDLMGYAQRKRCLEFTYMRFAEFTFVVKENGELVPQLQTMFV
PP"
ORIGIN
Alignment Scores:
Pred. No.: 835 Length: 313
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
US-10-029-756-12 (1-5) x AY208086 (1-313)
Qy 1 HisAenAlaHisHie 5
Db 117 CACAATGCCCATCAT 131
RESULT 13
LOCUS AY558170 315 bp DNA linear PLN 14-MAR-2004
DEFINITION Saccharomyces cerevisiae clone PLH110982.01X YAL069W gene, complete
cds.
ACCESSION AY558170
VERSION AY558170.1 GI:45270229
KEYWORDS Yeast ORF Project.
SOURCE Saccharomyces cerevisiae (baker's yeast)
ORGANISM Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE 1 (bases 1 to 315)

AUTHORS Marsischky, G., Rolfs, A., Richardson, A., Kane, M., Baqui, M., Taycher, E., Hu, Y., Vamberg, F., Weger, J., Kramer, J., Moreira, D., Kelley, F., Zuo, D., Raphael, J., Hogle, C., Jepson, D., Williamson, J., Camargo, A., Gonzaga, L., Vasconcelos, A.T., Simpson, A., Kolodner, R., Harlow, E. and LaBaer, J.

TITLE Creation of the YFLX clone resource: cloning of Saccharomyces cerevisiae ORFs in the Gateway recombinational cloning system

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 315)

AUTHORS Marsischky, G., Rolfs, A., Richardson, A., Kane, M., Baqui, M., Taycher, E., Hu, Y., Vamberg, F., Weger, J., Kramer, J., Moreira, D., Kelley, F., Zuo, D., Raphael, J., Hogle, C., Jepson, D., Williamson, J., Camargo, A., Gonzaga, L., Vasconcelos, A.T., Simpson, A., Kolodner, R., Harlow, E. and LaBaer, J.

TITLE Direct Submission

JOURNAL Submitted (17-FEB-2004) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA

COMMENT This clone is part of a collection of Saccharomyces cerevisiae full-length ORF clones generated by the Harvard Institute of Proteomics. Each CDS has been cloned with its native stop-codon. The CDS has been directionally cloned using the Gateway cloning system into the donor vectors pDONR 201 or pDONR 221. Additional sequences in the clone: 'TCCAGCTGACCAC' after the attL1 site and before the 'ATG' (from Research Genetics primers used to amplify the ORFs, including a Kozak consensus sequence); 'ATCCCGGAATGCCATG' after the stop codon and before the attL2 site (from the Research Genetics primers used to amplify the ORFs).

FEATURES source
 1..315
 /organism="Saccharomyces cerevisiae"
 /mol_type="genomic DNA"
 /db_xref="taxon:4932"
 /clone="FLH10982.01X"
 /lab_host="Escherichia coli DH5alpha T1 resistant"
 <1..>315
 /product="YAL069W"
 /codon_start=1
 1..315
 /product="YAL069W"
 /protein_id="AAS56496.1"
 /db_xref="GI:45270230"
 /translation="MIVNTHVLPLVLTITTTTCHTTHPLVTDFTYAGCYSIYHLKLT
 LLSDSTSLHGSPLESVPNALSTCLASAVYTLCHLPITPIIIHLISHSAPVN
 IV"

ORIGIN

Alignment Scores:
 Pred. No.: 840 Length: 315
 Score: 34.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-10-029-756-12 (1-5) x AY558170 (1-315)

Qy 1 HisAsnAlaHisHis 5

Db 249 CATAACGCCCATCAT 263

RESULT 14 AR358244/c

LOCUS AR358244/c

DEFINITION Sequence 4362 from patent US 6593114.

ACCESSION AR358244

VERSION AR358244.1 GI:33764328

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 316)

AUTHORS Kunsch, C.A., Choi, G.H., Barash, S., Dillon, P.J., Fannon, M.R. and

TITLE Rosen, C.A.

JOURNAL Staphylococcus aureus polynucleotides and sequences

FEATURES Patent: US 6593114-A 4362 15-JUL-2003;
 Location/Qualifiers
 source
 1..316
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Alignment Scores:
 Pred. No.: 842 Length: 316
 Score: 34.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR358244 (1-316)

Qy 1 HisAsnAlaHisHis 5

Db 205 CATAACGCCCATCAT 191

RESULT 15 AR539800/c

LOCUS AR539800

DEFINITION Sequence 4362 from patent US 6737248.

ACCESSION AR539800

VERSION AR539800.1 GI:53931017

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 316)

AUTHORS Kunsch, C.A., Choi, G.A., Barash, S.C., Dillon, P.J., Fannon, M.R. and Rosen, C.A.

TITLE Staphylococcus aureus polynucleotides and sequences

JOURNAL Patent: US 6737248-A 4362 18-MAY-2004;
 Location/Qualifiers
 source
 1..316
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Alignment Scores:
 Pred. No.: 842 Length: 316
 Score: 34.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR539800 (1-316)

Qy 1 HisAsnAlaHisHis 5

Db 205 CATAACGCCCATCAT 191

RESULT 16 CO433519

LOCUS CO433519

DEFINITION Sequence 18553 from Patent WO0151628.

ACCESSION CO433519

VERSION CO433519.1 GI:41385748

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE Lillie, J., Xu, Y., Wang, Y. and Steinmann, K.
 Novel genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of breast cancer

```

JOURNAL Patent: WO 0151628-A 18553 19-JUL-2001;
FEATURES Millennium Pharmaceuticals, Inc. (US)
SOURCE Location/Qualifiers
1.321
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 855 Length: 321
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x CQ433519 (1-321)

Qy 1 HisAenAlaHisHis 5
Db 83 CACAATGCACATCAT 97

RESULT 17
AY208082 AY208082 323 bp RNA linear VRL 19-APR-2003
LOCUS Human coxsackievirus A16 strain 98/01154-39/99 VP1 gene, partial
DEFINITION cds.
ACCESSION AY208082
VERSION AY208082.1 GI:30025142
SOURCE Human coxsackievirus A16
ORGANISM Human coxsackievirus A16
KEYWORDS Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 323)
AUTHORS Norder,H., Bjerregaard,L., Magnus,L.O., Lina,B., Aymard,M. and Chomel,J.J.
TITLE Sequencing of 'untypable' enteroviruses reveals two new types, EV-77 and EV-78, within human enterovirus type B and substitutions in the BC loop of the VP1 protein for known types
JOURNAL J. Gen. Virol. 84 (Pt 4), 827-836 (2003)
MEDLINE 22541853
PUBMED 12655083
REFERENCE 2 (bases 1 to 323)
AUTHORS Norder,H., Bjerregaard,L., Magnus,L.O., Lina,B., Aymard,M. and Chomel,J.J.
TITLE Direct Submission
JOURNAL Submitted (27-DEC-2002) Virological Department, Swedish Institute for Infectious Disease Control, Hepatitis Section, Solna SE- 171 82, Sweden
FEATURES source
1.323 Location/Qualifiers
/organism="Human coxsackievirus A16"
/mol_type="genomic RNA"
/strain="98/01154-39/99"
/db_xref="taxon:31704"
<1_->323
/codon_start=1
/product="VP1"
/protein_id="AAP04534.1"
/db_xref="GI:30025143"
/translation="QAATGASNASDKNLITRCVLNHHSTQETAINFFSRAGLVLS
IITWPTGTQNTDGVVNDIDLMGVAQLRRKCELFYRFDATFFVAKENGELVPG
LLQYM"

ORIGIN
Alignment Scores:
Pred. No.: 860 Length: 323
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

JOURNAL Patent: WO 0151628-A 18553 19-JUL-2001;
FEATURES Millennium Pharmaceuticals, Inc. (US)
SOURCE Location/Qualifiers
1.321
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 855 Length: 321
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AY208082 (1-323)

Qy 1 HisAenAlaHisHis 5
Db 138 CACAATGCCACCAC 152

RESULT 18
AX312622 AX312622 325 bp DNA linear PAT 14-DEC-2001
LOCUS Sequence 5607 from Patent WO0190366.
DEFINITION AX312622
ACCESSION AX312622
VERSION AX312622.1 GI:17897541
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Leach,M.D. and Shinkets,R.A.
TITLE Human polynucleotides and polypeptides encoded thereby
JOURNAL Patent: WO 0190366-A 5607 29-NOV-2001;
Curagen Corporation (US)
FEATURES Location/Qualifiers
source 1.325
/molecule="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 865 Length: 325
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AX312622 (1-325)

Qy 1 HisAenAlaHisHis 5
Db 217 CACAATGCCACCAC 231

RESULT 19
GI6708/c GI6708 329 bp DNA linear STS 06-MAR-1996
LOCUS human STS SHGC-3920 clone pg-1554, sequence tagged site.
DEFINITION GI6708
ACCESSION GI6708
VERSION GI6708.1 GI:1214134
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 329)
AUTHORS Myers,R.M.
JOURNAL Unpublished (1996)
COMMENT Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu

Primer A: TCTTTGTCCTTTTCGTCCATCC
Primer B: ATAAGTAGAGTTTCATATGCACAC
STS size: 176
PCR Profile:
Initial incubation: 94 degrees C for 90 seconds

```

Denaturation: 94 degrees C for 15 seconds
 Annealing: 62 degrees C for 23 seconds
 Polymerization: 72 degrees C for 30 seconds
 PCR Cycles: 30
 Thermal Cycler: Perkin Elmer 9600

Protocol:
 Template: 25 ng
 Primer: each 1 uM
 dNTPs: each 200 uM
 Taq Polymerase: 0.05 units/ul
 Total Vol: 10 ul

Buffer: MgCl2: 2.5 mM
 KCl: 50 mM
 Tris-HCl: 20 mM
 pH: 8.3

Chromosome 4.
 Location/Qualifiers
 source
 1..329
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /map="4"
 STS
 primer_bind
 primer_bind
 complement (154..178)

Alignment Scores:
 Pred. No.: 875 Length: 329
 Score: 34.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0

US-10-029-756-12 (1-5) x G16708 (1-329)

Qy 1 HisAenAlaHisHis 5

Db 166 CATAATGCACCAT 152

RESULT 20
 G34525/c
 LOCUS human STS SHGC-60109, sequence tagged site. linear STS 01-JUL-1997
 DEFINITION
 G34525
 G34525
 G34525.1 GI:2227829
 VERSION STS; STS sequence; primer; sequence tagged site.
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 329)
 Myers, R.M.
 Unpublished (1997)

Contact: Richard M. Myers
 Stanford Human Genome Center (SHGC)
 Stanford University School of Medicine
 Department of Genetics, M-344, Stanford, CA 94305, USA
 Tel: 4157259687
 Fax: 4157259689
 Email: myers@shgc.stanford.edu

Primer A: TTGTGTCCTCTTATGCTGTC
 Primer B: CTCATAACAGTGACTTCACCC
 STS size: 121
 PCR Profile:

Initial incubation: 94 degrees C for 90 seconds

Denaturation: 94 degrees C for 15 seconds
 Annealing: 62 degrees C for 23 seconds
 Polymerization: 72 degrees C for 30 seconds
 PCR Cycles: 30
 Thermal Cycler: Perkin Elmer 9600

Protocol:
 Template: 25 ng
 Primer: each 1 uM
 dNTPs: each 200 uM
 Taq Polymerase: 0.05 units/ul
 Total Vol: 10 ul

Buffer: MgCl2: 2.5 mM
 KCl: 50 mM
 Tris-HCl: 20 mM
 pH: 8.3

Redeveloped chromosome 21 markers for scoring on oligonucleotide arrays. Designed and developed at the Stanford Human Genome Center on sequences previously developed as STSs at the Stanford Human Genome Center, the Whitehead Institute or TIGR, as well as sequence available in the public databases for chromosome 21.

FEATURES
 source
 1..329
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /map="4"
 STS
 primer_bind
 primer_bind
 complement (236..259)

Alignment Scores:
 Pred. No.: 875 Length: 329
 Score: 34.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0

US-10-029-756-12 (1-5) x G34525 (1-329)

Qy 1 HisAenAlaHisHis 5

Db 166 CATAATGCACCAT 152

RESULT 21

AR378808/c

LOCUS

DEFINITION

SEQUENCE 3814 from patent US 6605709.

ACCESSION

AR378808

VERSION

AR378808.1 GI:40081990

KEYWORDS

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 333)

Breton, G.L.

Nucleic acid and amino acid sequences relating to Proteus mirabilis

for diagnostics and therapeutics

Patent: US 6605709-A 3814 12-AUG-2003;

JOURNAL

Location/Qualifiers

source

1..333

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.: 885 Length: 333

Score: 34.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR378808 (1-333)

Qy 1 HisaenAlaHis 5
 Db 205 CATAACGGCACCAC 191

RESULT 22
 CQ415760 343 bp DNA linear PAT 28-JAN-2004
 LOCUS
 DEFINITION Sequence 794 from Patent WO0151628.
 ACCESSION CQ415760
 VERSION CQ415760.1 GI:41367989
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 AUTHORS Lillie, J., Xu, Y., Wang, Y. and Steinmann, K.
 TITLE Novel genes, compositions, kits, and methods for identification,
 assessment, prevention, and therapy of breast cancer
 JOURNAL Patent: WO 0151628-A 794 19-JUL-2001;
 Millennium Pharmaceuticals, Inc. (US)

FEATURES
 Location/Qualifiers
 source
 1..343
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Alignment Scores:
 Pred. No.: 909 Length: 343
 Score: 34.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x CQ415760 (1-343)

Qy 1 HisaenAlaHis 5
 Db 104 CACAATGCACATCAT 118

RESULT 23
 CQ425403 345 bp DNA linear PAT 28-JAN-2004
 LOCUS
 DEFINITION Sequence 10437 from Patent WO0151628.
 ACCESSION CQ425403
 VERSION CQ425403.1 GI:41377632
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
 AUTHORS Lillie, J., Xu, Y., Wang, Y. and Steinmann, K.
 TITLE Novel genes, compositions, kits, and methods for identification,
 assessment, prevention, and therapy of breast cancer
 JOURNAL Patent: WO 0151628-A 10437 19-JUL-2001;
 Millennium Pharmaceuticals, Inc. (US)

FEATURES
 Location/Qualifiers
 source
 1..345
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Alignment Scores:
 Pred. No.: 914 Length: 345
 Score: 34.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x CQ425403 (1-345)

Qy 1 HisaenAlaHis 5
 Db 104 CACAATGCACATCAT 118

RESULT 24
 AR358018 348 bp DNA linear PAT 17-AUG-2003
 LOCUS
 DEFINITION Sequence 4136 from patent US 6593114.
 ACCESSION AR358018
 VERSION AR358018.1 GI:33764102
 KEYWORDS
 SOURCE Unknown.
 ORGANISM
 Unclassified.
 REFERENCE 1 (bases 1 to 348)
 AUTHORS Kunsch, C.A., Choi, G.H., Barash, S., Dillon, P.J., Fannon, M.R. and
 Rosen, C.A.
 TITLE Staphylococcus aureus polynucleotides and sequences
 JOURNAL Patent: US 6593114-A 4136 15-JUL-2003;
 FEATURES
 Location/Qualifiers
 source
 1..348
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Alignment Scores:
 Pred. No.: 922 Length: 348
 Score: 34.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR358018 (1-348)

Qy 1 HisaenAlaHis 5
 Db 144 CATAACGCACATCAT 158

RESULT 25
 AR539574 348 bp DNA linear PAT 08-OCT-2004
 LOCUS
 DEFINITION Sequence 4136 from patent US 6737248.
 ACCESSION AR539574
 VERSION AR539574.1 GI:53930791
 KEYWORDS
 SOURCE Unknown.
 ORGANISM
 Unclassified.
 REFERENCE 1 (bases 1 to 348)
 AUTHORS Kunsch, C.A., Choi, G.A., Barash, S.C., Dillon, P.J., Fannon, M.R. and
 Rosen, C.A.
 TITLE Staphylococcus aureus polynucleotides and sequences
 JOURNAL Patent: US 6737248-A 4136 18-MAY-2004;
 FEATURES
 Location/Qualifiers
 source
 1..348
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Alignment Scores:
 Pred. No.: 922 Length: 348
 Score: 34.00 Matches: 5

Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR539574 (1-348)

QY 1 HisAsnAlaHis 5
Db 144 CATAACGCATCAT 158

RESULT 26
AF154077/c
LOCUS AF154077 358 bp DNA linear PLN 16-FEB-2001
DEFINITION Rhizopogon vinicolor clone Rv15 microsatellite sequence.
ACCESSION AF154077
VERSION AF154077.1 GI:8347141
KEYWORDS
SOURCE Rhizopogon vinicolor
ORGANISM Rhizopogon vinicolor
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Boletales; Suillineae; Rhizopogonaceae; Rhizopogon.
REFERENCE 1 (bases 1 to 358)
AUTHORS Kretzer,A.M., Molina,R. and Spatafora,J.W.
TITLE Microsatellite markers for the ectomycorrhizal basidiomycete
Rhizopogon vinicolor
JOURNAL Mol. Ecol. 9 (8), 1190-1191 (2000)
MEDLINE 20427187
PUBMED 10964248
REFERENCE 2 (bases 1 to 358)
AUTHORS Kretzer,A.M.
TITLE Direct Submission
JOURNAL Submitted (26-MAY-1999) Botany and Plant Pathology, Oregon State
University, 2082 Cordley Hall, Corvallis, OR 97331, USA

FEATURES
source 1..358
 /organism="Rhizopogon vinicolor"
 /mol_type="genomic DNA"
 /strain="T20787"
 /db_xref="taxon:80600"
 /clones="Rv15"
repeat_region 1..358
 /notes="microsatellite"
 /rpt_type=tandem

ORIGIN
Alignment Scores:
Pred. No.: 947 Length: 358
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-029-756-12 (1-5) x AF154077 (1-358)

QY 1 HisAsnAlaHis 5
Db 84 CATAATGCCATCAT 70

RESULT 27
AX413277/c
LOCUS AX413277 366 bp DNA linear PAT 02-SEP-2002
DEFINITION Sequence 268 from Patent WO0228891.
ACCESSION AX413277
VERSION AX413277.1 GI:21445734
KEYWORDS Listeria innocua
SOURCE Listeria innocua
ORGANISM Listeria innocua
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
REFERENCE 1
AUTHORS Kunst,F. and Glaser,P.
TITLE Listeria innocua, genome and applications

JOURNAL Patent: WO 0228891-A 268 11-APR-2002;
INSTITUT PASTEUR (FR) ; CENTRE NATIONAL DE LA RECHERCHE
SCIENTIFIQUE (CNRS) (FR)

FEATURES
source 1..366
 /organism="Listeria innocua"
 /mol_type="unassigned DNA"
 /db_xref="taxon:1642"

ORIGIN
Alignment Scores:
Pred. No.: 966 Length: 366
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AX413277 (1-366)

QY 1 HisAsnAlaHis 5
Db 94 CACACGCTCACCAC 80

RESULT 28
AX415103/c
LOCUS AX415103 366 bp DNA linear PAT 02-SEP-2002
DEFINITION Sequence 2094 from Patent WO0228891.
ACCESSION AX415103
VERSION AX415103.1 GI:21447560
KEYWORDS Listeria innocua
SOURCE Listeria innocua
ORGANISM Listeria innocua
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
REFERENCE 1
AUTHORS Kunst,F. and Glaser,P.
TITLE Listeria innocua, genome and applications
JOURNAL Patent: WO 0228891-A 2094 11-APR-2002;
INSTITUT PASTEUR (FR) ; CENTRE NATIONAL DE LA RECHERCHE
SCIENTIFIQUE (CNRS) (FR)

FEATURES
source 1..366
 /organism="Listeria innocua"
 /mol_type="unassigned DNA"
 /db_xref="taxon:1642"

ORIGIN
Alignment Scores:
Pred. No.: 966 Length: 366
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AX415103 (1-366)

QY 1 HisAsnAlaHis 5
Db 94 CACACGCTCACCAC 80

RESULT 29
AR074124/c
LOCUS AR074124 380 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 33 from patent US 5952486.
ACCESSION AR074124
VERSION AR074124.1 GI:10000884
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 380)
AUTHORS Bloksberg,L.N., Havukkala,I. and Grierson,A.W.

TITLE Materials and methods for the modification of plant lignin content
JOURNAL Patent: US 5952486-A 33 14-SEP-1999;
FEATURES Location/Qualifiers
source 1..380
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
Pred. No.: 1e+03 Length: 380
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR074124 (1-380)

Qy 1 HisAenAlaHisHis 5

Db 50 CACAACGCTCACCAT 36

RESULT 10
BD224309/c
LOCUS BD224309 380 bp DNA linear PAT 17-JUL-2003
DEFINITION Materials and methods for the modification of plant lignin content.
ACCESSION BD224309
VERSION BD224309.1 GI:33034079
KEYWORDS JP 2002527058-A/33.
SOURCE Eucalyptus grandis
ORGANISM Eucalyptus grandis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Myrtales; Myrtaceae; Eucalyptus.
1 (bases 1 to 380)

REFERENCE Bloksberg,L.N. and Havukkala,I.J.
AUTHORS Materials and methods for the modification of plant lignin content
TITLE Patent: JP 2002527058-A 33 27-AUG-2002;
JOURNAL GENESIS RESEARCH AND DEVELOPMENT CORP LTD, FLETCHER CHALLENGE
FORESTS LTD

COMMENT OS Eucalyptus grandis
FN JP 2002527058-A/33
PD 27-AUG-2002
PF 06-OCT-1999 JP 2000575991
PR 09-OCT-1998 US 09/169789,14-JUL-1999 US 60/143811 PI
LEONARD NATHAN BLOKSBERG,ILKKA JAAKKO HAVUKKALA PC
C12N15/09,A01H5/00,C12N5/10,C12N9/02,C12N9/04,C12N9/ PC
10,C12N9/24,
PC C12N9/88,C12N15/00,C12N5/00
CC Materials and methods for the modification of plant lignin CC

FH Key Location/Qualifiers
FT source 1..380
/organism='Eucalyptus grandis'.
FT Location/Qualifiers

FEATURES
source 1..380
/organism="Eucalyptus grandis"
/mol_type="genomic DNA"
/db_xref="taxon:71139"

ORIGIN

Alignment Scores:
Pred. No.: 1e+03 Length: 380
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x BD224309 (1-380)

Qy 1 HisAenAlaHisHis 5

Db 50 CACAACGCTCACCAT 36

RESULT 31

BD273006/c

LOCUS BD273006 380 bp DNA linear PAT 17-JUL-2003

DEFINITION Materials and methods for the modification of isoprenoid content,
composition and metabolism.

ACCESSION BD273006

VERSION BD273006.1 GI:33082774

KEYWORDS JP 2002541764-A/73.

SOURCE Eucalyptus grandis

ORGANISM Eucalyptus grandis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Myrtales; Myrtaceae; Eucalyptus.
1 (bases 1 to 380)

REFERENCE Havukkala,I.J.

AUTHORS Materials and methods for the modification of isoprenoid content,
composition and metabolism

TITLE Patent: JP 2002541764-A 73 10-DEC-2002;
JOURNAL GENESIS RESEARCH AND DEVELOPMENT CORP LTD, FLETCHER CHALLENGE
FORESTS INDUSTRIES LTD

COMMENT OS Eucalyptus grandis (flooded gum)

PN JP 2002541764-A/73

PD 10-DEC-2002

PF 16-DEC-1999 JP 2000588332

PR 17-DEC-1998 US 09/215504,29-JUL-1999 US 60/146441 PI

ILKKA JAAKKO HAVUKKALA

PC C12N15/09,A01H5/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N5/

PC 10,C12N9/00,

PC C12Q1/68,C12N15/00,C12N5/00,C12N5/00

CC Materials and methods for the modification of isoprenoid CC

content,

CC composition and metabolism

FH Key Location/Qualifiers

FT source 1..380

/organism='Eucalyptus grandis (flooded gum)'.
FT Location/Qualifiers

1..380
/organism="Eucalyptus grandis"
/mol_type="genomic DNA"
/db_xref="taxon:71139"

ORIGIN

Alignment Scores:
Pred. No.: 1e+03 Length: 380
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x BD273006 (1-380)

Qy 1 HisAenAlaHisHis 5

Db 50 CACAACGCTCACCAT 36

RESULT 32

AR216359/c

LOCUS AR216359 380 bp DNA linear PAT 25-SEP-2002

DEFINITION Sequence 33 from patent US 6410718.

ACCESSION AR216359

VERSION AR216359.1 GI:23314839

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 380)

AUTHORS Bloksberg,L.N. and Havukkala,I.

TITLE Materials and methods for the modification of plant lignin content

JOURNAL Patent: US 6410718-A 33 25-JUN-2002;
FEATURES Location/Qualifiers

```

source      1. .380
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1e+03      Length: 380
Score: 34.00      Matches: 5
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 6      Gaps: 0

US-10-029-756-12 (1-5) x AR216359 (1-380)

Qy 1 HisAenAlaHisHis 5
Db 50 CACAACGCTCACCAT 36

RESULT 33
AR432761/c AR432761 380 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 33 from patent US 6653528.
ACCESSION AR432761
VERSION AR432761.1 GI:40195364
KEYWORDS
SOURCE unknown.
ORGANISM
REFERENCE 1 (bases 1 to 380)
AUTHORS Bloksberg,L.N. and Havukkala,I.
TITLE Pinus radiata nucleic acids encoding O-methyl transferase and
        methods for the modification of plant lignin content therewith
JOURNAL Patent: US 6653528-A 33 25-NOV-2003;
FEATURES
        source      1. .380
        /organism="unknown"
        /mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1e+03      Length: 380
Score: 34.00      Matches: 5
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 6      Gaps: 0

US-10-029-756-12 (1-5) x AR432761 (1-380)

Qy 1 HisAenAlaHisHis 5
Db 50 CACAACGCTCACCAT 36

RESULT 34
BD005672/c BD005672 380 bp DNA linear PAT 31-JAN-2002
LOCUS
DEFINITION Materials and methods for the modification of plant lignin content.
ACCESSION BD005672
VERSION BD005672.1 GI:18634043
KEYWORDS JP 2001500378-A/33.
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 380)
AUTHORS Bloksberg,L.N., Grierson,A.W. and Havukkala,I.J.
TITLE Materials and methods for the modification of plant lignin content
JOURNAL Patent: JP 2001500378-A 33 16-JAN-2001;
        GENESIS RESEARCH & DEVELOPMENT CO LTD, LETCHER CHALLENGE FORESTS
        LTD
COMMENT OS Unidentified
        PN JP 2001500378-A/33
        PD 16-JAN-2001

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PF 10-SEP-1997 JP 1998513535
PR 11-SEP-1996 US 08/713000
PI LEONARD NATHAN BLOKSBERG,ALISTAIR WALLACE GRIERSON, PI ILKKA
JAAKKO HAVUKKALA
PC C12N15/53,C12N15/54,C12N15/52,C12N15/60,C12N15/82,A01H5/00 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..380
        /organism="Unidentified".
        /organism="unidentified"
        /mol_type="genomic DNA"
        /db_xref="taxon:32644"

FEATURES
        source      1. .380
        Location/Qualifiers
        1..380
        /organism="unidentified"
        /mol_type="genomic DNA"
        /db_xref="taxon:32644"

ORIGIN
Alignment Scores:
Pred. No.: 1e+03      Length: 380
Score: 34.00      Matches: 5
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 6      Gaps: 0

US-10-029-756-12 (1-5) x BD005672 (1-380)

Qy 1 HisAenAlaHisHis 5
Db 50 CACAACGCTCACCAT 36

RESULT 35
HSA272XC9 380 bp DNA linear STS 09-SEP-2004
LOCUS
DEFINITION H.sapiens (D1S2682) DNA segment containing (CA) repeat; clone
        AFMa272xc9; single read, sequence tagged site.
ACCESSION Z52721
VERSION Z52721.1 GI:1234021
KEYWORDS STS; CA repeat; dinucleotide repeat; GT repeat; microsatellite DNA;
        microsatellite marker; repeat polymorphism.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 380)
AUTHORS Dib,C., Faure,S., Fizames,C., Samson,D., Drouot,N., Vignal,A.,
        Millasseau,P., Marc,S., Hazan,J., Seboun,E., Lathrop,M., Gyapay,G.,
        Morissette,J. and Weissenbach,J.
        A comprehensive genetic map of the human genome based on 5,264
        microsatellites
        Nature 380 (5570), 152-154 (1996)
JOURNAL 96176476
MEDLINE
PUBMED 8600387
REFERENCE 2 (bases 1 to 380)
AUTHORS Weissenbach,J.
TITLE Direct Submission
JOURNAL Submitted (01-SEP-1995) Genethon, B.P. 60, 91002 Evry Cedex France.
COMMENT E-mail: Jean.Weissenbach@genethon.fr
        full automatic.
FEATURES
        source      1. .380
        Location/Qualifiers
        1..380
        /organism="Homo sapiens"
        /mol_type="genomic DNA"
        /db_xref="taxon:9606"
        /chromosome="1"
        /cell_line="CEPH 134702"
        /clone_lib="genomic DNA"
        /note="Cloning vector is M13mp18"

ORIGIN
Alignment Scores:
Pred. No.: 1e+03      Length: 380
Score: 34.00      Matches: 5

```

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0

US-10-029-756-12 (1-5) x HSA272XC9 (1-380)

Qy 1 HisAenAlaHis 5

Db 290 CACAATGCATCAT 304

RESULT 36

HSPE48H04

LOCUS H.sapiens flow-sorted chromosome 1 linear STS 21-MAY-1998
 DEFINITION H.sapiens flow-sorted chromosome 1 HindIII fragment, SCIP48H04,
 sequence tagged site.

ACCESSION AL010086

VERSION AL010086.1 GI:2665248

KEYWORDS STS; single read.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

1 (bases 1 to 394) Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE Gregory, S., Kettleborough, R., Langford, C., Ross, M.T. and Hunt, S.E.

AUTHORS Direct Submission

JOURNAL Submitted (03-DEC-1997) E-mail contact: humquery@sanger.ac.uk

COMMENT Vector: pBS11SK+

Marker: stSG3252FS (Primer A : TCTCTGAGTCCCAACATC; Primer B :

AGGCGGTATCCAGCTG; amplicon size : 134 bp) was mapped to

chromosome 1 using Radiation Hybrid

panel Genebridge 4 (GB4).

FEATURES Location/Qualifiers

source 1..394

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="1"

/clone="SCIP48H04"

/sex="female"

/tissue_type="EBV lymphoblastoid cell line"

/clone_lib="SCIPe"

/dev_stage="adult"

ORIGIN

Alignment Scores: 1.04e+03 Length: 394
 Pred. No.: 34.00 Matches: 5
 Score: 34.00
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0

US-10-029-756-12 (1-5) x HSPE48H04 (1-394)

Qy 1 HisAenAlaHis 5

Db 118 CACAATGCATCAT 132

RESULT 37

AF333188/c

LOCUS AF333188

DEFINITION Oncorhynchus mykiss fructose-1,6-bisphosphatase mRNA, partial cds.

ACCESSION AF333188

VERSION AF333188.1 GI:15004314

KEYWORDS Oncorhynchus mykiss (rainbow trout)

SOURCE Oncorhynchus mykiss

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei;

Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

1 (bases 1 to 395)

REFERENCE Panseur, S., Plagnes-Juan, E. and Kaushik, S.

AUTHORS

TITLE

Nutritional regulation and tissue specificity of gene expression
 for proteins involved in hepatic glucose metabolism in rainbow
 trout (*Oncorhynchus mykiss*)

J. Exp. Biol. 204 (Pt 13), 2351-2360 (2001)

MEDLINE 21398391

PUBMED 11507117

REFERENCE 2 (bases 1 to 395)

Panseur, S., Plagnes-Juan, E. and Kaushik, S.

AUTHORS Direct Submission

TITLE Submitted (03-JAN-2001) INRA-IFREMER Fish Nutrition Laboratory,

JOURNAL INRA, St-Pee-sur-Nivelle 64310, France

FEATURES Location/Qualifiers

source 1..395

/organism="Oncorhynchus mykiss"

/mol_type="mRNA"

/db_xref="taxon:8022"

<1_>395

/EC_number="3.1.3.11"

/note="FBPase"

/codon_start=1

/product="fructose-1,6-bisphosphatase"

/protein_id="AAK77025.1"

/db_xref="GI:15004315"

/translation="PLDSSNIDCLVSGITFIAYRKTDDPNERDALQSRHIVAA

GYALYGSATMMVLSTGGVNCFLDPSIGEFILTDKDVKKRGIYSLNEGFAOHFY

PDVTEYLKKKYPEDSGAPYGRYVGSMA"

ORIGIN

Alignment Scores: 1.04e+03 Length: 395

Pred. No.: 34.00 Matches: 5

Score: 34.00

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 5 Gaps: 0

US-10-029-756-12 (1-5) x AF333188 (1-395)

Qy 1 HisAenAlaHis 5

Db 379 CATACGCCACCAT 365

RESULT 38

AF357625

LOCUS AR357625

DEFINITION Sequence 3743 from patent US 6593114.

ACCESSION AR357625

VERSION AR357625.1 GI:33763709

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 400)

AUTHORS Kunsch, C.A., Choi, G.H., Barash, S., Dillon, P.J., Fannon, M.R. and

Rosen, C.A.

TITLE Staphylococcus aureus polynucleotides and sequences

JOURNAL Patent: US 6593114-A 3743 15-JUL-2003;

FEATURES Location/Qualifiers

source 1..400

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Alignment Scores: 1.05e+03 Length: 400

Pred. No.: 34.00 Matches: 5

Score: 34.00

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR357625 (1-400)

Qy 1 HisAenAlaHisHis 5
 Db 79 CATAACGCACATCAT 93

RESULT 39
 AR539181
 LOCUS AR539181 400 bp DNA linear PAT 08-OCT-2004
 DEFINITION Sequence 3743 from patent US 6737248.
 ACCESSION AR539181
 VERSION AR539181.1 GI:53930398
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 400)
 AUTHORS Kunsch,C.A., Choi,G.A., Barash,S.C., Dillon,P.J., Fannon,M.R. and Rosen,C.A.
 TITLE Staphylococcus aureus polynucleotides and sequences
 JOURNAL Patent: US 6737248-A 3743 18-MAY-2004;
 FEATURES Location/Qualifiers
 source 1..400
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN
 Alignment Scores:
 Pred. No.: 1.05e+03 Length: 400
 Score: 34.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR539181 (1-400)

Qy 1 HisAenAlaHisHis 5
 Db 79 CATAACGCACATCAT 93

RESULT 40
 AX801776
 LOCUS AX801776 413 bp DNA linear PAT 24-NOV-2003
 DEFINITION Sequence 10 from Patent WO03057867.
 ACCESSION AX801776
 VERSION AX801776.1 GI:38500700
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Xiao,X.
 TITLE Regulation of human fatty acid CoA ligase-like AMP-binding enzyme
 JOURNAL Patent: WO 03057867-A 10 17-JUL-2003;
 Bayer Aktiengesellschaft (DE)
 FEATURES Location/Qualifiers
 source 1..413
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN
 Alignment Scores:
 Pred. No.: 1.08e+03 Length: 413
 Score: 34.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AX801776 (1-413)

Qy 1 HisAenAlaHisHis 5

Db 138 CACAATGCACATCAT 152

RESULT 41
 BD224391/c
 LOCUS BD224391 420 bp DNA linear PAT 17-JUL-2003
 DEFINITION Materials and methods for the modification of plant lignin content.
 ACCESSION BD224391
 VERSION BD224391.1 GI:33034161
 KEYWORDS JP 2002527058-A/115.
 SOURCE Eucalyptus grandis
 ORGANISM Eucalyptus grandis
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Myrtales; Myrtaceae; Eucalyptus.
 REFERENCE 1 (bases 1 to 420)
 AUTHORS Bloksberg,L.N. and Havukkala,I.J.
 TITLE Materials and methods for the modification of plant lignin content
 JOURNAL Patent: JP 2002527058-A 115 27-AUG-2002;
 GENESIS RESEARCH AND DEVELOPMENT CORP LTD, FLETCHER CHALLENGE FORESTS LTD
 COMMENT OS Eucalyptus grandis
 PN JP 2002527058-A/115
 PD 27-AUG-2002
 PF 06-OCT-1999 JP 2000575991
 PR 09-OCT-1998 US 09/169789, 14-JUL-1999 US 60/143811 PI
 LEONARD NATHAN BLOKSBERG,ILKKA JAAKKO HAVUKKALA PC
 C12N15/09,A01H5/00,C12N5/10,C12N9/00,C12N9/02,C12N9/04,C12N9/PC
 10,C12N9/24,
 PC C12N9/88,C12N15/00,C12N5/00
 CC Materials and methods for the modification of plant lignin CC
 content
 FH Key Location/Qualifiers
 FT source 1..420
 /organism='Eucalyptus grandis'.
 FEATURES source 1..420
 Location/Qualifiers
 /organism="Eucalyptus grandis"
 /mol_type="genomic DNA"
 /db_xref="taxon:71139"

ORIGIN
 Alignment Scores:
 Pred. No.: 1.1e+03 Length: 420
 Score: 34.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x BD224391 (1-420)

Qy 1 HisAenAlaHisHis 5
 Db 80 CACAACGCCTCACCAT 66

RESULT 42
 AR216441/c
 LOCUS AR216441 420 bp DNA linear PAT 25-SEP-2002
 DEFINITION Sequence 115 from patent US 6410718.
 ACCESSION AR216441
 VERSION AR216441.1 GI:23314921
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 420)
 AUTHORS Bloksberg,L.N. and Havukkala,I.
 TITLE Materials and methods for the modification of plant lignin content
 JOURNAL Patent: US 6410718-A 115 25-JUN-2002;
 FEATURES Location/Qualifiers
 source 1..420
 /organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 1.1e+03 Length: 420
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR216441 (1-420)

QY 1 HisAenAlaHisHis 5
|||||
DB 80 CACACGCTCACCAT 66

RESULT 43
AR432843/c
LOCUS AR432843 420 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 115 from patent US 6653528.
ACCESSION AR432843
VERSION AR432843.1 GI:40195446

KEYWORDS

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE 1 (bases 1 to 420)

Blosberg,L.N. and Havukkala,I.

Pinus radiata nucleic acids encoding O-methyl transferase and

methods for the modification of plant lignin content therewith

Patent: US 6653528-A 115 25-NOV-2003;

JOURNAL Location/Qualifiers

FEATURES

source

1..420

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 1.1e+03 Length: 420
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR432843 (1-420)

QY 1 HisAenAlaHisHis 5
|||||
DB 80 CACACGCTCACCAT 66

RESULT 44
AX896634
LOCUS AX896634 428 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 12497 from Patent EP1033401.
ACCESSION AX896634
VERSION AX896634.1 GI:40051518

KEYWORDS

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.

REFERENCE 1

Dumas Milne Edwards,J.B., Duclert,A. and Giordano,J.Y.

Expressed sequence tags and encoded human proteins

Patent: EP 1033401-A 12497 06-SEP-2000;

JOURNAL Genset (FR)

FEATURES

source

1..428

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 1.12e+03 Length: 428
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AX896634 (1-428)

QY 1 HisAenAlaHisHis 5
|||||
DB 109 CACATGCACACCAC 123

RESULT 45

BD032167

LOCUS

DEFINITION

Sequence tag and encoded human protein.

ACCESSION

BD032167

VERSION

BD032167.1 GI:22573909

KEYWORDS

JP 2001269182-A/8413.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.

REFERENCE 1 (bases 1 to 428)

Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.

Sequence tag and encoded human protein

Patent: JP 2001269182-A 8413 02-OCT-2001;

JOURNAL GENSET

COMMENT

OS Homo sapiens (human)

PN JP 2001269182-A/8413

PD 02-OCT-2001

PF 24-FEB-2000 JP 2000118773

PR 26-FEB-1999 US 60/122487

PI JEAN BAPTISTE DUMAS MILNE EDWARDS,EIMERIC DUCLAIR,JEAN YVES

PC C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21, PC

C12N5/10,

PC C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC

G06F15/40

CC

FH Key

Location/Qualifiers.

FEATURES

source

1..428

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 1.12e+03 Length: 428
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x BD032167 (1-428)

QY 1 HisAenAlaHisHis 5
|||||
DB 109 CACATGCACACCAC 123

RESULT 46

AR381260/c

LOCUS

DEFINITION

Sequence 7 from patent US 6607914.

ACCESSION

AR381260

VERSION

AR381260.1 GI:40089066

KEYWORDS

```

SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 432)
AUTHORS      Belyavsky,A.V., Luchinskaya,N.N. and Popsueva,A.E.
TITLE        Camello gene family and uses thereof
JOURNAL      Patent: US 6607914-A 7 19-AUG-2003;
FEATURES     Location/Qualifiers
             source
               1..432
               /organism="unknown"
               /mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.:      1.13e+03      Length:      432
Score:          34.00         Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             6           Gaps:        0

US-10-029-756-12 (1-5) x AR381260 (1-432)

Qy           1 HisAenAlaHisHis 5
Db           216 CACAATGCCACCAC 202

RESULT 47
AF221557
LOCUS        AF221557      437 bp      mRNA      linear      VRT 07-JUN-2001
DEFINITION   Gallus gallus bZIP transcription factor L-MAF mRNA, partial cds.
ACCESSION    AF221557
VERSION      AF221557.1 GI:7960153
KEYWORDS     .
SOURCE       Gallus gallus (chicken)
ORGANISM     Gallus gallus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
              Phasianinae; Gallus.
REFERENCE    1 (bases 1 to 437)
AUTHORS      Zhou,H., Liu,W. and Lamont,S.J.
TITLE        Genetic variation among chicken lines and mammalian species in
              specific genes
JOURNAL      Poult. Sci. 80 (3), 284-288 (2001)
MEDLINE      21158006
PUBMED       11261557
REFERENCE    2 (bases 1 to 437)
AUTHORS      Zhou,H. and Lamont,S.J.
TITLE        Direct Submission
JOURNAL      Submitted (06-JAN-2000) Animal Science, Iowa State University, 2255
              Kildee Hall, Ames, IA 50011, USA
FEATURES     Location/Qualifiers
             source
               1..437
               /organism="Gallus gallus"
               /mol_type="mRNA"
               /strain="breed Fayoumi"
               /db_xref="taxon:9031"
               /sex="female"
               /tissue type="spleen"
               <1..>437
               /note="MAFL"
               /codon_start=1
               /product="bZIP transcription factor L-MAF"
               /protein_id="AAF71239.1"
               /db_xref="GI:7960154"
               /translation="EALIGAPHHHHHHQSVESFRPQFPGGEELPPAAHHHNAHHHH
               HHHLRLEFRFSDQLVSMVRELNLQRLGFSKEVIRLKKRRTLKNRGYAQCRCYKR
               VQQRHILENEKCOLQSQVQLKQVSLAKERDLYKEKYEKLA"

CDS
Alignment Scores:
Pred. No.:      1.14e+03      Length:      437
Score:          34.00         Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             5           Gaps:        0

US-10-029-756-12 (1-5) x AF221558 (1-437)

Qy           1 HisAenAlaHisHis 5
Db           109 CACAACGCCACCAC 123

RESULT 48
AF221558
LOCUS        AF221558      437 bp      mRNA      linear      VRT 07-JUN-2001
DEFINITION   Gallus gallus bZIP transcription factor L-MAF mRNA, partial cds.
ACCESSION    AF221558
VERSION      AF221558.1 GI:7960155
KEYWORDS     .
SOURCE       Gallus gallus (chicken)
ORGANISM     Gallus gallus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
              Phasianinae; Gallus.
REFERENCE    1 (bases 1 to 437)
AUTHORS      Zhou,H., Liu,W. and Lamont,S.J.
TITLE        Genetic variation among chicken lines and mammalian species in
              specific genes
JOURNAL      Poult. Sci. 80 (3), 284-288 (2001)
MEDLINE      21158006
PUBMED       11261557
REFERENCE    2 (bases 1 to 437)
AUTHORS      Zhou,H. and Lamont,S.J.
TITLE        Direct Submission
JOURNAL      Submitted (06-JAN-2000) Animal Science, Iowa State University, 2255
              Kildee Hall, Ames, IA 50011, USA
FEATURES     Location/Qualifiers
             source
               1..437
               /organism="Gallus gallus"
               /mol_type="mRNA"
               /strain="breed Fayoumi"
               /db_xref="taxon:9031"
               /sex="female"
               /tissue type="spleen"
               <1..>437
               /note="MAFL"
               /codon_start=1
               /product="bZIP transcription factor L-MAF"
               /protein_id="AAF71240.1"
               /db_xref="GI:7960156"
               /translation="EALIGAPHHHHHHQSVESFRPQFPGGEELPPAAHHHNAHHHH
               HHHLRLEFRFSDQLVSMVRELNLQRLGFSKEVIRLKKRRTLKNRGYAQCRCYKR
               VQQRHILENEKCOLQSQVQLKQVSLAKERDLYKEKYEKLA"

ORIGIN
Alignment Scores:
Pred. No.:      1.14e+03      Length:      437
Score:          34.00         Matches:      5
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             5           Gaps:        0

US-10-029-756-12 (1-5) x AF221558 (1-437)

Qy           1 HisAenAlaHisHis 5
Db           109 CACAACGCCACCAC 123

RESULT 49
HPUEXPRT1/c
LOCUS        HPUEXPRT1     443 bp      DNA      linear      BCT 10-OCT-2003
DEFINITION   Helicobacter pylori ORF1 for hypothetical protein, isolate Pl-50.
ACCESSION    Z68311

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VERSION 268311.1 GI:1419554
KEYWORDS ORF1.
SOURCE Helicobacter pylori
ORGANISM Helicobacter pylori
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
Helicobacteraceae; Helicobacter.
REFERENCE 1 (bases 1 to 443)
AUTHORS Odenbreit,S., Till,M. and Haas,R.
TITLE Optimized Blam-transposon shuttle mutagenesis of Helicobacter
pylori allows the identification of novel genetic loci involved in
bacterial virulence
JOURNAL Mol. Microbiol. 20 (2), 361-373 (1996)
MEDLINE 96310373
PUBMED 8733234
REFERENCE 2 (bases 1 to 422)
AUTHORS Haas,R.
TITLE Direct Submission
JOURNAL Submitted (18-DEC-1995) Rainer Haas, Abteilung Infektionsbiologie,
Max-Planck-Institut, fuer Biologie, Spemannstr. 34, Tuebingen,
72076, GERMANY
FEATURES
source
    1..443
    /organism="Helicobacter pylori"
    /mol_type="genomic DNA"
    /strain="P1"
    /isolate="P1-50"
    /db_xref="taxon:210"
    /clone="pMu50"
    77..>443
    /function="involved in flagellar motility"
    /note="ORF1"
    /codon_start=1
    /transl_table=11
    /product="hypothetical protein"
    /protein_id="CA92653.1"
    /db_xref="GI:141955"
    /db_xref="UniProt/TREMBL:Q48273"
    /translation="MKKPKRIQSYAIVGGLSALVMSIVGCKSNADPKPEQSSLSQ
SVQKGAFVLSEQDKSVKVEEYPSSTRTHIVRDQLQGNRVLSNEEIQKLKEEAK
IDNGTSKLQVPPNGSGNESS"
CDS
    1..155+03
    /length=443
    /score=34.00
    /percent_similarity=100.00%
    /best_local_similarity=100.00%
    /query_match=100.00%
    /indels=0
    /gaps=0
    1
    /map="p22-2p21"
    /note="X01-F"
    276..409
    /gene="hypothetical BLOCK27"
    /number=1
    /evidence=not experimental
    complement(495..519)
    /note="X01-R"
ORIGIN
Alignment Scores:
Pred. No.: 1.15e+03 Length: 443
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0
US-10-029-756-12 (1-5) x HPUXPRT1 (1-443)
Qy 1 HisAenAlaHisHis 5
Db 154 CACAATGCTCACCAT 140
RESULT 50
LOCUS CQ681194 500 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 26120 from Patent WO02070737.
ACCESSION CQ681194
VERSION CQ681194.1 GI:42198347
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Liew,C.C., Marshall,W.E. and Zhang,H.
TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 26120 12-SEP-2002;
Chondrogene Inc. (CA)
FEATURES
    Location/Qualifiers
        1..155+03
        /length=500
        /score=34.00
        /percent_similarity=100.00%
        /best_local_similarity=100.00%
        /query_match=100.00%
        /indels=0
        /gaps=0
        1
        /map="p22-2p21"
        /note="X01-F"
        276..409
        /gene="hypothetical BLOCK27"
        /number=1
        /evidence=not experimental
        complement(495..519)
        /note="X01-R"
ORIGIN
Alignment Scores:
Pred. No.: 1.34e+03 Length: 519
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-10-029-756-12 (1-5) x AF449188S1 (1-519)
Qy 1 HisAenAlaHisHis 5
Db 92 CACAATGCCACCAC 78
RESULT 51
LOCUS AF449188S1 519 bp DNA linear PRI 28-MAY-2002
DEFINITION Homo sapiens hypothetical BLOCK27 gene, exon 1.
ACCESSION AF449188
VERSION AF449188.1 GI:21218162
KEYWORDS
SEGMENT 1 of 4
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 519)
AUTHORS Cortelli,J.R., Fallos,D. and Hart,T.C., Hart,P.S.,
Gorry,M.C., Zhang,Y., Marks,J.J., Suppe,B.,
Physical/Genetic Map of the 2p22-2p21 Region on Chromosome 2
Unpublished
JOURNAL
TITLE Submitted (20-NOV-2001) Oral Medicine/Pathology, University of
Pittsburgh, School of Dental Medicine, 3501 Terrace Street, 614
Salk Hall, Pittsburgh, PA 15261, USA
AUTHORS
    Location/Qualifiers
        1..519
        /organism="Homo sapiens"
        /mol_type="genomic DNA"
        /db_xref="taxon:9606"
        /chromosome="2"
        /map="2p22-2p21"
        /note="X01-F"
        276..409
        /gene="hypothetical BLOCK27"
        /number=1
        /evidence=not experimental
        complement(495..519)
        /note="X01-R"
ORIGIN
Alignment Scores:
Pred. No.: 1.34e+03 Length: 519
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-10-029-756-12 (1-5) x AF449188S1 (1-519)
Qy 1 HisAenAlaHisHis 5
Db 92 CACAATGCCACCAC 78
```

Db 46 CACAACGGCATCAC 60

RESULT 52
BD162240/c
LOCUS
DEFINITION Novel polynucleotide.
ACCESSION BD162240
VERSION BD162240.1 GI:27867997
KEYWORDS JP 2002191370-A/39.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 561)
Nakagawa, S., Mizoguchi, H., Ando, S., Hayashi, M., Ochiai, K.,
Yokoi, H., Tateishi, N., Senoh, A., Ikeda, M. and Ozaki, A.
TITLE Novel polynucleotide
JOURNAL PAT 17-JAN-2003
COMMENT OS Corynebacterium glutamicum
PN JP 2002191370-A/39
PD 09-JUL-2002
PF 15-DEC-2000 JP 2000405096
PI SATOSHI NAKAGAWA, HIROSHI MIZOGUCHI, SEIKO ANDO, MIKIO HAYASHI,
PI KEIKO OCHIAI,
PI HARUHIKO YOKOI, NAOKO TATEISHI, AKIHIRO SENOO, MASATO IKEDA, AKIO
PI OZAKI
PC C12N15/09, C12N15/09, C07K14/34, C07K16/12, C07K16/40, C12M1/00, PC
C12N1/15,
PC C12N1/19, C12N1/21, C12N5/10, C12N9/00, C12N9/02, C12P7/40, C12P13/
PC 04, C12P13/08,
PC C12P19/00, C12P19/34, C12P21/02, C12Q1/37, C12Q1/68, G01N33/53, PC
G01N33/566,
PC G01N33/569, G01N33/68, G01N37/00//C12P21/08, (C12N1/21, C12R1:15),
PC (C12N1/21, C12R1:13), (C12N1/21, C12R1:01), (C12P13/08, C12R1:15),
PC C12N5/00, C12N15/00
CC Novel polynucleotide
FH Key Location/Qualifiers
FT source 1. .561
FT /organism="Corynebacterium glutamicum".
FEATURES
source
1. .561
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

Alignment Scores:
Pred. No.: 1.44e+03 Length: 561
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x BD162240 (1-561)

Qy 1 HisAenAlaHisHis 5
|||||
Db 42 CATAACGCCCATCATC 28

RESULT 54
G88098
LOCUS
DEFINITION S209P6437RG4.T0 C3H/HeJ Mus musculus STS genomic, sequence tagged
site.
ACCESSION G88098
VERSION G88098.1 GI:22738854
KEYWORDS STS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 561)
Wade, C.
AUTHORS Polymorphism Structure in the Mouse
TITLE Unpublished (2002)
JOURNAL
COMMENT
Contact: Kerstin Lindblad-Toh
Whitehead Institute for Biomedical Research, Center for Genome
Research
320 Charles Street, Cambridge, MA 02141, USA
Tel: 6172521477
Fax: 6172580903
Email: kersli@genome.wi.mit.edu
Primer A: None
Primer B: None
STS size: 561
Protocol:
WGS-discovery: Paired-end low-coverage whole genome shotgun reads
were generated from 129S1/SvimJ C3H/HeJ, and BALB/cByJ The WGS
reads were placed uniquely on the WGS3 C57BL/6J assembly and SNP
detection was carried out by SSAHA-SNP. 225,000 reads were
annotated
as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J
and the strain from which the particular read came. The validation
rate for these SNPs was estimated at approximately 98%.

FEATURES
source
1. .561
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C3H/HeJ"
/db_xref="taxon:10090"
/map="3-22-508 48067552-48068038"
/clone_lib="C3H/HeJ"
<1..561

STS
ORIGIN

Alignment Scores:
Pred. No.: 1.44e+03 Length: 561
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x BD162240 (1-561)

Qy 1 HisAenAlaHisHis 5
|||||
Db 42 CATAACGCCCATCATC 28

RESULT 53
AX120123/c
LOCUS
DEFINITION Sequence 39 from Patent EP1108790.
ACCESSION AX120123
VERSION AX120123.1 GI:14036838
KEYWORDS
SOURCE Corynebacterium glutamicum
ORGANISM Corynebacterium glutamicum
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
REFERENCE 1

Alignment Scores:
 Pred. No.: 1.44e+03 Length: 561
 Score: 34.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0

US-10-029-756-12 (1-5) x G88098 (1-561)

Qy 1 HisaenAlaHisHis 5
 Db 206 CATATGCGCCATCAT 220

RESULT 55
 AR499461
 LOCUS AR499461 562 bp DNA linear PAT 22-SEP-2004
 DEFINITION Sequence 4421 from patent US 6703491.
 ACCESSION AR499461
 VERSION AR499461.1 GI:52434936
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.

REFERENCE 1 (bases 1 to 562)
 AUTHORS Homburger,S.A., Ebens,A.J. Jr., Erickson,C.S., Francis-Lang,H.L.,
 Margolis,J.S., Ruddy,B.P., Ruddy,D.A. and Buchman,A.R.
 TITLE Drosophila sequences
 JOURNAL Patent: US 6703491-A 4421 09-MAR-2004;
 FEATURES Location/Qualifiers
 source
 1..562
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Alignment Scores:
 Pred. No.: 1.44e+03 Length: 562
 Score: 34.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR499461 (1-562)

Qy 1 HisaenAlaHisHis 5
 Db 346 CATATGCGCCACAC 360

RESULT 56
 AR514743
 LOCUS AR514743 562 bp DNA linear PAT 22-SEP-2004
 DEFINITION Sequence 19703 from patent US 6703491.
 ACCESSION AR514743
 VERSION AR514743.1 GI:52450218
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.

REFERENCE 1 (bases 1 to 562)
 AUTHORS Homburger,S.A., Ebens,A.J. Jr., Erickson,C.S., Francis-Lang,H.L.,
 Margolis,J.S., Ruddy,B.P., Ruddy,D.A. and Buchman,A.R.
 TITLE Drosophila sequences
 JOURNAL Patent: US 6703491-A 19703 09-MAR-2004;
 FEATURES Location/Qualifiers
 source
 1..562
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Alignment Scores:
 Pred. No.: 1.44e+03 Length: 562
 Score: 34.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR514743 (1-562)

Qy 1 HisaenAlaHisHis 5
 Db 346 CATATGCGCCACAC 360

RESULT 57
 BV022000
 LOCUS BV022000 565 bp DNA linear STS 30-MAY-2003
 DEFINITION S212P6803PE1.T0 CZECHII/Ei Mus musculus STS genomic, sequence
 tagged site.
 ACCESSION BV022000
 VERSION BV022000.1 GI:31105895
 KEYWORDS STS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 565)
 Wade,C.M., Kulbokas,E.J. III, Kirby,A.W., Zody,M.C., Mullikin,J.C.,
 Lander,E.S., Lindblad-Toh,K. and Daly,M.J.
 TITLE The mosaic structure of variation in the laboratory mouse genome
 JOURNAL Nature 420 (6915), 574-578 (2002)
 MEDLINE 22354684
 PUBMED 12466852
 COMMENT

Contact: Kerstin Lindblad-Toh
 Whitehead Institute for Biomedical Research, Center for Genome
 Research
 320 Charles Street, Cambridge, MA 02141, USA
 Tel: 6172521477
 Fax: 6172580903
 Email: kersli@genome.wi.mit.edu
 Primer A: None
 Primer B: None
 STS size: 565
 Protocol:

WGS-discovery: Paired-end low-coverage whole genome shotgun reads
 were generated from 129S1/SvImJ, C3H/HeJ, and BALB/cByJ. The WGS
 reads were placed uniquely on the MGSCv3 C57BL/6J assembly and SNP
 detection was carried out by SSAHA-SNP. 225,000 reads were
 annotated
 as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J
 and the strain from which the particular read came. The validation
 rate for these SNPs was estimated at approximately 98%.

FEATURES
 source
 1..565
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="CZECHII/Ei"
 /db_xref="taxon:10090"
 /map="12 22-498 101043540-101043062"
 /clone_lib="CZECHII/Ei"
 <1..>565

STS
 ORIGIN

Alignment Scores:
 Pred. No.: 1.45e+03 Length: 565
 Score: 34.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0

US-10-029-756-12 (1-5) x BV022000 (1-565)

Qy 1 HisaenAlaHisHis 5
 Db 346 CATATGCGCCACAC 360

AUTHORS Baldwin,B.G. and Wessa,B.L.
TITLE Direct Submission
JOURNAL Submitted (20-JAN-2000) Jepson Herbarium and Department of Integrative Biology, University of California, Berkeley, 1001 Valley Life Sciences Building #2465, Berkeley, CA 94720-2465, USA

FEATURES
 source
 1..645
 /organism="Balduina uniflora"
 /mol_type="genomic DNA"
 /specimen_voucher="Urbatech 7579 (LSU, UC)"
 /db_xref="taxon:128714"
 misc_RNA
 1..259
 /product="internal transcribed spacer 1"
 rRNA
 260..423
 /product="5.8S ribosomal RNA"
 misc_RNA
 424..645
 /product="internal transcribed spacer 2"

ORIGIN
 Alignment Scores:
 Pred. No.: 1.64e+03 Length: 645
 Score: 34.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-10-029-756-12 (1-5) x AF229270 (1-645)

Qy 1 HisAenAlaHisHis 5
 |||||
Db 141 CATAATGCCCATCAT 127
 |||||

RESULT 62
HUMYR86G04/c
LOCUS HUMYR86G04 646 bp mRNA linear PRI 29-AUG-1998
DEFINITION Homo sapiens full length insert cDNA clone YR86G04.
ACCESSION AF085955
VERSION AF085955.1 GI:3483300
KEYWORDS FLI CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 646)
AUTHORS Woesner,J., Tan,F., Marra,M., Kucaba,T., Yandell,M., Martin,J., Math,G., Bowles,L., Wylie,T., Bowers,Y., Steptoe,M., Theising,B., Geisel,S., Allen,M., Underwood,K., Chappell,J., Person,B., Gibbons,M., Harvey,N., Pape,D., Chamberlain,A., Morales,R., Schurk,R., Ritter,E., Kohn,S., Swaller,T., Behymet,K., Hillier,L., Wilson,R. and Waterston,R.
TITLE Full Clone Sequencing of the Longest Available Member from Each Unigene Cluster
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 646)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (24-AUG-1998) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

COMMENT
 SUBMITTED BY: Genome Sequencing Center
 Department of Genetics
 Washington University
 St. Louis MO 63108, USA
 http://genome.wustl.edu/gsc
 mailto:est@watson.wustl.edu

NOTICE: This sequence represents the full insert of this cDNA. No attempt has been made to verify whether this corresponds to the full-length of the original mRNA from which it was derived. We have tried to obtain double-stranded, or double chemistry sequence across the entire clone, but potentially, there are areas in the sequence where this level of coverage was not achieved.

Nevertheless, we are confident of the accuracy of this sequence as all regions of low quality, as defined by PHRAP (P. Green, in preparation), were visually inspected and edited accordingly. The consensus quality values for this sequence have been submitted separately.

The location of this clone is unknown.

FEATURES
 Location/Qualifiers
 source
 1..646
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:212214"
 /clone_lib="Soares_fetal_liver_spleen_inFLS"

ORIGIN
 Alignment Scores:
 Pred. No.: 1.64e+03 Length: 646
 Score: 34.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-10-029-756-12 (1-5) x HUMYR86G04 (1-646)

Qy 1 HisAenAlaHisHis 5
 |||||
Db 91 CACATGACACACCAC 77
 |||||

RESULT 63
AJ606025/c
LOCUS AJ606025 647 bp mRNA linear PLN 05-JAN-2004
DEFINITION Triticum aestivum partial mRNA for putative integral membrane protein that regulates cation conductance (at2G03510 gene).
ACCESSION AJ606025
VERSION AJ606025.1 GI:40641592
KEYWORDS at2G03510 gene; integral membrane protein that regulates cation conductance.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Triticum.
REFERENCE 1
AUTHORS Ciaffi,M., Tanzarella,O.A., Porceddu,E., Paolacci,A.R. and d'Aloisio,E.
TITLE Identification and characterization of gene sequences expressed in wheat spikelets at the heading stage
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 647)
AUTHORS Ciaffi,M.
TITLE Direct Submission
JOURNAL Submitted (06-NOV-2003) Ciaffi M., Dipartimento Agrobiologia e Agrochimica, University of Tuscia, Via S. Camillo De Lellis, Italy 01100, ITALY

FEATURES
 Location/Qualifiers
 source
 1..647
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /cultivar="Chinese Spring"
 /db_xref="taxon:4565"
 /clone="P71A"
 /tissue_type="spike at heading stage"
 gene
 1..647
 /gene="at2G03510"
 <1..>645
 /codon_start=1
 /product="putative integral membrane protein that regulates cation conductance"
 /protein_id="CAE54276.1"
 /db_xref="GI:40641593"

/translation="TSAPSTLHVPSHVGCVYWRGGLLKTITTPGVHLKLPPITOF
EPIQVTLQTDQVKGIPCGTKGGWMISFDKIGVNRINKDPVWETLLNNGVHYDXTWLY
DKIHHEINQPCASHLSQVYIDFMDQALIAERQVAKAEATOKIALSBAEKNALV
SKILMQQMLTEKSSKRQQQIDNEMFLARERALADANYRITKEAEANKLKTPE"

ORIGIN

Alignment Scores:
Pred. No.: 1.65e+03 Length: 647
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-029-756-12 (1-5) x AJ506025 (1-647)

Qy 1 HisAsnAlaHisHis 5

Db 289 CATATGACACCAT 275

RESULT 64

AY454951

LOCUS AY454951 647 bp DNA linear PRI 21-JAN-2004
DEFINITION Alouatta caraya clone 1 olfactory receptor pseudogene, partial
sequence.

ACCESSION AY454951

VERSION AY454951.1 GI:38424539

KEYWORDS

SOURCE Alouatta caraya (black howler monkey)

ORGANISM

Alouatta caraya
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Alouattinae;
Alouatta.

REFERENCE 1 (bases 1 to 647)

AUTHORS Gilad,Y., Wiebe,V., Przeworski,M., Lancet,D. and Paabo,S.

TITLE Loss of Olfactory Receptor Genes Coincides with the Acquisition of

Full Trichromatic Vision in Primates

JOURNAL PLoS Biol. 2 (1), 0120-0125 (2004)

REFERENCE 2 (bases 1 to 647)

AUTHORS Gilad,Y., Wiebe,V., Przeworski,M., Lancet,D. and Paabo,S.

TITLE Direct Submission

JOURNAL Submitted (30-OCT-2003) Max Plank Institute for Evolutionary

Anthropology, Deutscher Platz 6, Leipzig 04103, Germany

FEATURES

source

1..647

/organism="Alouatta caraya"

/mol_type="genomic DNA"

/db_xref="taxon:9502"

/clone="1"

<1..>647

/gene="olfactory receptor"

/pseudo

ORIGIN

Alignment Scores:
Pred. No.: 1.65e+03 Length: 647
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-029-756-12 (1-5) x AY454951 (1-647)

Qy 1 HisAsnAlaHisHis 5

Db 443 CATATGCCCATCAT 457

RESULT 65

AX055282/c

LOCUS AX055282 648 bp DNA linear PAT 13-JAN-2001

DEFINITION Sequence 189 from Patent WO0073502.

ACCESSION AX055282

VERSION

AX055282.1 GI:12228586

KEYWORDS

Helicobacter sp.

SOURCE

Helicobacter sp.

ORGANISM

Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;

Helicobacteraceae; Helicobacter.

REFERENCE

1

Aufel,H., Fuchs,T.M., Gibbs,C.P., Hueck,C.J. and Meyer,T.F.

TITLE Essential gene and gene products for identifying, developing and

optimising immunological and pharmacological active ingredients for

the treatment of microbial infections

JOURNAL Patent: WO 0073502-A 189 07-DEC-2000;

Max-Planck-Gesellschaft zur Foerderung der Wissenschaften e.V. (DE)

; Creatogen GmbH (DE)

FEATURES

source

1..648

/organism="Helicobacter sp."

/mol_type="unassigned DNA"

/db_xref="taxon:218"

1..648

/notes="unnamed protein product"

/codon_start=1

/transl_table=11

/protein_id="CAC22068.1"

/db_xref="GI:12228587"

/translation="MKPYRKISDYAIVGGLSALVMVSIYCKSNADDPKEQSSLSQ

SVQKGFVILEEQDKSYKVVEYFSSRTHIIVRDLOGNERVLSNEIQKLKEEAK

IDNGTSKLQVPNKGSSSGFGLGSAIGLGAALIGSTIGNKLFPNNPYQQAQRT

YKSPQAYQRSONSFKSAPASSAMGGKSGGFFGSSRPTSPAVSSGTRGFNS"

ORIGIN

Alignment Scores:

Pred. No.: 1.65e+03 Length: 648

Score: 34.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AX055282 (1-648)

Qy 1 HisAsnAlaHisHis 5

Db 78 CACAATGCTCACCAT 64

RESULT 66

AY113693/c

LOCUS AY113693 650 bp mRNA linear VRT 03-SEP-2002

DEFINITION Oncorhynchus mykiss fructose-1,6-bisphosphatase-like mRNA, partial

sequence.

ACCESSION AY113693

VERSION AY113693.1 GI:22657376

KEYWORDS

SOURCE

ORGANISM

Oncorhynchus mykiss (rainbow trout)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei;

Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

REFERENCE 1 (bases 1 to 650)

AUTHORS Booth,H.L. and Mommsen,T.P.

TITLE Characterization of fructose-1,6-bisphosphatase in rainbow trout

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 650)

AUTHORS Booth,H.L. and Mommsen,T.P.

TITLE Direct Submission

JOURNAL Submitted (16-MAY-2002) Biochemistry and Microbiology, University

of Victoria, P.O. Box 3055, MS 7077, Victoria, BC V8W 3P6, Canada

COMMENT NCBI staff are still waiting for submitters to provide appropriate

coding region information.

FEATURES

source

1..650

/organism="Oncorhynchus mykiss"

/mol_type="mRNA"

misc_feature /db_xref=taxon:8022"
<1..650
/note="similar to fructose-1,6-bisphosphatase"

ORIGIN

Alignment Scores:
Pred. No.: 1.65e+03 Length: 650
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-029-756-12 (1-5) x AY113693 (1-650)

Qy 1 HisAsnAlaHisHis 5

Db 296 CATAACGCCACCAC 282

RESULT 67

AR273654 LOCUS linear PAT 10-APR-2003

DEFINITION Sequence 1397 from patent US 6504010.

ACCESSION AR273654

VERSION AR273654.1 GI:29705539

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 653)

AUTHORS Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S., Carter, D., Retter, M.W., Mannion, J., and Fan, L.
TITLE Compositions and methods for the therapy and diagnosis of lung cancer

JOURNAL Patent: US 6504010-A 1397 07-JAN-2003;

FEATURES

source

Location/Qualifiers

1..653

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 1.66e+03 Length: 653
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR273654 (1-653)

Qy 1 HisAsnAlaHisHis 5

Db 448 CACAATGCCACCAC 462

RESULT 68

AR277235 LOCUS linear PAT 10-APR-2003

DEFINITION Sequence 1397 from patent US 6509448.

ACCESSION AR277235

VERSION AR277235.1 GI:29710882

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 653)

AUTHORS Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S., Carter, D., Retter, M.W., Mannion, J., Fan, L. and Wang, A.
TITLE Compositions and methods for the therapy and diagnosis of lung cancer

JOURNAL Patent: US 6509448-A 1397 21-JAN-2003;

FEATURES

Location/Qualifiers

1..653

source

1..653

/organism="unknown"

/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 1.66e+03 Length: 653
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR277235 (1-653)

Qy 1 HisAsnAlaHisHis 5

Db 448 CACAATGCCACCAC 462

RESULT 69

AR407510 LOCUS linear PAT 18-DEC-2003

DEFINITION Sequence 1397 from patent US 6630574.

ACCESSION AR407510

VERSION AR407510.1 GI:40157321

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 653)

AUTHORS Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S., Carter, D., Retter, M.W., Mannion, J. and Fan, L.
TITLE Compositions and methods for the therapy and diagnosis of lung cancer

JOURNAL Patent: US 6630574-A 1397 07-OCT-2003;

FEATURES

source

Location/Qualifiers

1..653

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 1.66e+03 Length: 653
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR407510 (1-653)

Qy 1 HisAsnAlaHisHis 5

Db 448 CACAATGCCACCAC 462

RESULT 70

AR441360 LOCUS linear PAT 20-FEB-2004

DEFINITION Sequence 1397 from patent US 6667154.

ACCESSION AR441360

VERSION AR441360.1 GI:42667520

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 653)

AUTHORS Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S., Carter, D., Retter, M.W., Mannion, J. and Fan, L.
TITLE Compositions and methods for the therapy and diagnosis of lung cancer

JOURNAL Patent: US 6667154-A 1397 23-DEC-2003;

FEATURES

Location/Qualifiers

1..653

source

1..653

/organism="unknown"

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/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 1.66e+03 Length: 653
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-029-756-12 (1-5) x AR441360 (1-653)
Qy 1 HisAenAlaHisHis 5
Db 448 CACAATGCCACCAC 462
RESULT 71
LOCUS AR544171 653 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 1397 from patent US 6746846.
ACCESSION AR544171
VERSION AR544171.1 GI:53936847
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 653)
AUTHORS Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S.,
Carter, D., Retter, M.W., Mannion, J. and Fan, L.
TITLE Methods for diagnosing lung cancer
JOURNAL Patent: US 6746846-A 1397 08-JUN-2004;
FEATURES
source
1. .653
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 1.66e+03 Length: 653
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-029-756-12 (1-5) x AR544171 (1-653)
Qy 1 HisAenAlaHisHis 5
Db 448 CACAATGCCACCAC 462
RESULT 72
LOCUS AX368687 653 bp DNA linear PAT 16-FEB-2002
DEFINITION Sequence 1397 from Patent WO0204514.
ACCESSION AX368687
VERSION AX368687.1 GI:18856760
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
1
AUTHORS Wang, T., Watanabe, Y., Henderson, R.A., Johnson, J.C., Retter, M.W.,
Marnerakis, M., Carter, D., Fanger, G.R., Vedvick, T.S., Bangur, C.S.,
McNabb, A., Fanger, N., Switzer, A., McNeill, P.D. and Clapper, J.D.
TITLE Compositions and methods for the therapy and diagnosis of lung
cancer
JOURNAL Patent: WO 0204514-A 1397 17-JAN-2002;
CORIXA CORPORATION (US)
FEATURES
source
1. .653
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 1.66e+03 Length: 653
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-029-756-12 (1-5) x AX368687 (1-653)
Qy 1 HisAenAlaHisHis 5
Db 448 CACAATGCCACCAC 462
RESULT 73
LOCUS AY329324 662 bp DNA linear PLN 30-JUN-2004
DEFINITION Alternaria alternata strain EGS34-016 vacuolar membrane ATPase
catalytic subunit A (vmaA) gene, partial cds; and vmaA-vpsA
intergenic spacer, partial sequence.
ACCESSION AY329324
VERSION AY329324.1 GI:37594436
KEYWORDS
SOURCE
ORGANISM Alternaria alternata
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Alternaria;
Alternaria alternata group.
REFERENCE
1 (bases 1 to 662)
AUTHORS Inderbitzin, P. and Berbee, M.L.
TITLE Mating type gene evolution in Pleospora, the sexual state of
Stemphylium
JOURNAL Unpublished
AUTHORS Inderbitzin, P. and Berbee, M.L.
TITLE Direct Submission
JOURNAL Submitted (24-JUN-2003) Department of Botany, University of British
Columbia, #3529-6270 University Blvd., Vancouver, British Columbia
V6T1Z4, Canada
FEATURES
source
1. .662
/organism="Alternaria alternata"
/mol_type="genomic DNA"
/strain="EGS34-016"
/db_xref="taxon:5599"
<1..>39
/gene="vmaA"
/mRNA <1..>39
/gene="vmaA"
/CDs <1..>39
/product="vacuolar membrane ATPase catalytic subunit A"
/gene="vmaA"
/notes="similar to Aspergillus oryzae vmaA sequence in
Genbank Accession Number AB073302"
/codon_start=1
/product="vacuolar membrane ATPase catalytic subunit A"
/protein_id="AAQ94178.1"
/db_xref="GI:37594437"
/translation="GKLSQLLSYKC"
40..>662
/notes="vmaA-vpsA intergenic spacer"
misc_feature
ORIGIN
Alignment Scores:
Pred. No.: 1.68e+03 Length: 662
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-029-756-12 (1-5) x AY329324 (1-662)

QY 1 HisAenAlaHis 5
DB 241 CACAATGCCCATCAT 255

RESULT 74

LOCUS CQ715174/c 666 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 1108 from Patent WO02068579.

ACCESSION CQ715174

VERSION CQ715174.1 GI:42276031

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.

TITLE Kites, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof

JOURNAL

Patent: WO 02068579-A 1108 06-SEP-2002;

PE Corporation (NY) (US)

FEATURES

source Location/Qualifiers

1..666

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 1.69e+03 Length: 666
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x CQ715174 (1-666)

QY 1 HisAenAlaHis 5

DB 525 CACAATGCCCATCAT 511

RESULT 75

AY454977

LOCUS

DEFINITION Trachypithecus auratus clone 10 olfactory receptor pseudogene, partial sequence.

ACCESSION

AY454977.1 GI:38424583

VERSION

KEYWORDS

SOURCE

Trachypithecus auratus (Javan langur)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae; Trachypithecus.

REFERENCE

AUTHORS Gilad, Y., Wiebe, V., Przeworski, M., Lancet, D. and Paabo, S.

TITLE Loss of Olfactory Receptor Genes Coincides with the Acquisition of Full Trichromatic Vision in Primates

JOURNAL PLOS Biol. 2 (1), 0120-0125 (2004)

REFERENCE

AUTHORS Gilad, Y., Wiebe, V., Przeworski, M., Lancet, D. and Paabo, S.

TITLE Direct Submission

JOURNAL Submitted (30-OCT-2003) Max Planck Institute for Evolutionary

Anthropology, Deutscher Platz 6, Leipzig 04103, Germany

FEATURES

source Location/Qualifiers

1..675

/organism="Trachypithecus auratus"
/mol_type="genomic DNA"
/db_xref="taxon:222416"
/clone="10"
<1..>675
/gene="olfactory receptor"
/pseudo

gene

ORIGIN

Alignment Scores:

Pred. No.: 1.71e+03 Length: 675
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-029-756-12 (1-5) x AY454977 (1-675)

QY 1 HisAenAlaHis 5

DB 40 CACAATGCCCATCAC 54

RESULT 76

LOCUS CQ610128/c

DEFINITION Sequence 37886 from Patent WO0171042.

ACCESSION CQ610128

VERSION CQ610128.1 GI:41662065

KEYWORDS

SOURCE

ORGANISM

Drosophila sp.

Drosophila sp.

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

AUTHORS

TITLE

Detection kits, such as nucleic acid arrays, for detecting the expression of 10,000 or more Drosophila genes and uses thereof

JOURNAL

Patent: WO 0171042-A 37886 27-SEP-2001;

PE Corporation (NY) (US)

FEATURES

source Location/Qualifiers

1..679

/organism="Drosophila sp."

/mol_type="unassigned DNA"

/db_xref="taxon:7242"

ORIGIN

Alignment Scores:
Pred. No.: 1.72e+03 Length: 679
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x CQ610128 (1-679)

QY 1 HisAenAlaHis 5

DB 559 CACAATGCCCATCAC 545

RESULT 77

LOCUS BD010644/c

DEFINITION Helicobacter polypeptides and corresponding polynucleotide

moles.

ACCESSION BD010644

VERSION BD010644.1 GI:18639017

KEYWORDS JP 2001503637-A/82.

SOURCE unidentified

ORGANISM

unclassified.

unclassified.

```

REFERENCE 1 (bases 1 to 686)
AUTHORS Haas,R., Kleanthous,H., Tomb,J.F., Miller,C., Garawi,A.A.,
Odenbreit,S. and Meyer,T.
TITLE Helicobacter polypeptides and corresponding polynucleotide
molecules
JOURNAL Patent: JP 2001503637-A 82 21-MAR-2001;
MERIEUX ORAVAX, MAX PLANCK GESELLSCHAFT ZUR FORDERUNG DER
WISSENSCHAFTEN EV BERLIN, HUMAN GENOME SCIENCES INC
COMMENT OS Unidentified
PN JP 2001503637-A/82
PD 21-MAR-2001
PR 14-NOV-1997 JP 1998522949
PR 14-NOV-1996 US 08/749051,01-APR-1997 US 08/831309 PR
01-APR-1997 US 08/834705,01-APR-1997 US 08/833457 PR
24-JUN-1997 US 08/881227,29-JUL-1997 US 08/902615 PI RAINER
HAAS,HAROLD KLEANTHOS,JEAN FRANCOIS TOMB, PI CHARLES MILLER,
PI AMAL AL GARAWI,STEFAN ODENBREIT,THOMAS MEYER
PC C07H21/02,C07K1/00,A61K39/02,A01N37/18
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers
FT source 1..686
FT /organism="Unidentified".
FT /mol_type="genomic DNA"
FT /db_xref="taxon:32644"
FEATURES source
source 1..686
ORIGIN
Alignment Scores:
Pred. No.: 1.74e+03 Length: 686
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-029-756-12 (1-5) x BD010644 (1-686)
Qy 1 HisenAlaHis 5
Db 93 CACAATGCTCACCAT 79
RESULT 78
BD092839/c
LOCUS BD092839 686 bp DNA linear PAT 27-AUG-2002
DEFINITION Identification of polynucleotides encoding novel helicobacter
polypeptides in the helicobacter genome.
ACCESSION BD092839
VERSION BD092839.1 GI:22638450
KEYWORDS JP 2001527393-A/620.
SOURCE synthetic construct
ORGANISM other sequences: artificial sequences.
1 (bases 1 to 686)
REFERENCE Kleanthous,H., Garawi,A.A., Miller,C., Tomb,J.F. and Oomen,R.P.
AUTHORS Identification of polynucleotides encoding novel helicobacter
TITLE polypeptides in the helicobacter genome
JOURNAL Patent: JP 2001527393-A 620 25-DEC-2001;
MERIEUX ORAVAX SOCIETE EN NOM COLLECTIF PASTEUR MERIEUX SERUMS ET
VACCINS AGROBIOLOGICAL RESOURCES MINISTRY O SA, HUMAN GENOME
SCIENCES INC
COMMENT PN JP 2001527393-A/620
PD 25-DEC-2001
PF 01-APR-1998 JP 1998541947
PR 01-APR-1997 US 08/833457,24-JUN-1997 US 08/881227 PR
29-JUL-1997 US 08/902615
PI HAROLD KLEANTHOS,AMAL AL GARAWI,CHARLES MILLER,JEAN FRANCOIS
TOMB,
PI RAYMOND PETER OOMEN
PC A01N43/04,A61K31/70
CC Strandedness: Single;

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CC Topology: Linear;
FH Key Location/Qualifiers.
FEATURES source
source 1..686
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Alignment Scores:
Pred. No.: 1.74e+03 Length: 686
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-029-756-12 (1-5) x BD092839 (1-686)
Qy 1 HisenAlaHis 5
Db 93 CACAATGCTCACCAT 79
RESULT 79
AX414104/c
LOCUS AX414104 713 bp DNA linear PAT 02-SEP-2002
DEFINITION Sequence 1095 from Patent WO0228891.
ACCESSION AX414104
VERSION AX414104.1 GI:21446561
KEYWORDS Listeria monocytogenes ATCC 19115
SOURCE Listeria monocytogenes ATCC 19115
ORGANISM Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
REFERENCE 1
AUTHORS Kunst,F. and Glaser,P.
TITLE Listeria innocua, genome and applications
JOURNAL Patent: WO 0228891-A 1095 11-APR-2002;
INSTITUT PASTEUR (FR) ; CENTRE NATIONAL DE LA RECHERCHE
SCIENTIFIQUE (CNRS) (FR)
FEATURES source
source 1..713
/organism="Listeria monocytogenes ATCC 19115"
/mol_type="unassigned DNA"
/db_xref="taxon:176281"
ORIGIN
Alignment Scores:
Pred. No.: 1.8e+03 Length: 713
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-029-756-12 (1-5) x AX414104 (1-713)
Qy 1 HisenAlaHis 5
Db 407 CATAATGCACACCAC 393
RESULT 80
PM7E2G/c
LOCUS PM7E2G 723 bp DNA linear STS 29-MAY-2003
DEFINITION Penicillium marneffeii STS, clone pm7e2.g, sequence tagged site.
ACCESSION AL685153
VERSION AL685153.1 GI:19336504
KEYWORDS STS.
SOURCE Penicillium marneffeii
ORGANISM Penicillium marneffeii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
REFERENCE 1
AUTHORS Yuen,K.Y., Pascal,G., Wong,S.S., Glaser,P., Woo,P.C., Kunst,F.,

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Cai, J.J., Cheung, E.Y., Medigue, C. and Danchin, A.
 Exploring the Penicillium marneffei genome
 Arch. Microbiol. 179 (5), 339-353 (2003)
 MEDLINE 22595073
 PUBMED 12640520
 REFERENCE 2 (bases 1 to 723)
 AUTHORS Danchin, A. and Pascal, G.
 TITLE Direct Submission
 JOURNAL Submitted (08-MAR-2002) Danchin A., HKU-Pasteur Research Centre,
 Dexter HC Man Building 8, Sassoon Road, Pokfulam, Hong Kong
 FEATURES
 Location/Qualifiers
 source
 1..723
 /organism="Penicillium marneffei"
 /mol_type="genomic DNA"
 /db_xref="taxon:3772"
 /clone="pm7e2.g"

ORIGIN

Alignment Scores:
 Pred. No.: 1.83e+03 Length: 723
 Score: 34.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0
 US-10-029-756-12 (1-5) x PM7E2G (1-723)
 Qy 1 HisAenAlaHisHis 5
 Db 393 CACAATGCTCATCAT 379
 RESULT 81
 AF352352/c
 LOCUS AF352352 741 bp DNA linear PLN 12-APR-2002
 DEFINITION Cryptoperidinopsoid sp. clone V14 ChrVIMS14ITS1_3_6_12 internal
 transcribed spacer 1, 5.8S ribosomal RNA gene and internal
 transcribed spacer 2, complete sequence; and large subunit
 ribosomal RNA gene, partial sequence.

ACCESSION AF352352
 VERSION AF352352.1 GI:18462188

KEYWORDS cryptoperidinopsoid sp. clone V14
 SOURCE cryptoperidinopsoid sp. clone V14
 ORGANISM Eukaryota; Alveolata; Dinophyceae; unclassified Dinophyceae.

REFERENCE 1 (bases 1 to 741)
 AUTHORS Litaker, R.W., Reece, K.S., Stokes, N.A., Yonish, B.A., Vandersea, M.W.,
 Steidinger, K., and Tester, P.A.
 TITLE Genetic Variability in Dinoflagellate ITS Regions: Implications for
 species identification and phylogenetic analysis

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 741)
 AUTHORS Reece, K.S. and Stokes, N.A.
 TITLE Direct Submission
 JOURNAL Submitted (21-FEB-2001) Molecular Biology and Biotechnology,
 University of North Carolina at Chapel Hill, 442 Taylor Hall, CB
 7100, Chapel Hill, NC 27599, USA

FEATURES

source
 1..741
 /organism="cryptoperidinopsoid sp. clone V14"
 /mol_type="genomic DNA"
 /db_xref="taxon:155772"
 /clone="ChrVIMS14ITS1_3_6_12"
 /country="USA: Great Wicomico River, Virginia"
 /note="isolated in 1998"
 1..262
 /product="internal transcribed spacer 1"
 /note="ITS1"
 263..421
 /product="5.8S ribosomal RNA"
 422..716
 /product="internal transcribed spacer 2"
 /note="ITS2"
 misc_RNA
 rRNA
 misc_RNA

rRNA 717..5741
 /product="large subunit ribosomal RNA"

ORIGIN

Alignment Scores:
 Pred. No.: 1.87e+03 Length: 741
 Score: 34.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-10-029-756-12 (1-5) x AF352352 (1-741)

Qy 1 HisAenAlaHisHis 5

Db 333 CACAATGCTCATCAC 319

RESULT 82

AR253310
 LOCUS AR253310 824 bp DNA linear PAT 20-DEC-2002
 DEFINITION Sequence 56 from patent US 6479258.
 ACCESSION AR253310
 VERSION AR253310.1 GI:27301733

KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 824)

AUTHORS Short, J.M.

TITLE Non-stochastic generation of genetic vaccines

JOURNAL Patent: US 6479258-A 56 12-NOV-2002;

FEATURES Location/Qualifiers

source
 1..824
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Alignment Scores:
 Pred. No.: 2.06e+03 Length: 824
 Score: 34.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-10-029-756-12 (1-5) x AR253310 (1-824)

Qy 1 HisAenAlaHisHis 5

Db 523 CACAATGCCACCAC 537

RESULT 83

BD131771
 LOCUS BD131771 824 bp DNA linear PAT 18-SEP-2002
 DEFINITION Genetic vaccine vector engineering.
 ACCESSION BD131771
 VERSION BD131771.1 GI:23226716

KEYWORDS JP 2002503461-A/5.
 SOURCE Human herpesvirus 5

ORGANISM Human herpesvirus 5

REFERENCE 1 (bases 1 to 824)

AUTHORS Punnonen, J., Stemmer, W.P.C., Whalen, R.G. and Howard, R.

TITLE Genetic vaccine vector engineering

JOURNAL Patent: JP 2002503461-A 5 05-FEB-2002;

COMMENT MAXYGEN INC

OS Human cytomegalovirus

PN JP 2002503461-A/5

PD 05-FEB-2002

PF 10-FEB-1999 JP 2000531550

PR 11-FEB-1998 US 60/074294, 11-FEB-1998 US 09/021769 PI

JUHA PUNNONEN, WILLEM P C STEMMER, ROBERT GERALD WHALEN, RUSSELL PI
 HOWARD
 PC C12N15/09, A61K39/00, A61K48/00, A61P11/06, A61P29/00, A61P31/00,
 A61P35/00,
 PC A61P37/06, A61P37/08, A61K35/76, C12N15/00
 CC Intron A from human cytomegalovirus (CMV) AD169 strain FH
 Key Location/Qualifiers
 FT intron (1)..(824).

FEATURES
 source
 1..824
 /organism="Human herpesvirus 5"
 /mol_type="genomic DNA"
 /db_xref="taxon:10359"

ORIGIN

Alignment Scores:
 Pred. No.: 2.06e+03 Length: 824
 Score: 34.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x BD131771 (1-824)

Qy 1 HisAsnAlaHisHis 5
 Db 523 CACAATGCCACCCAC 537

RESULT 84

BD147586 826 bp DNA linear PAT 17-JAN-2003
 LOCUS
 DEFINITION Primer for synthesizing full-length cDNA and use thereof.
 ACCESSION BD147586
 VERSION BD147586.1 GI:27853344
 KEYWORDS JP 2002191363-A/2429.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J., Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
 TITLE Primer for synthesizing full-length cDNA and use thereof
 JOURNAL Patent: JP 2002191363-A 2429 09-JUL-2002;
 COMMENT HELIX RESEARCH INSTITUTE
 OS Homo sapiens (human)
 PN JP 2002191363-A/2429
 PD 09-JUL-2002
 PF 28-JUL-2000 JP 2000280990
 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
 PI SAITO,
 PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
 PI KEIICHI NAGAI, TETSUJI OTSUKI
 PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N5/02, C12Q1/68, C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
 Primer for synthesizing full-length cDNA and use thereof FH Key

FT source Location/Qualifiers
 FT 1..826
 /organism="Homo sapiens (human)"
 /db_xref="taxon:10359"

ORIGIN

Alignment Scores:
 Pred. No.: 2.07e+03 Length: 826
 Score: 34.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x BD147586 (1-826)

Qy 1 HisAsnAlaHisHis 5
 Db 447 CACAATGCCACCCAC 461

RESULT 85

AX867524 826 bp DNA linear PAT 17-DEC-2003
 LOCUS
 DEFINITION Sequence 2429 from Patent EP1074617.
 ACCESSION AX867524
 VERSION AX867524.1 GI:40022387
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J., Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
 TITLE Primers for synthesizing full-length cDNA and their use
 JOURNAL Patent: EP 1074617-A 2429 07-FEB-2001;
 RESEARCH Association for Biotechnology (JP)
 FEATURES Location/Qualifiers
 source 1..826
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
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ORIGIN

Alignment Scores:
 Pred. No.: 2.07e+03 Length: 826
 Score: 34.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AX867524 (1-826)

Qy 1 HisAsnAlaHisHis 5
 Db 447 CACAATGCCACCCAC 461

RESULT 86

AX451702 838 bp DNA linear PAT 03-JUL-2002
 LOCUS
 DEFINITION Sequence 1 from Patent WO0231137.
 ACCESSION AX451702
 VERSION AX451702.1 GI:21698617
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct

REFERENCE
 AUTHORS Thudium, K., Selby, M. and Ulmer, J.
 TITLE Cytomegalovirus intron a fragments
 JOURNAL Patent: WO 0231137-A 1 18-APR-2002;
 CHIRON CORPORATION (US)
 FEATURES Location/Qualifiers
 source 1..838
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="full length intron A"

ORIGIN

Alignment Scores:
 Pred. No.: 2.1e+03 Length: 838

Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AX451702 (1-838)

Qy 1 HisAenAlaHisHis 5
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Db 523 CACAATGCCACCAC 537

RESULT 87
BV208715/c
LOCUS
DEFINITION NRXN2 1011 Rhesus macaque genomic DNA Macaca mulatta STS 01-JUL-2004
ACCESSION BV208715
VERSION BV208715.1 GI:49533398
KEYWORDS STS.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM
Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Macaca.
1 (bases 1 to 847)
Spindel, E.R., Pauley, M., Jia, Y., Boyle, N., Jiang, S., Gravett, C.,
Lupo, S.L., Ali, H., Ojeda, S.R. and Norgren, R.B.
Targeted amplification of the 3' end of rhesus macaque orthologs of
human genes
human genes
Unpublished (2004)

Contact: Spindel ER
Division of Neuroscience
Oregon National Primate Research Center
505 NW 185th Avenue, Beaverton, OR 97006, USA
Tel: 403-690-5388
Fax: 503-690-5384
Email: spindel@ohsu.edu
Primer A: aacctcaggacagatgg
Primer B: cagtggacatttacaacac
STS size: 847
PCR Profile:
Hot Start: 95 degrees C for 2.00 min
Denaturation: 95 degrees C for 0.50 min
Annealing: 48 degrees C for 0.50 min
Polymerization: 72 degrees C for 1.00 min
PCR Cycles: 35
Extension: 72 degrees C for 7.0 min
Thermal Cycler: MJ Instruments PTC100

Protocol:
Template: 200 ng
Primer: each 1uM
dNTP's: each 200 uM
Tag Polymerase: 0.05 units/ul (Fast Start High Fidelity, Roche)
Total Vol: 50 ul

Buffer: MgCl2: 1.8 mM
Fast Start polymerase reaction buffer (Roche)

Bases 1-847 are 98% homologous (Blast) to bases 1999-2844 of NM_138734.1. Primers were chosen to amplify genomic DNA in the 3' region of NRXN2. As human sequence was used to design the primers, the primer sequences are not included in the rhesus sequence provided below. To obtain additional information regarding primers or clones contact: Dr. Robert Norgren; Dept of Genetics, Cell Biology & Anatomy; University of Nebraska Medical Center; 986395 Nebraska Medical Center; Omaha, NE 68198. Email: rnorgren@unmc.edu
A database containing sequences associated with this project can be found at: <http://rhesusgenomechip.unomaha.edu/index.html>.

FEATURES
source
Location/Qualifiers
1..847
/organism="Macaca mulatta"
/mol_type="genomic DNA"
/strain="Indian origin"
/db_xref="taxon:9544"
/clone="MMA1011"
/clone_lib="Rhesus macaque genomic DNA"
/dev_stage="Adult"
/note="Organ: Liver; Vector: pGEM-T Easy; V-type: Plasmid; cDNA amplified from rhesus genomic DNA with the human forward and reverse primers listed above and subcloned into pGEM-T Easy-"
1..847
/gene="NRXN2"
/note="neurexin 2"
<1..>847
/gene="NRXN2"

gene
STS
ORIGIN

Alignment Scores:
Pred. No.: 2.12e+03 Length: 847
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-10-029-756-12 (1-5) x BV208715 (1-847)

Qy 1 HisAenAlaHisHis 5
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Db 304 CACAATGCCACCAC 290

RESULT 88
AR508033
LOCUS
DEFINITION Sequence 12993 from patent US 6703491.
ACCESSION AR508033
VERSION AR508033.1 GI:52443508
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 881)
Homburger, S.A., Ebens, A.J. Jr., Erickson, C.S., Francis-Lang, H.L., Margolis, J.S., Reddy, B.P., Ruddy, D.A. and Buchman, A.R.
Drosophila sequences
Patent: US 6703491-A 12993 09-MAR-2004;
Location/Qualifiers
1..881
/source
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 2.2e+03 Length: 881
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x AR508033 (1-881)

Qy 1 HisAenAlaHisHis 5
|||||

Db 858 CACAATGCCACCAC 872

RESULT 89
AX790445/c
LOCUS
DEFINITION Sequence 2909 from Patent WO02066501.
895 bp DNA
linear PAT 17-JUL-2003

```

ACCESSION   AX790445
VERSION     AX790445.1  GI:32956066
SOURCE      Helicobacter pylori
ORGANISM    Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
            Helicobacteraceae; Helicobacter.
REFERENCE   1
AUTHORS     Legrain, P., Rain, J.C., Colland, F., de Reuse, H. and Labigne, A.
TITLE       Protein-protein interactions in Helicobacter pylori
JOURNAL     Patent: WO 0206501-A 2909 29-AUG-2002;
            Hybrigenics (FR) ; INSTITUT PASTEUR (FR)
FEATURES    Location/Qualifiers
             source          1..895
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ORIGIN
Alignment Scores:  2.23e+03  Length: 895
Pred. No.:        34.00     Matches: 5
Score:            100.00%    Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match:      100.00%   Gaps: 0
DB:               6
US-10-029-756-12 (1-5) x AX790445 (1-895)
Oy          1 HisAsnAlaHisHis 5
Db          881 CACAATGCTCACCAT 867
RESULT 90
CNS01BZ5   900 bp  mRNA  linear  PLN 20-MAR-2004
LOCUS      Botrytis cinerea strain T4 cDNA library.
ACCESSION  AL114873
VERSION    AL114873.1  GI:5829492
KEYWORDS   cDNA library; EST; nitrate deprivation.
SOURCE     Botryotinia fuckeliana
ORGANISM   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
            Helotiales; Sclerotiniaceae; Botryotinia.
REFERENCE   1 (bases 1 to 900)
AUTHORS     Bitton, F., Lewis, C., Fortini, D., Pradier, J.M. and Brygoo, Y.
TITLE       Direct Submission
JOURNAL     Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr,
            78026 Versailles, France
REFERENCE   2 (bases 1 to 900)
AUTHORS     Genoscope.
TITLE       Direct Submission
JOURNAL     Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage :
            CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
            - Web : www.genoscope.cns.fr)
COMMENT     The cDNA library was made by using Botrytis cinerea T4 strain grown
            under nitrate deprivation conditions. The cDNA were cloned
            directionally in the pBSII vector.
            Location/Qualifiers
             source          1..900
                           /organism="Botryotinia fuckeliana"
                           /mol_type="mRNA"
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                           /db_xref="taxon:40559"
                           /note="Genoscope sequence ID : W11H121"
FEATURES    Location/Qualifiers
             source          1..900
                           /organism="Botryotinia fuckeliana"
                           /mol_type="mRNA"
                           /strain="T4"
                           /db_xref="taxon:40559"
                           /note="Genoscope sequence ID : W11H121"
ORIGIN
Alignment Scores:  2.24e+03  Length: 900
Pred. No.:        34.00     Matches: 5
Score:            100.00%    Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match:      100.00%   Gaps: 0

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DB:          8  Gaps: 0
US-10-029-756-12 (1-5) x CNS01BZ5 (1-900)
Oy          1 HisAsnAlaHisHis 5
Db          241 CACAACGCACACCAC 255
RESULT 91
AY061549/c 922 bp  mRNA  linear  INV 22-JAN-2003
LOCUS      Drosophila melanogaster LP07806 full insert cDNA.
DEFINITION AY061549
ACCESSION  AY061549
VERSION    AY061549.1  GI:16769755
KEYWORDS   FLY_CDNA.
SOURCE     Drosophila melanogaster (fruit fly)
ORGANISM   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1 (bases 1 to 922)
AUTHORS     Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
            Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R.,
            Gonzalez, M., Guarin, H., Li, P., Liao, G., Miranda, A., Mungall, C.J.,
            Nunoo, J., Pacleb, J., Paragas, V., Park, S., Phouanavong, S., Wan, K.,
            Yu, C., Lewis, S.E., Rubin, G.M. and Celniker, S.
TITLE       Direct Submission
JOURNAL     Submitted (30-OCT-2001) Berkeley Drosophila Genome Project,
            Lawrence Berkeley National Laboratory, One Cyclotron Road,
            Berkeley, CA 94720, USA
REFERENCE   2 (bases 1 to 922)
AUTHORS     Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
            Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E.,
            George, R., Gonzalez, M., Guarin, H., Krommiller, B., Li, P., Liao, G.,
            Miranda, A., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,
            Patel, S., Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin, G.M.
            and Celniker, S.
TITLE       Direct Submission
JOURNAL     Submitted (22-JAN-2003) Berkeley Drosophila Genome Project,
            Lawrence Berkeley National Laboratory, One Cyclotron Road,
            Berkeley, CA 94720, USA
COMMENT     Sequence submitted by:
            Lawrence Berkeley National Laboratory
            Berkeley Drosophila Genome Project
            Berkeley, CA 94720
            This clone was sequenced as part of a high-throughput process to
            sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
            Science 2000). The sequence has been subjected to integrity checks
            for sequence accuracy, presence of a polyA tail and contiguity
            within 100 kb in the genome. Thus we believe the sequence to
            reflect accurately this particular cDNA clone. However, there are
            artifacts associated with the generation of cDNA clones that may
            have not been detected in our initial analyses such as internal
            priming, priming from contaminating genomic DNA, retained introns
            due to reverse transcription of unspliced precursor RNAs, and
            reverse transcriptase errors that result in single base changes.
            For further information about this sequence, including its location
            and relationship to other sequences, please visit our Web site
            (http://fruitfly.berkeley.edu) or send email to
            cdna@fruitfly.berkeley.edu.
            Location/Qualifiers
             source          1..922
                           /organism="Drosophila melanogaster"
                           /mol_type="mRNA"
                           /strain="Y; cn bw sp"
                           /db_xref="taxon:7227"
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                           /db_xref="FLYBASE:FBgn0000640"
                           /note="Longest ORF"
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FEATURES    Location/Qualifiers
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                           /db_xref="taxon:7227"
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/product="LP07806p"
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PFRSGMDKMIYQKTGVFMAMCPGLTNSMTMNLTRDNTVTHHSSMVEATESAKRQMP
EEAAMQIMHMEMKNGSNWIVSMGQLKEVTPFTWQW"

ORIGIN
Alignment Scores:
Pred. No.: 2.29e+03 Length: 922
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x AY061549 (1-922)

QY 1 HisAsnAlaHis 5
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Db 174 CACAATGCCATCAT 160

RESULT 92
HSA324083 948 bp DNA linear PRI 18-JUL-2002
LOCUS Homo sapiens genomic sequence surrounding NotI site, clone
DEFINITION NLI-VL24C.
ACCESSION AJ324083
VERSION AJ324083.1 GI:15868462
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 948)
AUTHORS Kutsenko, A.S., Gizatullin, R.Z., Al-Amin, A.N., Wang, F., Kvasha, S.M.,
Podowski, R.M., Matuehkin, Y.G., Gvanchandani, A., Muravenko, O.V.,
Levitsky, V.G., Kolchanov, N.A., Protodopov, A.I., Kashuba, V.I.,
Kiselev, L.L., Wasserman, W., Wahlstedt, C. and Zabarovsky, E.R.
NOTI flanking sequences: a tool for gene discovery and verification
of the human genome
TITLE Nucleic Acids Res. 30 (14), 3163-3170 (2002)
JOURNAL Nucleic Acids Res. 30 (14), 3163-3170 (2002)
MEDLINE 22131767
PubMed 12136098
REFERENCE 2 (bases 1 to 948)
AUTHORS Zabarovsky, E.R.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
Sweden

FEATURES
Location/Qualifiers
source 1..948
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="NLI-VL24C"

ORIGIN
Alignment Scores:
Pred. No.: 2.35e+03 Length: 948
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-029-756-12 (1-5) x HSA324083 (1-948)

QY 1 HisAsnAlaHis 5
|||||
Db 174 CACAATGCCATCAT 160

RESULT 92
HSA324083 948 bp DNA linear PRI 18-JUL-2002
LOCUS Homo sapiens genomic sequence surrounding NotI site, clone
DEFINITION NLI-VL24C.
ACCESSION AJ324083
VERSION AJ324083.1 GI:15868462
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 948)
AUTHORS Kutsenko, A.S., Gizatullin, R.Z., Al-Amin, A.N., Wang, F., Kvasha, S.M.,
Podowski, R.M., Matuehkin, Y.G., Gvanchandani, A., Muravenko, O.V.,
Levitsky, V.G., Kolchanov, N.A., Protodopov, A.I., Kashuba, V.I.,
Kiselev, L.L., Wasserman, W., Wahlstedt, C. and Zabarovsky, E.R.
NOTI flanking sequences: a tool for gene discovery and verification
of the human genome
TITLE Nucleic Acids Res. 30 (14), 3163-3170 (2002)
JOURNAL Nucleic Acids Res. 30 (14), 3163-3170 (2002)
MEDLINE 22131767
PubMed 12136098
REFERENCE 2 (bases 1 to 948)
AUTHORS Zabarovsky, E.R.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
Sweden

FEATURES
Location/Qualifiers
source 1..948
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="NLI-VL24C"

ORIGIN
Alignment Scores:
Pred. No.: 2.35e+03 Length: 948
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-029-756-12 (1-5) x HSA324083 (1-948)

QY 1 HisAsnAlaHis 5
|||||
Db 174 CACAATGCCATCAT 160

RESULT 92
HSA324083 948 bp DNA linear PRI 18-JUL-2002
LOCUS Homo sapiens genomic sequence surrounding NotI site, clone
DEFINITION NLI-VL24C.
ACCESSION AJ324083
VERSION AJ324083.1 GI:15868462
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 948)
AUTHORS Kutsenko, A.S., Gizatullin, R.Z., Al-Amin, A.N., Wang, F., Kvasha, S.M.,
Podowski, R.M., Matuehkin, Y.G., Gvanchandani, A., Muravenko, O.V.,
Levitsky, V.G., Kolchanov, N.A., Protodopov, A.I., Kashuba, V.I.,
Kiselev, L.L., Wasserman, W., Wahlstedt, C. and Zabarovsky, E.R.
NOTI flanking sequences: a tool for gene discovery and verification
of the human genome
TITLE Nucleic Acids Res. 30 (14), 3163-3170 (2002)
JOURNAL Nucleic Acids Res. 30 (14), 3163-3170 (2002)
MEDLINE 22131767
PubMed 12136098
REFERENCE 2 (bases 1 to 948)
AUTHORS Zabarovsky, E.R.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
Sweden

FEATURES
Location/Qualifiers
source 1..948
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="NLI-VL24C"

ORIGIN
Alignment Scores:
Pred. No.: 2.35e+03 Length: 948
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-029-756-12 (1-5) x HSA324083 (1-948)

QY 1 HisAsnAlaHis 5
|||||
Db 174 CACAATGCCATCAT 160

RESULT 92
HSA324083 948 bp DNA linear PRI 18-JUL-2002
LOCUS Homo sapiens genomic sequence surrounding NotI site, clone
DEFINITION NLI-VL24C.
ACCESSION AJ324083
VERSION AJ324083.1 GI:15868462
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 948)
AUTHORS Kutsenko, A.S., Gizatullin, R.Z., Al-Amin, A.N., Wang, F., Kvasha, S.M.,
Podowski, R.M., Matuehkin, Y.G., Gvanchandani, A., Muravenko, O.V.,
Levitsky, V.G., Kolchanov, N.A., Protodopov, A.I., Kashuba, V.I.,
Kiselev, L.L., Wasserman, W., Wahlstedt, C. and Zabarovsky, E.R.
NOTI flanking sequences: a tool for gene discovery and verification
of the human genome
TITLE Nucleic Acids Res. 30 (14), 3163-3170 (2002)
JOURNAL Nucleic Acids Res. 30 (14), 3163-3170 (2002)
MEDLINE 22131767
PubMed 12136098
REFERENCE 2 (bases 1 to 948)
AUTHORS Zabarovsky, E.R.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
Sweden

FEATURES
Location/Qualifiers
source 1..948
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="NLI-VL24C"

ORIGIN
Alignment Scores:
Pred. No.: 2.35e+03 Length: 948
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-029-756-12 (1-5) x HSA324083 (1-948)

QY 1 HisAsnAlaHis 5
|||||
Db 174 CACAATGCCATCAT 160

RESULT 92
HSA324083 948 bp DNA linear PRI 18-JUL-2002
LOCUS Homo sapiens genomic sequence surrounding NotI site, clone
DEFINITION NLI-VL24C.
ACCESSION AJ324083
VERSION AJ324083.1 GI:15868462
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 948)
AUTHORS Kutsenko, A.S., Gizatullin, R.Z., Al-Amin, A.N., Wang, F., Kvasha, S.M.,
Podowski, R.M., Matuehkin, Y.G., Gvanchandani, A., Muravenko, O.V.,
Levitsky, V.G., Kolchanov, N.A., Protodopov, A.I., Kashuba, V.I.,
Kiselev, L.L., Wasserman, W., Wahlstedt, C. and Zabarovsky, E.R.
NOTI flanking sequences: a tool for gene discovery and verification
of the human genome
TITLE Nucleic Acids Res. 30 (14), 3163-3170 (2002)
JOURNAL Nucleic Acids Res. 30 (14), 3163-3170 (2002)
MEDLINE 22131767
PubMed 12136098
REFERENCE 2 (bases 1 to 948)
AUTHORS Zabarovsky, E.R.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
Sweden

FEATURES
Location/Qualifiers
source 1..948
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="NLI-VL24C"

ORIGIN
Alignment Scores:
Pred. No.: 2.35e+03 Length: 948
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-029-756-12 (1-5) x HSA324083 (1-948)

QY 1 HisAsnAlaHis 5
|||||
Db 174 CACAATGCCATCAT 160

RESULT 92
HSA324083 948 bp DNA linear PRI 18-JUL-2002
LOCUS Homo sapiens genomic sequence surrounding NotI site, clone
DEFINITION NLI-VL24C.
ACCESSION AJ324083
VERSION AJ324083.1 GI
```

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Korn, B., Zuo, D., Hu, Y. and LaBaer, J.
 Cloning of human full open reading frames in Gateway(TM) system
 entry vector (pDONR201)
 2 (bases 1 to 990)
 Halleck, A., Ebert, L., Moundinya, M., Schick, M., Eisenstein, S.,
 Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mar, W.,
 Korn, B., Zuo, D., Hu, Y. and LaBaer, J.
 Direct Submission
 Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
 Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
 Germany
 RZPD: RZPD0834H0232D, ORFNo 3794
 www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPD0834H0232D RZPDLIB;
 Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
 834
 www.rzpd.de/cgi-bin/products/showLib.pl.cgi?response?libNo=834
 www.rzpd.de/products/orfclones/
 Contact: Inge Arlart
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
 Heubnerweg 6, D-14059 Berlin, Germany
 Tel: +49 30 32639 100
 Fax: +49 30 32639 111
 www.rzpd.de
 This clone is available from RZPD;
 Contact RZPD (customer.service@rzpd.de) for further information.
 Clone name at Harvard Institute of Proteomics
 (www.hip.harvard.edu): FLH130889.01L
 This CDS clone is part of a collection of human full ORF clones
 jointly established and verified by the Harvard Institute of
 Proteomics (HIP) and RZPD.
 This CDS has been cloned without stopcodon.
 The CDS has been inserted into pDONR201 via a BP Clonase(TM)
 reaction. Additional sequence has been added in front of the start
 codon: att. .AAAAA GCA GGC TCC ACC (ATG).
 The last codon is followed by the 3', att site: GACCCAGCTTCTT. .att
 The clone is validated by full sequence check.
 Compared to the reference sequence NM_004810 (GI:19913386) we found
 AA exchange(s) at position (first base of changed triplet):
 586(gln->arg)
 Clone distribution: http://www.rzpd.de/products/orfclones/.
FEATURES
 source
 1. .990
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="RZPD0834H0232D"
 /clone_lib="Human Full ORF Clones Gateway(TM) - RZPD"
 /lab_host="DH5Alpha"
 /note="Vector: pDONR201, Site_1: attP1; Site_2: attP2"
 1. .990
 /gene="GRAP2"
 1. .>990
 /gene="GRAP2"
 /codon_start=1
 /protein_id="CAG46647.1"
 /db_xref="GI:49456653"
 /translation="MEAVAKPDTFASGEDELSPHTGVDVLKILSNQEWFKAEIGSQEG
 YVPKNFDIDQPKWFHGLSRHQAEILMGKEVFFIIRASQSPGDFISVVRHEDDV
 DRKVMKNGNYLWTEKPSNLKLVYRTKNSISRKQIFLDRPTREQGHGNSL
 DRRSQGGPHLSGAVGEIRPSMNRKLDHPPTLPLROHQPOPPQVAPAPAOQQPP
 QQRVLQHHHFEQRGSLDINDGCHCTGLGSENNALMHRHTDPVLOQAGVRWA
 RALYDFEALEDDELGFHSGVEVVDSSNFSNWTGRLNKLGLLPPANYVAPMTR"

ORIGIN

Alignment Scores:
 Pred. No.: 2.45e+03 Length: 990
 Score: 34.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-10-029-756-12 (1-5) x CR541849 (1-990)

Qy 1 HisAsnAlaHisHis 5
 |||||
Db 733 CACAATGCCCATCAT 719

RESULT 95
LOCUS BD235644/c
DEFINITION GRIP and GRB2 family member-associated human adaptor proteins.
ACCESSION BD235644
VERSION BD235644.1 GI:33045414
KEYWORDS JP 2002523429-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 993)
AUTHORS Ellis, J.H.
TITLE GRIP and GRB2 family member-associated human adaptor proteins
JOURNAL Patent: JP 2002523429-A 3 30-JUL-2002;
COMMENT GLAXO GROUP LTD
 OS Homo sapiens (human)
 PN JP 2002523429-A/3
 PD 30-JUL-2002
 PR 18-AUG-1999 JP 2000566414
 PR 19-AUG-1998 GB 9818124.1
 PI JONATHAN HENRY ELLIS
 PC C07K14/47,A61K45/00,A61P35/00,A61P37/06,C12N15/09,G01N33/15,
 PC G01N33/50,
 PC G01N33/566,C12N15/00
 CC GRIP and GRB2 family member-associated human adaptor proteins
 FH Key Location/Qualifiers
 FT CDS (1)..(993).

FEATURES
 source
 1. .993
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

ORIGIN

Alignment Scores:
 Pred. No.: 2.45e+03 Length: 993
 Score: 34.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x BD235644 (1-993)

Qy 1 HisAsnAlaHisHis 5
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Db 733 CACAATGCCCATCAT 719

RESULT 96
LOCUS BD235645
DEFINITION GRIP and GRB2 family member-associated human adaptor proteins.
ACCESSION BD235645
VERSION BD235645.1 GI:33045415
KEYWORDS JP 2002523429-A/4.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 993)
AUTHORS Ellis, J.H.
TITLE GRIP and GRB2 family member-associated human adaptor proteins
JOURNAL Patent: JP 2002523429-A 4 30-JUL-2002;
COMMENT GLAXO GROUP LTD
 OS Homo sapiens (human)
 PN JP 2002523429-A/4


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PD 30-JUL-2002
PF 18-AUG-1999 JP 2000566414
PI 19-AUG-1998 GB 9818124.1
PI JONATHAN HENRY ELLIS
PC C07K14/47, A61K45/00, A61P35/00, A61P37/06, C12N15/09, G01N33/15,
G01N33/50
PC G01N33/566, C12N15/00
CC GRIP and GRB2 family member-associated human adaptor proteins
FH Key Location/Qualifiers
FT source 1..993
FT /organism='Homo sapiens (human)'.

FEATURES
    source
        1..993
            Location/Qualifiers
                /organism="Homo sapiens"
                /mol_type="genomic DNA"
                /db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 2.46e+03 Length: 993
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-12 (1-5) x BD235645 (1-993)

QY 1 HisaenAlaHis 5
DB 261 CACAATGCCCATCAT 275

RESULT 97
AF236120/c
LOCUS AF236120 993 bp mRNA linear PRI 30-JUN-2000
DEFINITION Homo sapiens cell-line Jurkat J6 T cell lymphoma adaptor protein
ACCESSION AF236120
VERSION AF236120.1 GI:7331202
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
    1 (bases 1 to 993)
    Ellis J.H., Ashman, C., Burden, M.N., Kilpatrick, K.E., Morse, M.A. and
    Hamblin, P.A.
    GRID: a novel Grb-2-related adaptor protein that interacts with the
    activated T cell costimulatory receptor CD28
    J. Immunol. 164 (11), 5805-5814 (2000)
JOURNAL MEDLINE
PUBMED 20281669
REFERENCE
    2 (bases 1 to 993)
    Ellis, J.H., Ashman, C., Burden, M.N., Kilpatrick, K.E., Morse, M.A. and
    Hamblin, P.A.
    Submitted (18-FEB-2000) Immunopathology Unit, GlaxoWellcome
    Medicine Research Centre, Gunnels Wood Road, Stevenage,
    Hertfordshire SG1 2NY, UK
JOURNAL
PUBMED 10820259
REFERENCE
    2 (bases 1 to 993)
    Hamblin, P.A.
    Direct Submission
    Submitted (18-FEB-2000) Immunopathology Unit, GlaxoWellcome
    Medicine Research Centre, Gunnels Wood Road, Stevenage,
    Hertfordshire SG1 2NY, UK
FEATURES
    source
        1..993
            Location/Qualifiers
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /chromosome="22"
                /map="22q12-22qter"
                /cell_line="Jurkat J6 T cell lymphoma"
                /gene="GRID"
                /gene="GRID"
                /note="similar to Homo sapiens adaptor protein Gads
                encoded by GenBank Accession Number Y18051"

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/codon_start=1
/product="adaptor protein GRID"
/protein_id="AAF60320.1"
/db_xref="GI:7331203"
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YVKNFIDIOFPKWFHGLSLHQAEILLMGKEVGFFIIRASQSSPGDFSI5VRHEDDV
RRKMDKNGNYFLWTEKFPKSLNKLVDYRTNISRQKQIFLDRDTRDQGRGNSL
QRRSGGPHLSGAVEEIRPNNRKLSDHPPTLPQQHQHQFQPPYAPAPQQLQPP
QOQYLIQHHEFHQERRGSLDINDGCGTGLGSENNALMHRHTDPVQLQAGRVRA
RALYDFEALEDDELGFHSGVEVLDSSNPSWMTGRLNKLGLFPANTVAPMTR"

ORIGIN
Alignment Scores:
Pred. No.: 2.46e+03 Length: 993
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-029-756-12 (1-5) x AF236120 (1-993)

QY 1 HisaenAlaHis 5
DB 733 CACAATGCCCATCAT 719

RESULT 98
CR536524/c
LOCUS CR536524 993 bp mRNA linear PRI 23-JUN-2004
DEFINITION Homo sapiens full open reading frame cDNA clone RZPD0834F0120D for
gene GRAP2, GRB2-related adaptor protein 2; complete cds, incl.
stopcodon.
ACCESSION CR536524
VERSION CR536524.1 GI:49168531
KEYWORDS Full ORF shuttle clone, Gateway(TM), complete cds.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
    1 (bases 1 to 993)
    Hallett, A., Ebert, L., Moundinya, M., Schick, M., Eisenstein, S.,
    Neubert, P., Ketrang, K., Schatten, R., Shen, B., Henze, S., Mar, W.,
    Korn, B., Zuo, D., Hu, Y. and Labaer, J.
    Cloning of human full open reading frames in Gateway(TM) system
    entry vector (pDONR201)
    Unpublished
JOURNAL
PUBMED 10820259
REFERENCE
    2 (bases 1 to 993)
    Hallett, A., Ebert, L., Moundinya, M., Schick, M., Eisenstein, S.,
    Neubert, P., Ketrang, K., Schatten, R., Shen, B., Henze, S., Mar, W.,
    Korn, B., Zuo, D., Hu, Y. and Labaer, J.
    Direct Submission
    Submitted (23-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
    Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
    Germany
JOURNAL
PUBMED 10820259
REFERENCE
    2 (bases 1 to 993)
    Hallett, A., Ebert, L., Moundinya, M., Schick, M., Eisenstein, S.,
    Neubert, P., Ketrang, K., Schatten, R., Shen, B., Henze, S., Mar, W.,
    Korn, B., Zuo, D., Hu, Y. and Labaer, J.
    Direct Submission
    Submitted (23-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
    Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
    Germany
COMMENT
    RZPD: RZPD0834F0120D, ORFNo 3096
    www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=RZPD0834F0120D RZPDLib;
    Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD Lib No.
    834
    www.rzpd.de/cgi-bin/products/showLib.pl.cgi?response?libNo=834
    www.rzpd.de/products/orfclones/
    Contact: Inge Arian
    RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
    Heubnerweg 6, D-14059 Berlin, Germany
    Tel.: +49 30 32639 100
    Fax: +49 30 32639 111
    www.rzpd.de
    This clone is available from RZPD;
    contact RZPD (customer.service@rzpd.de) for further information.
    This CDS clone is a part of a collection of human full ORF clones
    jointly established and verified by the Harvard Institute of
    Proteomics and RZPD.
    This CDS has been inserted into stopcodon.
    The CDS has been inserted into pDONR201 via a BP Clonase(TM)

```

reaction. Additional sequence has been added in front of the start codon: att..AAAAA GCA GGC TCC ACC (ATG).
The stopcodon is followed by the 3' att site:
(stop)GACCAGCTTTCCTT..att Compared to the reference sequence
NM_004810 (g119913386) we did not find any amino acid exchanges.
Clone distribution: <http://www.rzpd.de/products/orfclones/>.

FEATURES

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source      location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="RZPD0834F0120D"
/clone_lib="Human Full ORF Clones Gateway(TM) - RZPD"
/lab_host="DH10B"
/notice=Vector: pDONR201, Site_1: attP1; Site_2: attP2"
1..993
gene

```

gene

CDS

ORIGIN

| | | |
|------------------------|----------|-----------------|
| Alignment Scores: | | |
| Pred. No.: | 2,46e+03 | 993 |
| Score: | 34.00 | 5 |
| Percent Similarity: | 100.00% | Conservative: 0 |
| Best Local Similarity: | 100.00% | Mismatches: 0 |
| Query Match: | 100.00% | Indels: 0 |
| DB: | 9 | Gaps: 0 |

US-10-029-756-12 (1-5) x CR536524 (1-993)

Qy 1 HisAsnAlaHisHis 5
Db 733 CACAATGCCCATCAT 719

| | |
|------------|--|
| RESULT | 99 |
| AX925633 | . |
| LOCUS | |
| DEFINITION | Sequence 12 from Patent WO03083098. |
| ACCESSION | AX925633 |
| VERSION | AX925633.1 GI:40244035 |
| KEYWORDS | |
| SOURCE | Alternaria alternata |
| ORGANISM | Alternaria alternata |
| | Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes; |
| | Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Alternaria; |
| | Alternaria alternata group. |

| REFERENCE AUTHORS | TITLE | JOURNAL |
|--|---|---------------------------------------|
| Simon-Nobbe, B., Schneider, P., Denk, U., Wally, V., Richter, K., Radauer, C., Teigel, M., Ebner, C. and Breitenbach, M. | Nucleic acid sequence and protein in addition to polypeptides coding for mannitol-dehydrogenases or parts thereof and the production and use thereof in diagnosis and therapy | Patent: WO 03083098-A 12 09-OCT-2003; |

FEATURES
SOURCE

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source
1. .1026
/organism="Alternaria alternata"
/mol_type="unassigned DNA"
/db xref="taxon:5599"
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ORIGIN

Alignment Scores:
Pred. No.: 2.53e+03 Length: 1026

| | | | |
|------------------------|---------|---------------|---|
| Score: | 34.00 | Matches: | 5 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 6 | Gaps: | 0 |

US-10-029-756-12 (1-5) x AX925633 (1-1026)

Qy 1 HisAsnAlaHisHis 5
|||
Db 83 CACAATGCCCATCAC 97

RESULT 100

| | | | | |
|------------|--|---------|------------|-----------------|
| | AF034693 | 1027 bp | DNA linear | VRT 23-JUL-1998 |
| LOCUS | AF034693 | 1027 bp | DNA linear | VRT 23-JUL-1998 |
| DEFINITION | Coturnix coturnix japonica bzip transcription factor Mafa (mafa) | | | |
| | gene, complete cds. | | | |

AF034693
AF034693.1 GI:2654142
VERSION
KEYWORDS
SOURCE Coturnix japonica (Japanese mail)

| SOURCE | ORGANISM |
|------------------------------------|--|
| Coturnix japonica (Japanese quail) | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi |
| Coturnix japonica | Archosauria; Aves; Neognathae; Galliformes; Phasianidae; |
| | Phasianinae; Coturnix |

REFERENCE

1 (bases 1 to 1027)

AUTHORS

Benkheifala S., Provot S., Lecog O., Pouponnot C., Cal
Frasigianne, Colunna.

BEHNERT, S.; FLOVOC, S.;
FELDER-SCHMITTBUEHL, M.P.

| TITLE | JOURNAL |
|--|---------------------------------|
| mafa, a novel member of the maf proto-oncogene family, is involved in the developmental regulation and mitogenic activation of neuroretina cells | Oncogene 17 (2), 247-254 (1998) |

| | |
|-----------|---|
| MEDLINE | 98337467 |
| PUBLISHED | 9674710 |
| REFERENCE | 2 (bases 1 to 1027) |
| AUTHORS | Benkeliaf S., Felder-Schmittbuhl M.P. and Calothy G. |
| TITLE | Direct Submission |
| JOURNAL | Submitted (17-NOV-1997) UMR 146 CNRS, Institut Curie, Bat 110 |
| FEATURES | Centre universitaire, Orsay 91405, France |
| source | Location/Qualifiers 1. .1027 |

gene

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CDS
161..1021
/genes="mafa"
/codon_start=1
/product="bzip transcription factor MafA"
/protein_id="AAC60377.1"
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[illegible]

ORIGIN

Alignment Scores:

| | | | |
|------------------------|----------|---------------|------|
| Pred. No.: | 2.53e+03 | Length: | 1027 |
| Score: | 34.00 | Matches: | 5 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 5 | Gaps: | 0 |

US-10-029-756-12 (1-5) x AF034693 (1-1027)

Qy 1 HisAsnAlaHisHis 5

Db 623 CACACGCTCATCAT 637

Search completed: June 8, 2005, 13:16:20
Job time : 1104.6 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein. - nucleic search, using frame_plus_p2n model

Run on: June 8, 2005, 11:36:25 ; Search time 76.3158 Seconds
(without alignments)
107.204 Million cell updates/sec

Title: US-10-029-756-12

Perfect score: 34

Sequence: 1 HNAH 5

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Command line parameters:

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-DB=Issued_Patents_NA -QFMT=fastcap -SURFIX=p2n.rn1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=1000 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=100
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10029756 @cgn 1.1 177 @runat_07062005_122751_28805 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:

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4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 1 | 34 | 100.0 | 25 | 4 | US-09-396-196G-33466 |
| 2 | 34 | 100.0 | 82 | 4 | US-09-270-767-8295 |
| 3 | 34 | 100.0 | 82 | 4 | US-09-270-767-23577 |
| 4 | 34 | 100.0 | 206 | 4 | US-09-270-767-28874 |
| 5 | 34 | 100.0 | 316 | 4 | US-08-956-171E-4362 |
| 6 | 34 | 100.0 | 316 | 4 | US-08-781-986A-4362 |
| 7 | 34 | 100.0 | 333 | 4 | US-09-543-681A-3814 |
| 8 | 34 | 100.0 | 348 | 4 | US-08-956-171E-4136 |
| 9 | 34 | 100.0 | 348 | 4 | US-08-781-986A-4136 |
| 10 | 34 | 100.0 | 380 | 2 | US-08-975-316-33 |
| 11 | 34 | 100.0 | 380 | 3 | US-09-615-192A-33 |
| 12 | 34 | 100.0 | 380 | 4 | US-09-169-789-33 |
| 13 | 34 | 100.0 | 400 | 4 | US-08-956-171E-3743 |
| 14 | 34 | 100.0 | 400 | 4 | US-08-781-986A-3743 |
| 15 | 34 | 100.0 | 420 | 3 | US-09-615-192A-115 |
| 16 | 34 | 100.0 | 420 | 3 | US-09-169-789-115 |
| 17 | 34 | 100.0 | 428 | 4 | US-09-513-999C-12497 |
| 18 | 34 | 100.0 | 432 | 4 | US-09-593-887-7 |
| 19 | 34 | 100.0 | 562 | 4 | US-09-270-767-4421 |
| 20 | 34 | 100.0 | 562 | 4 | US-09-270-767-13703 |
| 21 | 34 | 100.0 | 601 | 4 | US-09-949-016-94983 |
| 22 | 34 | 100.0 | 601 | 4 | US-09-949-016-95095 |
| 23 | 34 | 100.0 | 601 | 4 | US-09-949-016-150166 |
| 24 | 34 | 100.0 | 601 | 4 | US-09-949-016-153056 |
| 25 | 34 | 100.0 | 601 | 4 | US-09-949-016-165560 |
| 26 | 34 | 100.0 | 601 | 4 | US-09-949-016-181710 |
| 27 | 34 | 100.0 | 601 | 4 | US-09-949-016-181829 |
| 28 | 34 | 100.0 | 601 | 4 | US-09-949-016-181948 |
| 29 | 34 | 100.0 | 653 | 4 | US-09-702-705-1397 |
| 30 | 34 | 100.0 | 653 | 4 | US-09-736-457-1397 |
| 31 | 34 | 100.0 | 653 | 4 | US-09-614-124B-1397 |
| 32 | 34 | 100.0 | 653 | 4 | US-09-671-325-1397 |
| 33 | 34 | 100.0 | 653 | 4 | US-09-658-824-1397 |
| 34 | 34 | 100.0 | 824 | 4 | US-09-495-052-56 |
| 35 | 34 | 100.0 | 881 | 4 | US-09-270-767-12993 |
| 36 | 34 | 100.0 | 1068 | 4 | US-09-252-991A-10187 |
| 37 | 34 | 100.0 | 1081 | 4 | US-09-949-016-5053 |
| 38 | 34 | 100.0 | 1086 | 4 | US-09-328-352-1975 |
| 39 | 34 | 100.0 | 1179 | 4 | US-09-543-681A-1032 |
| 40 | 34 | 100.0 | 1281 | 4 | US-09-857-583B-3 |
| 41 | 34 | 100.0 | 1293 | 4 | US-09-540-236-1347 |
| 42 | 34 | 100.0 | 1323 | 4 | US-09-248-796A-442 |
| 43 | 34 | 100.0 | 1425 | 4 | US-09-540-236-1678 |
| 44 | 34 | 100.0 | 1479 | 4 | US-09-489-039A-4667 |
| 45 | 34 | 100.0 | 1499 | 4 | US-09-949-016-4296 |
| 46 | 34 | 100.0 | 1517 | 4 | US-09-814-915A-41 |
| 47 | 34 | 100.0 | 1661 | 2 | US-08-815-176-2 |
| 48 | 34 | 100.0 | 1661 | 3 | US-09-197-344-2 |
| 49 | 34 | 100.0 | 1684 | 2 | US-08-831-570-1 |
| 50 | 34 | 100.0 | 1684 | 2 | US-08-831-575-1 |
| 51 | 34 | 100.0 | 1685 | 1 | US-08-366-779-4 |
| 52 | 34 | 100.0 | 1685 | 1 | US-08-789-936-4 |
| 53 | 34 | 100.0 | 1685 | 3 | US-08-934-254-4 |
| 54 | 34 | 100.0 | 1685 | 4 | US-09-685-775-4 |
| 55 | 34 | 100.0 | 1702 | 3 | US-08-934-254-26 |
| 56 | 34 | 100.0 | 1702 | 4 | US-09-685-775-26 |
| 57 | 34 | 100.0 | 1800 | 4 | US-09-489-039A-5879 |
| 58 | 34 | 100.0 | 2022 | 4 | US-08-252-991A-9887 |
| 59 | 34 | 100.0 | 2373 | 4 | US-09-614-221A-602 |
| 60 | 34 | 100.0 | 2418 | 3 | US-08-549-515-2 |
| 61 | 34 | 100.0 | 2591 | 4 | US-09-023-655-1000 |
| 62 | 34 | 100.0 | 2970 | 4 | US-09-540-236-217 |
| 63 | 34 | 100.0 | 3304 | 4 | US-09-919-172-63 |
| 64 | 34 | 100.0 | 3989 | 4 | US-08-956-171E-816 |
| 65 | 34 | 100.0 | 3989 | 4 | US-08-781-986A-816 |
| 66 | 34 | 100.0 | 4051 | 3 | US-08-549-515-1 |
| 67 | 34 | 100.0 | 4276 | 4 | US-09-721-480-1 |
| 68 | 34 | 100.0 | 4326 | 3 | US-08-760-615-7 |
| 69 | 34 | 100.0 | 4328 | 3 | US-09-132-808-1 |
| 70 | 34 | 100.0 | 4328 | 3 | US-08-910-647-2 |
| 71 | 34 | 100.0 | 4328 | 3 | US-09-620-925-2 |
| 72 | 34 | 100.0 | 4328 | 4 | US-09-620-260-1 |
| 73 | 34 | 100.0 | 4328 | 4 | US-09-620-259-1 |
| 74 | 34 | 100.0 | 4336 | 4 | US-08-956-171E-546 |
| 75 | 34 | 100.0 | 4336 | 4 | US-08-781-986A-546 |
| 76 | 34 | 100.0 | 4531 | 4 | US-09-949-016-1943 |
| 77 | 34 | 100.0 | 4818 | 3 | US-08-910-647-4 |
| 78 | 34 | 100.0 | 4818 | 3 | US-09-620-925-4 |
| 79 | 34 | 100.0 | 4928 | 1 | US-08-345-913-1 |
| 80 | 34 | 100.0 | 4928 | 3 | US-08-818-562-1 |
| 81 | 34 | 100.0 | 4928 | 3 | US-09-628-445-1 |
| 82 | 34 | 100.0 | 5107 | 3 | US-08-910-647-3 |
| 83 | 34 | 100.0 | 5107 | 3 | US-09-620-925-3 |
| 84 | 34 | 100.0 | 5108 | 4 | US-09-628-730-51 |
| 85 | 34 | 100.0 | 5108 | 4 | US-09-628-730-52 |

| | | | | | | | | | | | | | |
|-----|----|-------|---------|---|----------------------|--------------------|-------|----|------|------|---|---------------------|--------------------|
| 86 | 34 | 100.0 | 5111 | 4 | US-09-628-730-55 | Sequence 55, Appl | c 159 | 31 | 91.2 | 702 | 4 | US-09-540-236-397 | Sequence 397, App |
| 87 | 34 | 100.0 | 5128 | 4 | US-09-721-480-2 | Sequence 2, Appli | c 160 | 31 | 91.2 | 753 | 3 | US-08-811-682-16 | Sequence 12, Appl |
| 88 | 34 | 100.0 | 5185 | 4 | US-09-628-730-47 | Sequence 47, Appl | c 161 | 31 | 91.2 | 813 | 3 | US-08-479-040-22 | Sequence 26, Appl |
| 89 | 34 | 100.0 | 5188 | 4 | US-09-628-730-59 | Sequence 59, Appl | c 162 | 31 | 91.2 | 908 | 3 | US-08-991-789A-46 | Sequence 46, Appl |
| 90 | 34 | 100.0 | 5215 | 3 | US-09-173-053-8 | Sequence 8, Appli | c 163 | 31 | 91.2 | 908 | 3 | US-09-062-451-46 | Sequence 46, Appl |
| 91 | 34 | 100.0 | 5254 | 4 | US-09-628-730-60 | Sequence 60, Appl | c 164 | 31 | 91.2 | 908 | 3 | US-09-598-326-46 | Sequence 46, Appl |
| 92 | 34 | 100.0 | 5459 | 4 | US-09-721-480-4 | Sequence 4, Appli | c 165 | 31 | 91.2 | 908 | 4 | US-09-289-198-46 | Sequence 46, Appl |
| 93 | 34 | 100.0 | 5882 | 4 | US-09-721-480-6 | Sequence 6, Appli | c 166 | 31 | 91.2 | 908 | 4 | US-09-429-755-46 | Sequence 46, Appl |
| 94 | 34 | 100.0 | 7015 | 3 | US-09-770-315-1 | Sequence 1, Appli | c 167 | 31 | 91.2 | 908 | 4 | US-09-699-295-46 | Sequence 46, Appl |
| 95 | 34 | 100.0 | 9600 | 3 | US-08-910-647-1 | Sequence 1, Appli | c 168 | 31 | 91.2 | 927 | 4 | US-09-248-796A-7190 | Sequence 7190, Ap |
| 96 | 34 | 100.0 | 9600 | 3 | US-09-620-925-1 | Sequence 1, Appli | c 169 | 31 | 91.2 | 970 | 3 | US-09-735-935-1 | Sequence 1, Appli |
| 97 | 34 | 100.0 | 15538 | 4 | US-09-554-337-1 | Sequence 1, Appli | c 170 | 31 | 91.2 | 970 | 4 | US-10-162-639-1 | Sequence 1, Appli |
| 98 | 34 | 100.0 | 21893 | 4 | US-09-949-016-16407 | Sequence 16407, A | c 171 | 31 | 91.2 | 1002 | 4 | US-09-248-796A-5029 | Sequence 5029, Ap |
| 99 | 34 | 100.0 | 22406 | 4 | US-09-949-016-14958 | Sequence 14958, A | c 172 | 31 | 91.2 | 1089 | 4 | US-09-543-681A-120 | Sequence 120, App |
| 100 | 34 | 100.0 | 24056 | 4 | US-09-949-016-14320 | Sequence 14320, A | c 173 | 31 | 91.2 | 1197 | 4 | US-09-710-279-1497 | Sequence 1497, Ap |
| 101 | 34 | 100.0 | 25165 | 3 | US-09-453-702B-39 | Sequence 39, Appl | c 174 | 31 | 91.2 | 1227 | 4 | US-09-248-796A-377 | Sequence 377, App |
| 102 | 34 | 100.0 | 28063 | 4 | US-09-949-016-16795 | Sequence 16795, A | c 175 | 31 | 91.2 | 1254 | 3 | US-09-134-001C-973 | Sequence 973, App |
| 103 | 34 | 100.0 | 31214 | 4 | US-09-949-016-17097 | Sequence 17097, A | c 176 | 31 | 91.2 | 1254 | 3 | US-09-614-912-177 | Sequence 177, App |
| 104 | 34 | 100.0 | 31214 | 4 | US-09-949-016-17098 | Sequence 17098, A | c 177 | 31 | 91.2 | 1314 | 4 | US-09-234-186-2 | Sequence 2, Appli |
| 105 | 34 | 100.0 | 41180 | 4 | US-09-949-016-12088 | Sequence 12088, A | c 178 | 31 | 91.2 | 1315 | 3 | US-09-234-186-4 | Sequence 4, Appli |
| 106 | 34 | 100.0 | 60304 | 4 | US-09-949-016-11995 | Sequence 11995, A | c 179 | 31 | 91.2 | 1315 | 3 | US-09-234-186-5 | Sequence 5, Appli |
| 107 | 34 | 100.0 | 60304 | 4 | US-09-949-016-17264 | Sequence 17264, A | c 180 | 31 | 91.2 | 1315 | 3 | US-09-234-186-6 | Sequence 6, Appli |
| 108 | 34 | 100.0 | 60465 | 4 | US-09-949-016-15995 | Sequence 15995, A | c 181 | 31 | 91.2 | 1315 | 3 | US-09-233-527-2 | Sequence 2, Appli |
| 109 | 34 | 100.0 | 87562 | 4 | US-09-949-016-13685 | Sequence 13685, A | c 182 | 31 | 91.2 | 1315 | 3 | US-09-233-527-4 | Sequence 4, Appli |
| 110 | 34 | 100.0 | 90618 | 4 | US-09-949-016-15964 | Sequence 15964, A | c 183 | 31 | 91.2 | 1315 | 3 | US-09-233-527-5 | Sequence 5, Appli |
| 111 | 34 | 100.0 | 91933 | 4 | US-09-949-016-11855 | Sequence 11855, A | c 184 | 31 | 91.2 | 1315 | 3 | US-09-233-527-6 | Sequence 6, Appli |
| 112 | 34 | 100.0 | 91933 | 4 | US-09-949-016-14628 | Sequence 14628, A | c 185 | 31 | 91.2 | 1315 | 3 | PCT-US93-05651-2 | Sequence 2, Appli |
| 113 | 34 | 100.0 | 99629 | 4 | US-09-596-002-37 | Sequence 37, Appl | c 186 | 31 | 91.2 | 1315 | 5 | US-09-543-681A-2896 | Sequence 2896, App |
| 114 | 34 | 100.0 | 152393 | 4 | US-09-949-016-14514 | Sequence 14514, A | c 187 | 31 | 91.2 | 1410 | 4 | US-09-799-451-323 | Sequence 323, App |
| 115 | 34 | 100.0 | 152393 | 4 | US-09-949-016-14515 | Sequence 14515, A | c 188 | 31 | 91.2 | 1546 | 4 | US-08-600-656-6 | Sequence 6, Appli |
| 116 | 34 | 100.0 | 156894 | 4 | US-09-949-016-12765 | Sequence 12765, A | c 189 | 31 | 91.2 | 1548 | 3 | US-09-170-670-11 | Sequence 11, Appl |
| 117 | 34 | 100.0 | 156894 | 4 | US-09-949-016-12766 | Sequence 12766, A | c 190 | 31 | 91.2 | 1548 | 3 | US-09-193-068-11 | Sequence 11, Appl |
| 118 | 34 | 100.0 | 156895 | 4 | US-09-949-016-16957 | Sequence 16957, A | c 191 | 31 | 91.2 | 1548 | 3 | US-09-183-412-11 | Sequence 11, Appl |
| 119 | 34 | 100.0 | 156895 | 4 | US-09-949-016-16958 | Sequence 16958, A | c 192 | 31 | 91.2 | 1548 | 3 | US-09-354-191A-6 | Sequence 6, Appli |
| 120 | 34 | 100.0 | 156895 | 4 | US-09-949-016-16959 | Sequence 16959, A | c 193 | 31 | 91.2 | 1548 | 3 | US-09-290-734-11 | Sequence 11, Appl |
| 121 | 34 | 100.0 | 166698 | 4 | US-09-949-016-16038 | Sequence 16038, A | c 194 | 31 | 91.2 | 1548 | 3 | US-09-537-168-7 | Sequence 7, Appli |
| 122 | 34 | 100.0 | 183202 | 4 | US-09-949-016-13614 | Sequence 13614, A | c 195 | 31 | 91.2 | 1548 | 4 | US-09-545-586-11 | Sequence 11, Appl |
| 123 | 34 | 100.0 | 199945 | 4 | US-09-949-016-15436 | Sequence 15436, A | c 196 | 31 | 91.2 | 1548 | 4 | US-09-749-864-11 | Sequence 11, Appl |
| 124 | 34 | 100.0 | 269223 | 4 | US-09-596-002-41 | Sequence 41, Appl | c 197 | 31 | 91.2 | 1739 | 4 | US-09-949-016-4226 | Sequence 4226, Ap |
| 125 | 34 | 100.0 | 580073 | 4 | US-08-545-528D-1 | Sequence 1, Appli | c 198 | 31 | 91.2 | 1814 | 1 | US-08-720-899-5 | Sequence 5, Appli |
| 126 | 34 | 100.0 | 1830121 | 4 | US-09-557-884-1 | Sequence 1, Appli | c 199 | 31 | 91.2 | 1814 | 1 | US-08-459-610-5 | Sequence 5, Appli |
| 127 | 34 | 100.0 | 1830121 | 4 | US-09-643-990A-1 | Sequence 1, Appli | c 200 | 31 | 91.2 | 1814 | 1 | US-08-343-804-5 | Sequence 5, Appli |
| 128 | 34 | 100.0 | 4403765 | 3 | US-09-103-840A-2 | Sequence 2, Appli | c 201 | 31 | 91.2 | 1814 | 2 | US-08-687-399-5 | Sequence 5, Appli |
| 129 | 34 | 100.0 | 4411529 | 3 | US-09-103-840A-1 | Sequence 1, Appli | c 202 | 31 | 91.2 | 1814 | 2 | US-08-600-908A-5 | Sequence 5, Appli |
| 130 | 31 | 91.2 | 25 | 4 | US-09-396-136G-44377 | Sequence 44377, A | c 203 | 31 | 91.2 | 1814 | 2 | US-08-683-838A-5 | Sequence 5, Appli |
| 131 | 31 | 91.2 | 45 | 4 | US-09-069-827A-65 | Sequence 65, Appl | c 204 | 31 | 91.2 | 1814 | 3 | US-09-182-859-5 | Sequence 5, Appli |
| 132 | 31 | 91.2 | 50 | 4 | US-09-554-929-43 | Sequence 43, Appl | c 205 | 31 | 91.2 | 1814 | 3 | US-09-672-459-5 | Sequence 5, Appli |
| 133 | 31 | 91.2 | 50 | 4 | US-09-513-999C-32775 | Sequence 32775, A | c 206 | 31 | 91.2 | 1814 | 3 | US-09-636-252A-5 | Sequence 5, Appli |
| 134 | 31 | 91.2 | 99 | 4 | US-09-513-999C-9545 | Sequence 9545, Ap | c 207 | 31 | 91.2 | 1814 | 4 | US-10-186-042-5 | Sequence 5, Appli |
| 135 | 31 | 91.2 | 137 | 4 | US-09-513-999C-9553 | Sequence 9553, Ap | c 208 | 31 | 91.2 | 1845 | 1 | US-08-652-207A-1 | Sequence 1, Appli |
| 136 | 31 | 91.2 | 210 | 4 | US-09-248-796A-9553 | Sequence 9553, Ap | c 209 | 31 | 91.2 | 1845 | 3 | US-09-488-857B-3 | Sequence 3, Appli |
| 137 | 31 | 91.2 | 411 | 4 | US-09-248-796A-6520 | Sequence 6520, Ap | c 210 | 31 | 91.2 | 1845 | 3 | US-09-949-016-1358 | Sequence 1358, Ap |
| 138 | 31 | 91.2 | 413 | 4 | US-09-513-999C-23181 | Sequence 23181, A | c 211 | 31 | 91.2 | 1978 | 4 | US-09-799-451-318 | Sequence 318, App |
| 139 | 31 | 91.2 | 453 | 4 | US-09-621-976-19159 | Sequence 19159, A | c 212 | 31 | 91.2 | 2225 | 4 | US-09-248-796A-633 | Sequence 633, App |
| 140 | 31 | 91.2 | 482 | 4 | US-09-621-976-15665 | Sequence 15665, A | c 213 | 31 | 91.2 | 2271 | 4 | US-09-543-681A-1562 | Sequence 1562, App |
| 141 | 31 | 91.2 | 601 | 4 | US-09-949-016-42885 | Sequence 42885, A | c 214 | 31 | 91.2 | 2766 | 4 | US-07-882-232-1 | Sequence 1, Appli |
| 142 | 31 | 91.2 | 601 | 4 | US-09-949-016-42886 | Sequence 42886, A | c 215 | 31 | 91.2 | 2830 | 1 | US-08-331-644-1 | Sequence 1, Appli |
| 143 | 31 | 91.2 | 601 | 4 | US-09-949-016-42873 | Sequence 42873, A | c 216 | 31 | 91.2 | 2830 | 5 | PCT-US93-04102-1 | Sequence 1, Appli |
| 144 | 31 | 91.2 | 601 | 4 | US-09-949-016-72936 | Sequence 72936, A | c 217 | 31 | 91.2 | 2830 | 5 | US-09-710-279-4053 | Sequence 4053, Ap |
| 145 | 31 | 91.2 | 601 | 4 | US-09-949-016-72937 | Sequence 72937, A | c 218 | 31 | 91.2 | 3264 | 4 | US-08-851-567B-33 | Sequence 33, Appl |
| 146 | 31 | 91.2 | 601 | 4 | US-09-949-016-72938 | Sequence 72938, A | c 219 | 31 | 91.2 | 3288 | 4 | US-09-710-279-3745 | Sequence 3745, Ap |
| 147 | 31 | 91.2 | 601 | 4 | US-09-949-016-77647 | Sequence 77647, A | c 220 | 31 | 91.2 | 3314 | 4 | US-09-710-279-3746 | Sequence 3746, Ap |
| 148 | 31 | 91.2 | 601 | 4 | US-09-949-016-80314 | Sequence 80314, A | c 221 | 31 | 91.2 | 3314 | 4 | US-09-488-857B-12 | Sequence 12, Appl |
| 149 | 31 | 91.2 | 601 | 4 | US-09-949-016-156337 | Sequence 156337, A | c 222 | 31 | 91.2 | 3436 | 3 | US-09-248-796A-3954 | Sequence 3954, Ap |
| 150 | 31 | 91.2 | 601 | 4 | US-09-949-016-156627 | Sequence 156627, A | c 223 | 31 | 91.2 | 3771 | 4 | US-08-811-682-13 | Sequence 13, Appl |
| 151 | 31 | 91.2 | 601 | 4 | US-09-949-016-156628 | Sequence 156628, A | c 224 | 31 | 91.2 | 3841 | 3 | US-09-949-016-2718 | Sequence 2718, Ap |
| 152 | 31 | 91.2 | 601 | 4 | US-09-949-016-176395 | Sequence 176395, A | c 225 | 31 | 91.2 | 3897 | 4 | US-09-554-929-1 | Sequence 1, Appli |
| 153 | 31 | 91.2 | 601 | 4 | US-09-949-016-178140 | Sequence 178140, A | c 226 | 31 | 91.2 | 4800 | 4 | US-08-386-435-9 | Sequence 9, Appli |
| 154 | 31 | 91.2 | 601 | 4 | US-09-949-016-178141 | Sequence 178141, A | c 227 | 31 | 91.2 | 4835 | 5 | PCT-US96-02331-9 | Sequence 9, Appli |
| 155 | 31 | 91.2 | 601 | 4 | US-09-949-016-180793 | Sequence 180793, A | c 228 | 31 | 91.2 | 5044 | 3 | US-09-735-935-3 | Sequence 3, Appli |
| 156 | 31 | 91.2 | 601 | 4 | US-09-949-016-180794 | Sequence 180794, A | c 229 | 31 | 91.2 | 5044 | 4 | US-10-162-639-3 | Sequence 3, Appli |
| 157 | 31 | 91.2 | 601 | 4 | US-09-949-016-180795 | Sequence 180795, A | c 230 | 31 | 91.2 | 5044 | 4 | US-09-814-915A-79 | Sequence 79, Appl |
| 158 | 31 | 91.2 | 645 | 4 | US-09-107-532A-2083 | Sequence 2083, Ap | c 231 | 31 | 91.2 | 5177 | 4 | | |

| | | | | | | | | | | | | | | |
|-------|----|------|--------|---|----------------------|--------------------|--------------------|-------|----|------|---------|---|----------------------|--------------------|
| 232 | 31 | 91.2 | 5552 | 3 | US-08-155-888-1 | Sequence 1, Appli | Sequence 1, Appli | c 305 | 31 | 91.2 | 331814 | 4 | US-09-949-016-17056 | Sequence 17056, A |
| c 233 | 31 | 91.2 | 5609 | 3 | US-09-313-677-14 | Sequence 14, Appl | Sequence 14, Appl | c 306 | 31 | 91.2 | 451924 | 4 | US-09-949-016-12896 | Sequence 12896, A |
| c 234 | 31 | 91.2 | 5609 | 3 | US-09-313-677-15 | Sequence 15, Appl | Sequence 15, Appl | c 307 | 31 | 91.2 | 451925 | 4 | US-09-949-016-17305 | Sequence 17305, A |
| c 235 | 31 | 91.2 | 6559 | 3 | US-09-234-186-1 | Sequence 1, Appli | Sequence 1, Appli | c 308 | 31 | 91.2 | 1664976 | 4 | US-08-916-421B-1 | Sequence 1, Appli |
| c 236 | 31 | 91.2 | 6559 | 3 | US-09-233-527-1 | Sequence 1, Appli | Sequence 1, Appli | c 309 | 31 | 91.2 | 1664976 | 4 | US-09-692-570-1 | Sequence 1, Appli |
| c 237 | 31 | 91.2 | 6560 | 5 | PCU-US93-05651-1 | Sequence 1, Appli | Sequence 1, Appli | c 310 | 30 | 88.2 | 23 | 4 | US-09-280-428A-1 | Sequence 1, Appli |
| c 238 | 31 | 91.2 | 7838 | 4 | US-09-761-466-4 | Sequence 4, Appli | Sequence 4, Appli | c 311 | 30 | 88.2 | 25 | 4 | US-09-396-186G-47969 | Sequence 47969, A |
| c 239 | 31 | 91.2 | 7916 | 4 | US-09-479-040-1 | Sequence 1, Appli | Sequence 1, Appli | c 312 | 30 | 88.2 | 25 | 4 | US-09-396-196G-74247 | Sequence 74247, A |
| c 240 | 31 | 91.2 | 8773 | 4 | US-09-593-580B-1 | Sequence 1, Appli | Sequence 1, Appli | c 313 | 30 | 88.2 | 27 | 2 | US-08-558-823-11 | Sequence 11, Appli |
| c 241 | 31 | 91.2 | 9464 | 4 | US-09-378-847-1 | Sequence 1, Appli | Sequence 1, Appli | c 314 | 30 | 88.2 | 45 | 4 | US-09-769-863-2 | Sequence 2, Appli |
| c 242 | 31 | 91.2 | 9464 | 4 | US-09-378-810-1 | Sequence 1, Appli | Sequence 1, Appli | c 315 | 30 | 88.2 | 45 | 4 | US-09-769-863-3 | Sequence 3, Appli |
| c 243 | 31 | 91.2 | 9471 | 3 | US-08-811-682-1 | Sequence 1, Appli | Sequence 1, Appli | c 316 | 30 | 88.2 | 169 | 4 | US-09-401-064-145 | Sequence 145, App |
| c 244 | 31 | 91.2 | 9471 | 3 | US-08-811-682-1 | Sequence 1, Appli | Sequence 1, Appli | c 317 | 30 | 88.2 | 205 | 4 | US-09-513-999C-20710 | Sequence 20710, A |
| c 245 | 31 | 91.2 | 9975 | 3 | US-08-977-171-1 | Sequence 2, Appli | Sequence 2, Appli | c 318 | 30 | 88.2 | 207 | 4 | US-09-328-352-2816 | Sequence 2816, Ap |
| c 246 | 31 | 91.2 | 9934 | 3 | US-08-977-171-2 | Sequence 2, Appli | Sequence 2, Appli | c 319 | 30 | 88.2 | 208 | 4 | US-09-471-276-153 | Sequence 153, App |
| c 247 | 31 | 91.2 | 16302 | 4 | US-09-949-016-17212 | Sequence 17212, A | Sequence 17212, A | c 320 | 30 | 88.2 | 233 | 4 | US-08-956-171E-4577 | Sequence 4577, Ap |
| c 248 | 31 | 91.2 | 17607 | 4 | US-09-949-016-15968 | Sequence 15968, A | Sequence 15968, A | c 321 | 30 | 88.2 | 233 | 4 | US-08-781-986A-4577 | Sequence 4577, Ap |
| c 249 | 31 | 91.2 | 22143 | 4 | US-09-949-016-15983 | Sequence 15983, A | Sequence 15983, A | c 322 | 30 | 88.2 | 279 | 4 | US-09-313-294A-3402 | Sequence 3402, Ap |
| c 250 | 31 | 91.2 | 22375 | 4 | US-09-949-016-15987 | Sequence 15987, A | Sequence 15987, A | c 323 | 30 | 88.2 | 281 | 4 | US-09-313-294A-5256 | Sequence 5256, Ap |
| c 251 | 31 | 91.2 | 24538 | 4 | US-09-949-016-13100 | Sequence 13100, A | Sequence 13100, A | c 324 | 30 | 88.2 | 285 | 4 | US-09-313-294A-1903 | Sequence 1903, Ap |
| c 252 | 31 | 91.2 | 26777 | 4 | US-09-949-016-13015 | Sequence 13015, A | Sequence 13015, A | c 325 | 30 | 88.2 | 288 | 4 | US-09-313-294A-2785 | Sequence 2785, Ap |
| c 253 | 31 | 91.2 | 28366 | 4 | US-09-949-016-15763 | Sequence 15763, A | Sequence 15763, A | c 326 | 30 | 88.2 | 301 | 4 | US-09-313-294A-7039 | Sequence 7039, Ap |
| c 254 | 31 | 91.2 | 29970 | 4 | US-09-949-016-14460 | Sequence 14460, A | Sequence 14460, A | c 327 | 30 | 88.2 | 316 | 3 | US-08-905-223-92 | Sequence 92, Appl |
| c 255 | 31 | 91.2 | 35881 | 4 | US-08-311-731A-127 | Sequence 127, App | Sequence 127, App | c 328 | 30 | 88.2 | 392 | 4 | US-09-621-976-3686 | Sequence 3686, Ap |
| c 256 | 31 | 91.2 | 37715 | 4 | US-09-949-016-13846 | Sequence 13846, A | Sequence 13846, A | c 329 | 30 | 88.2 | 411 | 3 | US-09-134-001C-1518 | Sequence 1518, Ap |
| c 257 | 31 | 91.2 | 38969 | 4 | US-09-949-016-14051 | Sequence 14051, A | Sequence 14051, A | c 330 | 30 | 88.2 | 454 | 4 | US-09-513-999C-851 | Sequence 851, App |
| c 258 | 31 | 91.2 | 41798 | 4 | US-09-949-016-16058 | Sequence 16058, A | Sequence 16058, A | c 331 | 30 | 88.2 | 454 | 4 | US-09-513-999C-13119 | Sequence 13119, A |
| c 259 | 31 | 91.2 | 43986 | 4 | US-09-949-016-17155 | Sequence 17155, A | Sequence 17155, A | c 332 | 30 | 88.2 | 480 | 4 | US-09-513-999C-960 | Sequence 960, App |
| c 260 | 31 | 91.2 | 51928 | 4 | US-09-949-016-13184 | Sequence 13184, A | Sequence 13184, A | c 333 | 30 | 88.2 | 493 | 4 | US-09-621-976-2468 | Sequence 2468, Ap |
| c 261 | 31 | 91.2 | 52202 | 4 | US-09-949-016-17006 | Sequence 17006, A | Sequence 17006, A | c 334 | 30 | 88.2 | 508 | 4 | US-09-621-976-2834 | Sequence 2834, Ap |
| c 262 | 31 | 91.2 | 55851 | 4 | US-09-949-016-13732 | Sequence 13732, A | Sequence 13732, A | c 335 | 30 | 88.2 | 522 | 4 | US-09-270-767-5998 | Sequence 5998, Ap |
| c 263 | 31 | 91.2 | 64319 | 4 | US-09-949-016-13204 | Sequence 13204, A | Sequence 13204, A | c 336 | 30 | 88.2 | 535 | 4 | US-09-270-767-30953 | Sequence 30953, A |
| c 264 | 31 | 91.2 | 74527 | 4 | US-09-949-016-15939 | Sequence 15939, A | Sequence 15939, A | c 337 | 30 | 88.2 | 541 | 3 | US-08-642-274D-37 | Sequence 37, Appl |
| c 265 | 31 | 91.2 | 74528 | 4 | US-09-949-016-13275 | Sequence 13275, A | Sequence 13275, A | c 338 | 30 | 88.2 | 541 | 3 | US-08-952-014C-37 | Sequence 37, Appl |
| c 266 | 31 | 91.2 | 82496 | 4 | US-09-596-002-36 | Sequence 36, Appl | Sequence 36, Appl | c 339 | 30 | 88.2 | 546 | 2 | US-08-558-823-9 | Sequence 9, Appli |
| c 267 | 31 | 91.2 | 82497 | 4 | US-09-596-002-36 | Sequence 36, Appl | Sequence 36, Appl | c 340 | 30 | 88.2 | 546 | 2 | US-08-558-823-9 | Sequence 9, Appli |
| c 268 | 31 | 91.2 | 93510 | 4 | US-09-949-016-115095 | Sequence 115095, A | Sequence 115095, A | c 341 | 30 | 88.2 | 552 | 4 | US-09-513-999C-850 | Sequence 850, App |
| c 269 | 31 | 91.2 | 94755 | 4 | US-09-949-016-11839 | Sequence 11839, A | Sequence 11839, A | c 342 | 30 | 88.2 | 552 | 4 | US-09-328-352-3792 | Sequence 3792, Ap |
| c 270 | 31 | 91.2 | 96109 | 4 | US-09-596-002-35 | Sequence 35, Appl | Sequence 35, Appl | c 343 | 30 | 88.2 | 564 | 4 | US-09-540-236-1898 | Sequence 1898, Ap |
| c 271 | 31 | 91.2 | 98302 | 4 | US-09-949-016-15847 | Sequence 15847, A | Sequence 15847, A | c 344 | 30 | 88.2 | 568 | 3 | US-09-385-983-380 | Sequence 380, App |
| c 272 | 31 | 91.2 | 98439 | 4 | US-09-949-016-15957 | Sequence 15957, A | Sequence 15957, A | c 345 | 30 | 88.2 | 598 | 4 | US-09-949-016-42230 | Sequence 42230, A |
| c 273 | 31 | 91.2 | 100550 | 4 | US-09-949-016-11835 | Sequence 11835, A | Sequence 11835, A | c 346 | 30 | 88.2 | 601 | 4 | US-09-949-016-42231 | Sequence 42231, A |
| c 274 | 31 | 91.2 | 100551 | 4 | US-09-949-016-16207 | Sequence 16207, A | Sequence 16207, A | c 347 | 30 | 88.2 | 601 | 4 | US-09-949-016-42297 | Sequence 42297, A |
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| c 279 | 31 | 91.2 | 105679 | 4 | US-09-949-016-13260 | Sequence 13260, A | Sequence 13260, A | c 352 | 30 | 88.2 | 601 | 4 | US-09-949-016-61414 | Sequence 61414, A |
| c 280 | 31 | 91.2 | 110585 | 4 | US-09-949-016-13427 | Sequence 13427, A | Sequence 13427, A | c 353 | 30 | 88.2 | 601 | 4 | US-09-949-016-62959 | Sequence 62959, A |
| c 281 | 31 | 91.2 | 110585 | 4 | US-09-949-016-13427 | Sequence 13427, A | Sequence 13427, A | c 354 | 30 | 88.2 | 601 | 4 | US-09-949-016-63789 | Sequence 63789, A |
| c 282 | 31 | 91.2 | 149543 | 4 | US-09-949-016-15947 | Sequence 15947, A | Sequence 15947, A | c 355 | 30 | 88.2 | 601 | 4 | US-09-949-016-63790 | Sequence 63790, A |
| c 283 | 31 | 91.2 | 150780 | 4 | US-09-949-016-14711 | Sequence 14711, A | Sequence 14711, A | c 356 | 30 | 88.2 | 601 | 4 | US-09-949-016-74695 | Sequence 74695, A |
| c 284 | 31 | 91.2 | 162465 | 4 | US-09-949-016-14264 | Sequence 14264, A | Sequence 14264, A | c 357 | 30 | 88.2 | 601 | 4 | US-09-949-016-74894 | Sequence 74894, A |
| c 285 | 31 | 91.2 | 174259 | 4 | US-09-949-016-11968 | Sequence 11968, A | Sequence 11968, A | c 358 | 30 | 88.2 | 601 | 4 | US-09-949-016-75093 | Sequence 75093, A |
| c 286 | 31 | 91.2 | 174262 | 4 | US-09-949-016-14259 | Sequence 14259, A | Sequence 14259, A | c 359 | 30 | 88.2 | 601 | 4 | US-09-949-016-75292 | Sequence 75292, A |
| c 287 | 31 | 91.2 | 176006 | 4 | US-09-949-016-16804 | Sequence 16804, A | Sequence 16804, A | c 360 | 30 | 88.2 | 601 | 4 | US-09-949-016-75491 | Sequence 75491, A |
| c 288 | 31 | 91.2 | 183770 | 4 | US-09-949-016-15494 | Sequence 15494, A | Sequence 15494, A | c 361 | 30 | 88.2 | 601 | 4 | US-09-949-016-80634 | Sequence 80634, A |
| c 289 | 31 | 91.2 | 187916 | 4 | US-09-949-016-12980 | Sequence 12980, A | Sequence 12980, A | c 362 | 30 | 88.2 | 601 | 4 | US-09-949-016-82721 | Sequence 82721, A |
| c 290 | 31 | 91.2 | 194537 | 4 | US-09-949-016-12928 | Sequence 12928, A | Sequence 12928, A | c 363 | 30 | 88.2 | 601 | 4 | US-09-949-016-87243 | Sequence 87243, A |
| c 291 | 31 | 91.2 | 194714 | 4 | US-09-949-016-11869 | Sequence 11869, A | Sequence 11869, A | c 364 | 30 | 88.2 | 601 | 4 | US-09-949-016-92155 | Sequence 92155, A |
| c 292 | 31 | 91.2 | 196714 | 4 | US-09-949-016-15474 | Sequence 15474, A | Sequence 15474, A | c 365 | 30 | 88.2 | 601 | 4 | US-09-949-016-92325 | Sequence 92325, A |
| c 293 | 31 | 91.2 | 201529 | 4 | US-09-949-016-13740 | Sequence 13740, A | Sequence 13740, A | c 366 | 30 | 88.2 | 601 | 4 | US-09-949-016-96376 | Sequence 96376, A |
| c 294 | 31 | 91.2 | 212449 | 4 | US-09-949-016-15419 | Sequence 15419, A | Sequence 15419, A | c 367 | 30 | 88.2 | 601 | 4 | US-09-949-016-96642 | Sequence 96642, A |
| c 295 | 31 | 91.2 | 221545 | 4 | US-09-949-016-13875 | Sequence 13875, A | Sequence 13875, A | c 368 | 30 | 88.2 | 601 | 4 | US-09-949-016-96908 | Sequence 96908, A |
| c 296 | 31 | 91.2 | 229354 | 4 | US-09-705-400-64 | Sequence 64, Appl | Sequence 64, Appl | c 369 | 30 | 88.2 | 601 | 4 | US-09-949-016-97174 | Sequence 97174, A |
| c 297 | 31 | 91.2 | 231129 | 4 | US-09-949-016-16110 | Sequence 16110, A | Sequence 16110, A | c 370 | 30 | 88.2 | 601 | 4 | US-09-949-016-97440 | Sequence 97440, A |
| c 298 | 31 | 91.2 | 235064 | 4 | US-09-949-016-15390 | Sequence 15390, A | Sequence 15390, A | c 371 | 30 | 88.2 | 601 | 4 | US-09-949-016-97706 | Sequence 97706, A |
| c 299 | 31 | 91.2 | 237863 | 4 | US-09-949-016-13404 | Sequence 13404, A | Sequence 13404, A | c 372 | 30 | 88.2 | 601 | 4 | US-09-949-016-97972 | Sequence 97972, A |
| c 300 | 31 | 91.2 | 253375 | 4 | US-09-949-016-12849 | Sequence 12849, A | Sequence 12849, A | c 373 | 30 | 88.2 | 601 | 4 | US-09-949-016-98238 | Sequence 98238, A |
| c 301 | 31 | 91.2 | 254366 | 4 | US-09-822-871-3 | Sequence 3, Appli | Sequence 3, Appli | c 374 | 30 | 88.2 | 601 | 4 | US-09-949-016-98504 | Sequence 98504, A |
| c 302 | 31 | 91.2 | 266293 | 4 | US-09-949-016-11934 | Sequence 11934, A | Sequence 11934, A | c 375 | 30 | 88.2 | 601 | 4 | US-09-949-016-98770 | Sequence 98770, A |
| c 303 | 31 | 91.2 | 269223 | 4 | US-09-596-002-41 | Sequence 41, Appl | Sequence 41, Appl | c 376 | 30 | 88.2 | 601 | 4 | US-09-949-016-99036 | Sequence 99036, A |
| c 304 | 31 | 91.2 | 331814 | | | | | | | | | | | |

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| C 378 | 30 | 88.2 | 601 | 4 | US-09-949-016-39568 | Sequence 99568, A | 451 | 30 | 88.2 | 1362 | 4 | US-09-769-863-13 | Sequence 13, Appl |
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| C 380 | 30 | 88.2 | 601 | 4 | US-09-949-016-100100 | Sequence 100100, A | C 453 | 30 | 88.2 | 1377 | 4 | US-09-543-681A-2152 | Sequence 2152, Ap |
| C 381 | 30 | 88.2 | 601 | 4 | US-09-949-016-100366 | Sequence 100366, A | C 454 | 30 | 88.2 | 1386 | 4 | US-09-602-787A-359 | Sequence 359, App |
| C 382 | 30 | 88.2 | 601 | 4 | US-09-949-016-100632 | Sequence 100632, A | C 455 | 30 | 88.2 | 1387 | 4 | US-09-567-003C-19 | Sequence 19, Appl |
| C 383 | 30 | 88.2 | 601 | 4 | US-09-949-016-100936 | Sequence 100936, A | C 456 | 30 | 88.2 | 1398 | 4 | US-09-489-039A-3060 | Sequence 3060, Ap |
| C 384 | 30 | 88.2 | 601 | 4 | US-09-949-016-101202 | Sequence 101202, A | C 457 | 30 | 88.2 | 1454 | 2 | US-08-713-000-7 | Sequence 7, Appl |
| C 385 | 30 | 88.2 | 601 | 4 | US-09-949-016-101468 | Sequence 101468, A | C 458 | 30 | 88.2 | 1454 | 2 | US-08-975-316-7 | Sequence 7, Appl |
| C 386 | 30 | 88.2 | 601 | 4 | US-09-949-016-101734 | Sequence 101734, A | C 459 | 30 | 88.2 | 1454 | 3 | US-09-211-710-7 | Sequence 7, Appl |
| C 387 | 30 | 88.2 | 601 | 4 | US-09-949-016-106049 | Sequence 106049, A | C 460 | 30 | 88.2 | 1454 | 3 | US-09-615-192A-7 | Sequence 7, Appl |
| C 388 | 30 | 88.2 | 601 | 4 | US-09-949-016-106248 | Sequence 106248, A | C 461 | 30 | 88.2 | 1454 | 3 | US-09-169-789-7 | Sequence 7, Appl |
| C 389 | 30 | 88.2 | 601 | 4 | US-09-949-016-106248 | Sequence 106248, A | C 462 | 30 | 88.2 | 1460 | 3 | US-09-615-192A-95 | Sequence 95, Appl |
| C 390 | 30 | 88.2 | 601 | 4 | US-09-949-016-106447 | Sequence 106447, A | C 463 | 30 | 88.2 | 1460 | 3 | US-09-567-003C-20 | Sequence 20, Appl |
| C 391 | 30 | 88.2 | 601 | 4 | US-09-949-016-106646 | Sequence 106646, A | C 464 | 30 | 88.2 | 1460 | 4 | US-09-169-789-95 | Sequence 95, Appl |
| C 392 | 30 | 88.2 | 601 | 4 | US-09-949-016-106845 | Sequence 106845, A | C 465 | 30 | 88.2 | 1461 | 4 | US-09-857-583B-1 | Sequence 1, Appl |
| C 393 | 30 | 88.2 | 601 | 4 | US-09-949-016-117009 | Sequence 117009, A | C 466 | 30 | 88.2 | 1473 | 4 | US-09-543-681A-3766 | Sequence 3766, Ap |
| C 394 | 30 | 88.2 | 601 | 4 | US-09-949-016-117618 | Sequence 117618, A | C 467 | 30 | 88.2 | 1474 | 2 | US-08-975-316-71 | Sequence 71, Appl |
| C 395 | 30 | 88.2 | 601 | 4 | US-09-949-016-120023 | Sequence 120023, A | C 468 | 30 | 88.2 | 1474 | 3 | US-09-615-192A-71 | Sequence 71, Appl |
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| C 397 | 30 | 88.2 | 601 | 4 | US-09-949-016-120936 | Sequence 120936, A | C 470 | 30 | 88.2 | 1474 | 3 | US-09-325-932A-202 | Sequence 202, App |
| C 398 | 30 | 88.2 | 601 | 4 | US-09-949-016-130886 | Sequence 130886, A | C 471 | 30 | 88.2 | 1474 | 4 | US-09-169-789-71 | Sequence 71, Appl |
| C 399 | 30 | 88.2 | 601 | 4 | US-09-949-016-140911 | Sequence 140911, A | C 472 | 30 | 88.2 | 1474 | 4 | US-09-169-789-184 | Sequence 184, App |
| C 400 | 30 | 88.2 | 601 | 4 | US-09-949-016-169045 | Sequence 169045, A | C 473 | 30 | 88.2 | 1476 | 4 | US-09-248-796A-8230 | Sequence 8230, Ap |
| C 401 | 30 | 88.2 | 601 | 4 | US-09-949-016-169046 | Sequence 169046, A | C 474 | 30 | 88.2 | 1491 | 4 | US-09-249-020A-3 | Sequence 3, Appl |
| C 402 | 30 | 88.2 | 601 | 4 | US-09-949-016-176848 | Sequence 176848, A | C 475 | 30 | 88.2 | 1491 | 4 | US-09-668-286-3 | Sequence 3, Appl |
| C 403 | 30 | 88.2 | 601 | 4 | US-09-949-016-180641 | Sequence 180641, A | C 476 | 30 | 88.2 | 1491 | 4 | US-09-668-283-3 | Sequence 3, Appl |
| C 404 | 30 | 88.2 | 601 | 4 | US-09-949-016-196671 | Sequence 196671, A | C 477 | 30 | 88.2 | 1491 | 4 | US-10-442-173-3 | Sequence 3, Appl |
| C 405 | 30 | 88.2 | 601 | 4 | US-09-949-016-203969 | Sequence 203969, A | C 478 | 30 | 88.2 | 1503 | 4 | US-09-543-681A-1943 | Sequence 1943, Ap |
| C 406 | 30 | 88.2 | 624 | 4 | US-09-252-991A-6954 | Sequence 9954, App | C 479 | 30 | 88.2 | 1617 | 2 | US-08-834-655-1 | Sequence 1, Appl |
| C 407 | 30 | 88.2 | 632 | 4 | US-09-513-999C-12584 | Sequence 12584, A | C 480 | 30 | 88.2 | 1617 | 3 | US-08-834-655A-1 | Sequence 1, Appl |
| C 408 | 30 | 88.2 | 654 | 3 | US-09-385-982-336 | Sequence 336, App | C 481 | 30 | 88.2 | 1617 | 3 | US-09-363-574-1 | Sequence 1, Appl |
| C 409 | 30 | 88.2 | 654 | 3 | US-09-328-352-2942 | Sequence 352, App | C 482 | 30 | 88.2 | 1617 | 3 | US-09-363-526-1 | Sequence 1, Appl |
| C 410 | 30 | 88.2 | 665 | 3 | US-09-385-982-348 | Sequence 348, App | C 483 | 30 | 88.2 | 1617 | 3 | US-09-330-235-17 | Sequence 17, Appl |
| C 411 | 30 | 88.2 | 669 | 4 | US-09-328-352-2741 | Sequence 328, App | C 484 | 30 | 88.2 | 1701 | 4 | US-09-328-352-683 | Sequence 683, App |
| C 412 | 30 | 88.2 | 673 | 4 | US-09-640-211A-328 | Sequence 328, App | C 485 | 30 | 88.2 | 1884 | 4 | US-09-328-352-3421 | Sequence 3421, Ap |
| C 413 | 30 | 88.2 | 678 | 4 | US-09-540-236-392 | Sequence 392, App | C 486 | 30 | 88.2 | 1987 | 4 | US-09-774-528-158 | Sequence 158, App |
| C 414 | 30 | 88.2 | 694 | 4 | US-09-270-767-3952 | Sequence 3952, App | C 487 | 30 | 88.2 | 2043 | 4 | US-09-248-796A-2264 | Sequence 2264, Ap |
| C 415 | 30 | 88.2 | 694 | 4 | US-09-270-767-19234 | Sequence 19234, A | C 488 | 30 | 88.2 | 2234 | 4 | US-09-949-016-3362 | Sequence 3362, Ap |
| C 416 | 30 | 88.2 | 702 | 4 | US-09-252-991A-6780 | Sequence 6780, Ap | C 489 | 30 | 88.2 | 2394 | 4 | US-09-620-312D-592 | Sequence 592, App |
| C 417 | 30 | 88.2 | 732 | 4 | US-09-248-796A-3894 | Sequence 3894, Ap | C 490 | 30 | 88.2 | 2421 | 1 | US-08-063-552-1 | Sequence 1, Appl |
| C 418 | 30 | 88.2 | 745 | 4 | US-09-513-999C-3929 | Sequence 3929, Ap | C 491 | 30 | 88.2 | 2421 | 5 | PCT-US93-05704-1 | Sequence 1, Appl |
| C 419 | 30 | 88.2 | 756 | 4 | US-09-248-796A-4002 | Sequence 4002, Ap | C 492 | 30 | 88.2 | 2430 | 4 | US-09-620-312D-176 | Sequence 176, App |
| C 420 | 30 | 88.2 | 840 | 4 | US-09-489-039A-2990 | Sequence 2990, Ap | C 493 | 30 | 88.2 | 2430 | 4 | US-09-620-312D-591 | Sequence 591, App |
| C 421 | 30 | 88.2 | 868 | 4 | US-09-270-767-13287 | Sequence 13287, A | C 494 | 30 | 88.2 | 2436 | 3 | US-08-983-275-1 | Sequence 1, Appl |
| C 422 | 30 | 88.2 | 879 | 4 | US-09-107-532A-214 | Sequence 214, App | C 495 | 30 | 88.2 | 2508 | 4 | US-09-248-796A-971 | Sequence 971, App |
| C 423 | 30 | 88.2 | 957 | 4 | US-09-902-540-8470 | Sequence 8470, Ap | C 496 | 30 | 88.2 | 2593 | 4 | US-09-624-912-89 | Sequence 89, Appl |
| C 424 | 30 | 88.2 | 960 | 4 | US-09-949-016-5223 | Sequence 5223, Ap | C 497 | 30 | 88.2 | 2743 | 3 | US-09-060-482-3 | Sequence 3, Appl |
| C 425 | 30 | 88.2 | 996 | 4 | US-09-270-767-10797 | Sequence 10797, A | C 498 | 30 | 88.2 | 2880 | 4 | US-09-949-016-2952 | Sequence 2952, Ap |
| C 426 | 30 | 88.2 | 1022 | 4 | US-09-270-767-14723 | Sequence 14723, A | C 499 | 30 | 88.2 | 2881 | 4 | US-09-702-705-1794 | Sequence 1794, Ap |
| C 427 | 30 | 88.2 | 1068 | 4 | US-09-567-003C-21 | Sequence 21, Appl | C 500 | 30 | 88.2 | 2881 | 4 | US-09-736-457-1794 | Sequence 1794, Ap |
| C 428 | 30 | 88.2 | 1093 | 4 | US-09-023-655-1169 | Sequence 1169, Ap | C 501 | 30 | 88.2 | 2895 | 3 | US-09-671-325-1794 | Sequence 171, App |
| C 429 | 30 | 88.2 | 1095 | 4 | US-09-540-236-712 | Sequence 712, App | C 502 | 30 | 88.2 | 2895 | 3 | US-09-556-877-183 | Sequence 183, App |
| C 430 | 30 | 88.2 | 1111 | 4 | US-09-016-434-1297 | Sequence 1297, Ap | C 503 | 30 | 88.2 | 2895 | 4 | US-09-598-419-171 | Sequence 171, App |
| C 431 | 30 | 88.2 | 1116 | 4 | US-09-252-991A-6913 | Sequence 6913, Ap | C 504 | 30 | 88.2 | 2934 | 3 | US-09-556-877-183 | Sequence 183, App |
| C 432 | 30 | 88.2 | 1122 | 4 | US-09-543-681A-245 | Sequence 245, App | C 505 | 30 | 88.2 | 2934 | 3 | US-09-620-412C-183 | Sequence 183, App |
| C 433 | 30 | 88.2 | 1143 | 4 | US-09-328-352-415 | Sequence 2115, Ap | C 506 | 30 | 88.2 | 2934 | 4 | US-09-598-419-183 | Sequence 183, App |
| C 434 | 30 | 88.2 | 1203 | 4 | US-09-828-509-430 | Sequence 490, App | C 507 | 30 | 88.2 | 2934 | 4 | US-09-598-419-183 | Sequence 7, Appl |
| C 435 | 30 | 88.2 | 1208 | 4 | US-09-721-870-7 | Sequence 7, Appl | C 508 | 30 | 88.2 | 3159 | 3 | US-09-437-054A-7 | Sequence 7, Appl |
| C 436 | 30 | 88.2 | 1211 | 4 | US-09-023-655-793 | Sequence 793, App | C 509 | 30 | 88.2 | 3209 | 4 | US-09-949-016-3688 | Sequence 3688, Ap |
| C 437 | 30 | 88.2 | 1214 | 4 | US-09-721-870-9 | Sequence 9, Appl | C 510 | 30 | 88.2 | 3237 | 2 | US-08-419-075-26 | Sequence 26, Appl |
| C 438 | 30 | 88.2 | 1220 | 4 | US-09-721-870-5 | Sequence 5, Appl | C 511 | 30 | 88.2 | 3348 | 4 | US-09-312-762A-2 | Sequence 2, Appl |
| C 439 | 30 | 88.2 | 1251 | 4 | US-09-252-991A-6829 | Sequence 6829, Ap | C 512 | 30 | 88.2 | 3356 | 4 | US-09-634-238-8 | Sequence 8, Appl |
| C 440 | 30 | 88.2 | 1251 | 4 | US-09-540-236-645 | Sequence 645, App | C 513 | 30 | 88.2 | 3442 | 4 | US-09-814-915A-39 | Sequence 39, Appl |
| C 441 | 30 | 88.2 | 1254 | 4 | US-09-248-796A-3831 | Sequence 3831, Ap | C 514 | 30 | 88.2 | 3466 | 3 | US-09-438-906-1 | Sequence 1, Appl |
| C 442 | 30 | 88.2 | 1261 | 3 | US-08-475-742-16 | Sequence 16, Appl | C 515 | 30 | 88.2 | 3492 | 3 | US-09-438-906-3 | Sequence 3, Appl |
| C 443 | 30 | 88.2 | 1261 | 4 | US-08-261-293-16 | Sequence 16, Appl | C 516 | 30 | 88.2 | 3496 | 4 | US-09-949-016-1688 | Sequence 1688, Ap |
| C 444 | 30 | 88.2 | 1263 | 4 | US-09-543-681A-3749 | Sequence 3749, Ap | C 517 | 30 | 88.2 | 3539 | 4 | US-09-949-016-2396 | Sequence 2396, Ap |
| C 445 | 30 | 88.2 | 1308 | 4 | US-09-489-039A-2917 | Sequence 2917, Ap | C 518 | 30 | 88.2 | 3556 | 1 | US-07-971-624E-1 | Sequence 1, Appl |
| C 446 | 30 | 88.2 | 1318 | 4 | US-09-721-870-11 | Sequence 11, Appl | C 519 | 30 | 88.2 | 3572 | 1 | US-07-971-624E-2 | Sequence 2, Appl |
| C 447 | 30 | 88.2 | 1335 | 4 | US-09-249-020A-1 | Sequence 1, Appl | C 520 | 30 | 88.2 | 3601 | 3 | US-09-668-680-2 | Sequence 2, Appl |
| C 448 | 30 | 88.2 | 1335 | 4 | US-09-668-286-1 | Sequence 1, Appl | C 521 | 30 | 88.2 | 3616 | 4 | US-09-976-594-465 | Sequence 285, App |
| C 449 | 30 | 88.2 | 1335 | 4 | US-09-668-283-1 | Sequence 1, Appl | C 522 | 30 | 88.2 | 3934 | 4 | US-09-023-655-1066 | Sequence 1066, Ap |
| C 450 | 30 | 88.2 | 1335 | 4 | US-10-442-173-1 | Sequence 1, Appl | C 523 | 30 | 88.2 | 4032 | 1 | US-08-107-748-3 | Sequence 3, Appl |

| | | | | | | | | | | | | | |
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| 524 | 30 | 88.2 | 4032 | 1 | US-08-245-809-4 | Sequence 4, Appl1 | c 597 | 30 | 88.2 | 46492 | 4 | US-09-949-016-13954 | Sequence 12954, A |
| 525 | 30 | 88.2 | 4032 | 5 | PCT-US92-01385-3 | Sequence 3, Appl1 | 598 | 30 | 88.2 | 46885 | 4 | US-09-949-016-13848 | Sequence 13848, A |
| 526 | 30 | 88.2 | 4071 | 3 | US-09-513-057C-5 | Sequence 5, Appl1 | c 599 | 30 | 88.2 | 47858 | 4 | US-09-949-016-14965 | Sequence 14965, A |
| 527 | 30 | 88.2 | 4071 | 4 | US-09-746-801A-5 | Sequence 5, Appl1 | c 600 | 30 | 88.2 | 47968 | 4 | US-09-949-016-15240 | Sequence 15240, A |
| 528 | 30 | 88.2 | 4087 | 4 | US-09-799-451-262 | Sequence 262, App | c 601 | 30 | 88.2 | 48328 | 4 | US-09-596-002-27 | Sequence 27, Appl |
| 529 | 30 | 88.2 | 4771 | 4 | US-09-620-312D-121 | Sequence 121, App | c 602 | 30 | 88.2 | 47995 | 3 | US-09-453-702B-60 | Sequence 60, Appl |
| c 530 | 30 | 88.2 | 5325 | 4 | US-10-164-595-17 | Sequence 17, Appl | c 603 | 30 | 88.2 | 49971 | 4 | US-09-949-016-16888 | Sequence 16888, A |
| c 531 | 30 | 88.2 | 5334 | 4 | US-10-164-595-21 | Sequence 21, Appl | c 604 | 30 | 88.2 | 55195 | 4 | US-09-949-016-15854 | Sequence 15854, A |
| c 532 | 30 | 88.2 | 5455 | 1 | US-08-342-930-1 | Sequence 1, Appl1 | c 605 | 30 | 88.2 | 58829 | 4 | US-09-949-016-13146 | Sequence 13146, A |
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| c 535 | 30 | 88.2 | 5512 | 3 | US-08-642-274D-1 | Sequence 1, Appl1 | c 608 | 30 | 88.2 | 62663 | 4 | US-09-453-702B-62 | Sequence 62, Appl |
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| c 537 | 30 | 88.2 | 5912 | 3 | US-08-952-014C-1 | Sequence 1, Appl1 | c 610 | 30 | 88.2 | 83617 | 4 | US-09-949-016-12254 | Sequence 12254, A |
| c 538 | 30 | 88.2 | 6298 | 4 | US-09-830-123-20 | Sequence 20, Appl | c 611 | 30 | 88.2 | 87205 | 4 | US-09-949-016-13430 | Sequence 13430, A |
| c 539 | 30 | 88.2 | 6380 | 4 | US-09-902-540-891 | Sequence 891, App | c 612 | 30 | 88.2 | 90150 | 4 | US-09-949-016-17383 | Sequence 17383, A |
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| c 549 | 30 | 88.2 | 9171 | 3 | US-08-642-274D-2 | Sequence 2, Appl1 | c 622 | 30 | 88.2 | 112623 | 4 | US-09-949-016-14374 | Sequence 14374, A |
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| c 554 | 30 | 88.2 | 9385 | 3 | US-09-360-416-1 | Sequence 1, Appl1 | c 627 | 30 | 88.2 | 125188 | 4 | US-09-949-016-11980 | Sequence 11980, A |
| c 555 | 30 | 88.2 | 9389 | 4 | US-09-949-016-4409 | Sequence 4409, Ap | c 628 | 30 | 88.2 | 129778 | 4 | US-09-949-016-11291 | Sequence 12191, A |
| c 556 | 30 | 88.2 | 9558 | 4 | US-09-949-016-13026 | Sequence 13026, A | c 629 | 30 | 88.2 | 129778 | 4 | US-09-949-016-17075 | Sequence 17075, A |
| c 557 | 30 | 88.2 | 9870 | 1 | US-08-508-836A-9 | Sequence 9, Appl1 | c 630 | 30 | 88.2 | 131631 | 4 | US-09-949-016-11757 | Sequence 11757, A |
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| c 560 | 30 | 88.2 | 12032 | 4 | US-09-949-016-15080 | Sequence 15080, A | c 633 | 30 | 88.2 | 148640 | 4 | US-09-949-016-16151 | Sequence 16151, A |
| c 561 | 30 | 88.2 | 12032 | 4 | US-09-949-016-15081 | Sequence 15081, A | c 634 | 30 | 88.2 | 148783 | 4 | US-09-949-016-15729 | Sequence 15729, A |
| c 562 | 30 | 88.2 | 14600 | 4 | US-09-949-016-16450 | Sequence 16450, A | c 635 | 30 | 88.2 | 160759 | 4 | US-09-949-016-16514 | Sequence 16514, A |
| c 563 | 30 | 88.2 | 14635 | 4 | US-09-949-016-13927 | Sequence 13927, A | c 636 | 30 | 88.2 | 165651 | 4 | US-09-949-016-13032 | Sequence 13032, A |
| c 564 | 30 | 88.2 | 15164 | 4 | US-09-919-497-20 | Sequence 20, Appl | c 637 | 30 | 88.2 | 167708 | 4 | US-09-949-016-16423 | Sequence 16423, A |
| c 565 | 30 | 88.2 | 16883 | 4 | US-09-949-016-14694 | Sequence 14694, A | c 638 | 30 | 88.2 | 174639 | 4 | US-09-949-016-16509 | Sequence 16509, A |
| c 566 | 30 | 88.2 | 18157 | 4 | US-09-949-016-16193 | Sequence 16193, A | c 639 | 30 | 88.2 | 187595 | 4 | US-09-949-016-15546 | Sequence 15546, A |
| c 567 | 30 | 88.2 | 18620 | 4 | US-09-949-016-13010 | Sequence 13010, A | c 640 | 30 | 88.2 | 191433 | 4 | US-09-949-016-16144 | Sequence 16144, A |
| c 568 | 30 | 88.2 | 18994 | 2 | US-08-459-586-4 | Sequence 4, Appl1 | c 641 | 30 | 88.2 | 192956 | 4 | US-09-949-016-14382 | Sequence 14382, A |
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| c 570 | 30 | 88.2 | 19566 | 4 | US-09-949-016-12096 | Sequence 12096, A | c 643 | 30 | 88.2 | 208433 | 4 | US-09-949-016-13527 | Sequence 13527, A |
| c 571 | 30 | 88.2 | 19567 | 4 | US-09-949-016-14114 | Sequence 14114, A | c 644 | 30 | 88.2 | 213456 | 4 | US-09-820-007-3 | Sequence 3, Appl1 |
| c 572 | 30 | 88.2 | 22294 | 4 | US-09-949-016-14020 | Sequence 14020, A | c 645 | 30 | 88.2 | 229354 | 4 | US-09-705-400-64 | Sequence 64, Appl |
| c 573 | 30 | 88.2 | 23219 | 4 | US-09-949-016-13556 | Sequence 13556, A | c 646 | 30 | 88.2 | 236341 | 4 | US-09-949-016-13978 | Sequence 13978, A |
| c 574 | 30 | 88.2 | 24319 | 4 | US-09-949-016-14068 | Sequence 14068, A | c 647 | 30 | 88.2 | 254778 | 4 | US-09-949-016-13417 | Sequence 12417, A |
| c 575 | 30 | 88.2 | 24645 | 4 | US-09-949-016-14062 | Sequence 14062, A | c 648 | 30 | 88.2 | 276237 | 4 | US-09-949-016-17504 | Sequence 17504, A |
| c 576 | 30 | 88.2 | 25333 | 4 | US-09-949-016-14069 | Sequence 14069, A | c 649 | 30 | 88.2 | 278866 | 4 | US-09-949-016-13922 | Sequence 13922, A |
| c 577 | 30 | 88.2 | 26173 | 3 | US-09-453-702B-69 | Sequence 69, Appl | c 650 | 30 | 88.2 | 278866 | 4 | US-09-949-016-13924 | Sequence 13924, A |
| c 578 | 30 | 88.2 | 26664 | 3 | US-09-564-805-28 | Sequence 28, Appl | c 651 | 30 | 88.2 | 278866 | 4 | US-09-949-016-13924 | Sequence 13924, A |
| c 579 | 30 | 88.2 | 28585 | 4 | US-09-949-016-17311 | Sequence 17311, A | c 652 | 30 | 88.2 | 278866 | 4 | US-09-949-016-13925 | Sequence 13925, A |
| c 580 | 30 | 88.2 | 28720 | 3 | US-09-341-587-7 | Sequence 7, Appl1 | c 653 | 30 | 88.2 | 278866 | 4 | US-09-949-016-13926 | Sequence 13926, A |
| c 581 | 30 | 88.2 | 29123 | 4 | US-09-949-016-12694 | Sequence 12694, A | c 654 | 30 | 88.2 | 278866 | 4 | US-09-949-016-14699 | Sequence 14699, A |
| c 582 | 30 | 88.2 | 29598 | 4 | US-09-949-016-15607 | Sequence 15607, A | c 655 | 30 | 88.2 | 278866 | 4 | US-09-949-016-14700 | Sequence 14700, A |
| c 583 | 30 | 88.2 | 30444 | 4 | US-09-949-016-14997 | Sequence 14997, A | c 656 | 30 | 88.2 | 278866 | 4 | US-09-949-016-14701 | Sequence 14701, A |
| c 584 | 30 | 88.2 | 33908 | 4 | US-09-949-016-15104 | Sequence 15104, A | c 657 | 30 | 88.2 | 278866 | 4 | US-09-949-016-14702 | Sequence 14702, A |
| c 585 | 30 | 88.2 | 35913 | 4 | US-09-949-016-15586 | Sequence 15586, A | c 658 | 30 | 88.2 | 278866 | 4 | US-09-949-016-14703 | Sequence 14703, A |
| c 586 | 30 | 88.2 | 36203 | 4 | US-09-949-016-15430 | Sequence 15430, A | c 659 | 30 | 88.2 | 323820 | 4 | US-09-949-016-14139 | Sequence 14139, A |
| c 587 | 30 | 88.2 | 36618 | 4 | US-09-949-016-15935 | Sequence 15935, A | c 660 | 30 | 88.2 | 325034 | 4 | US-09-949-016-14957 | Sequence 14957, A |
| c 588 | 30 | 88.2 | 36820 | 4 | US-09-949-016-16665 | Sequence 16665, A | c 661 | 30 | 88.2 | 340380 | 4 | US-09-949-016-14179 | Sequence 14179, A |
| c 589 | 30 | 88.2 | 36938 | 4 | US-09-949-016-13484 | Sequence 13484, A | c 662 | 30 | 88.2 | 346112 | 4 | US-09-949-016-13165 | Sequence 13165, A |
| c 590 | 30 | 88.2 | 37996 | 4 | US-09-949-016-16472 | Sequence 16472, A | c 663 | 30 | 88.2 | 389504 | 4 | US-09-949-016-11774 | Sequence 11774, A |
| c 591 | 30 | 88.2 | 38479 | 4 | US-09-949-016-16730 | Sequence 16730, A | c 664 | 30 | 88.2 | 389080 | 4 | US-09-949-016-14720 | Sequence 14720, A |
| c 592 | 30 | 88.2 | 40586 | 4 | US-09-949-016-16965 | Sequence 16965, A | c 665 | 30 | 88.2 | 767677 | 4 | US-09-949-016-12147 | Sequence 12147, A |
| c 593 | 30 | 88.2 | 42894 | 4 | US-09-949-016-13201 | Sequence 12301, A | c 666 | 30 | 88.2 | 767677 | 4 | US-09-949-016-17361 | Sequence 17361, A |
| c 594 | 30 | 88.2 | 42898 | 4 | US-09-949-016-15904 | Sequence 15904, A | c 667 | 30 | 88.2 | 818128 | 4 | US-09-949-016-14546 | Sequence 14546, A |
| c 595 | 30 | 88.2 | 42917 | 4 | US-09-949-016-13795 | Sequence 13795, A | c 668 | 30 | 88.2 | 818128 | 4 | US-09-949-016-14547 | Sequence 14547, A |
| c 596 | 30 | 88.2 | 46492 | 4 | US-09-949-016-12953 | Sequence 12953, A | c 669 | 30 | 88.2 | 818128 | 4 | US-09-949-016-14548 | Sequence 14548, A |

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| C 670 | 30 | 88.2 | 818128 | 4 | US-09-949-016-14549 | Sequence 14549, A | 743 | 29 | 85.3 | 310 | 4 | US-09-270-767-18054 | Sequence 18054, A |
| C 671 | 30 | 88.2 | 818128 | 4 | US-09-949-016-14550 | Sequence 14550, A | C 744 | 29 | 85.3 | 313 | 4 | US-09-270-767-7295 | Sequence 7295, Ap |
| C 672 | 30 | 88.2 | 818128 | 4 | US-09-949-016-14551 | Sequence 14551, A | C 745 | 29 | 85.3 | 313 | 4 | US-09-270-767-22577 | Sequence 22577, A |
| C 673 | 30 | 88.2 | 818128 | 4 | US-09-949-016-14552 | Sequence 14552, A | 746 | 29 | 85.3 | 314 | 3 | US-08-905-223-91 | Sequence 91, Appl |
| C 674 | 30 | 88.2 | 818128 | 4 | US-09-949-016-14553 | Sequence 14553, A | C 747 | 29 | 85.3 | 315 | 4 | US-09-902-540-8453 | Sequence 8453, Ap |
| C 675 | 30 | 88.2 | 818128 | 4 | US-09-949-016-14554 | Sequence 14554, A | C 748 | 29 | 85.3 | 316 | 2 | US-08-799-173A-16 | Sequence 16, Appl |
| C 676 | 30 | 88.2 | 818128 | 4 | US-09-949-016-14555 | Sequence 14555, A | C 749 | 29 | 85.3 | 316 | 2 | US-08-799-173A-17 | Sequence 17, Appl |
| C 677 | 30 | 88.2 | 818128 | 4 | US-09-949-016-14556 | Sequence 14556, A | C 750 | 29 | 85.3 | 316 | 4 | US-09-170-042A-17 | Sequence 17, Appl |
| C 678 | 30 | 88.2 | 818128 | 4 | US-09-949-016-14557 | Sequence 14557, A | C 751 | 29 | 85.3 | 316 | 4 | US-09-170-042A-18 | Sequence 18, Appl |
| C 679 | 30 | 88.2 | 818128 | 4 | US-09-949-016-14558 | Sequence 14558, A | C 752 | 29 | 85.3 | 321 | 4 | US-09-902-540-9225 | Sequence 9225, Ap |
| C 680 | 30 | 88.2 | 818128 | 4 | US-09-949-016-14559 | Sequence 14559, A | 753 | 29 | 85.3 | 321 | 4 | US-09-248-796A-11993 | Sequence 11993, A |
| C 681 | 30 | 88.2 | 818128 | 4 | US-09-949-016-14560 | Sequence 14560, A | 754 | 29 | 85.3 | 322 | 1 | US-08-421-356-2 | Sequence 2, Appl1 |
| C 682 | 30 | 88.2 | 818128 | 4 | US-09-949-016-14561 | Sequence 14561, A | 755 | 29 | 85.3 | 322 | 3 | US-09-046-783-2 | Sequence 2, Appl1 |
| C 683 | 30 | 88.2 | 818128 | 4 | US-09-949-016-14562 | Sequence 14562, A | C 756 | 29 | 85.3 | 324 | 3 | US-09-134-001C-151 | Sequence 151, App |
| C 684 | 30 | 88.2 | 818128 | 4 | US-09-949-016-14563 | Sequence 14563, A | 757 | 29 | 85.3 | 334 | 4 | US-09-270-767-28697 | Sequence 28697, A |
| C 685 | 30 | 88.2 | 818128 | 4 | US-09-949-016-14564 | Sequence 14564, A | C 758 | 29 | 85.3 | 338 | 4 | US-09-640-211A-1443 | Sequence 1443, Ap |
| C 686 | 30 | 88.2 | 818128 | 4 | US-09-949-016-14565 | Sequence 14565, A | 759 | 29 | 85.3 | 342 | 4 | US-09-107-433-1625 | Sequence 1625, Ap |
| C 687 | 30 | 88.2 | 818128 | 4 | US-09-949-016-14566 | Sequence 14566, A | C 760 | 29 | 85.3 | 348 | 2 | US-08-853-659A-33 | Sequence 33, Appl |
| C 688 | 30 | 88.2 | 1230025 | 4 | US-09-198-452A-1 | Sequence 1, Appl1 | 761 | 29 | 85.3 | 353 | 4 | US-09-513-999C-31652 | Sequence 31652, A |
| C 689 | 30 | 88.2 | 1230230 | 4 | US-09-438-185A-1 | Sequence 1, Appl1 | C 762 | 29 | 85.3 | 357 | 4 | US-09-775-932-23 | Sequence 23, Appl |
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| C 691 | 30 | 88.2 | 4411529 | 3 | US-09-103-840A-2 | Sequence 1, Appl1 | C 764 | 29 | 85.3 | 366 | 3 | US-09-020-956-115 | Sequence 115, App |
| C 692 | 29 | 85.3 | 25 | 2 | US-08-859-998-105 | Sequence 105, App | 765 | 29 | 85.3 | 366 | 3 | US-09-030-607-115 | Sequence 115, App |
| C 693 | 29 | 85.3 | 25 | 3 | US-09-225-928-105 | Sequence 105, App | C 766 | 29 | 85.3 | 366 | 3 | US-09-439-313-115 | Sequence 115, App |
| C 694 | 29 | 85.3 | 25 | 4 | US-09-225-201B-105 | Sequence 105, App | C 767 | 29 | 85.3 | 366 | 3 | US-09-352-616A-115 | Sequence 115, App |
| C 695 | 29 | 85.3 | 25 | 4 | US-09-396-196G-1004 | Sequence 1004, Ap | C 768 | 29 | 85.3 | 366 | 3 | US-09-232-149A-115 | Sequence 115, App |
| C 696 | 29 | 85.3 | 71 | 2 | US-08-477-527A-60 | Sequence 60, Appl | C 769 | 29 | 85.3 | 366 | 4 | US-09-159-812-115 | Sequence 115, App |
| C 697 | 29 | 85.3 | 71 | 3 | US-08-481-710-60 | Sequence 60, Appl | C 770 | 29 | 85.3 | 366 | 4 | US-09-636-215-115 | Sequence 115, App |
| C 698 | 29 | 85.3 | 71 | 5 | PCT-US96-09537-60 | Sequence 60, Appl | C 771 | 29 | 85.3 | 366 | 4 | US-09-685-166A-115 | Sequence 115, App |
| C 699 | 29 | 85.3 | 105 | 4 | US-09-513-999C-19529 | Sequence 19529, Ap | C 772 | 29 | 85.3 | 366 | 4 | US-09-115-453-115 | Sequence 115, App |
| C 700 | 29 | 85.3 | 114 | 4 | US-09-902-540-5774 | Sequence 5774, Ap | C 773 | 29 | 85.3 | 366 | 4 | US-09-688-489-115 | Sequence 115, App |
| C 701 | 29 | 85.3 | 140 | 4 | US-09-270-767-25601 | Sequence 25601, A | C 774 | 29 | 85.3 | 366 | 4 | US-09-679-426-115 | Sequence 115, App |
| C 702 | 29 | 85.3 | 140 | 4 | US-09-513-999C-21615 | Sequence 21615, A | C 775 | 29 | 85.3 | 366 | 4 | US-09-759-143-115 | Sequence 115, App |
| C 703 | 29 | 85.3 | 178 | 3 | US-08-991-789A-188 | Sequence 188, App | C 776 | 29 | 85.3 | 366 | 4 | US-09-651-236-115 | Sequence 115, App |
| C 704 | 29 | 85.3 | 178 | 3 | US-09-062-451-188 | Sequence 188, App | C 777 | 29 | 85.3 | 369 | 4 | US-09-248-796A-7832 | Sequence 7832, Ap |
| C 705 | 29 | 85.3 | 178 | 3 | US-09-598-326-188 | Sequence 188, App | C 778 | 29 | 85.3 | 369 | 4 | US-10-083-424-17 | Sequence 17, Appl |
| C 706 | 29 | 85.3 | 178 | 4 | US-09-289-198-188 | Sequence 188, App | C 779 | 29 | 85.3 | 375 | 4 | US-09-621-976-17190 | Sequence 17190, A |
| C 707 | 29 | 85.3 | 178 | 4 | US-09-429-755-188 | Sequence 188, App | 780 | 29 | 85.3 | 375 | 4 | US-09-640-211A-1413 | Sequence 1413, Ap |
| C 708 | 29 | 85.3 | 178 | 4 | US-09-699-295-188 | Sequence 188, App | C 781 | 29 | 85.3 | 381 | 4 | US-09-134-000C-593 | Sequence 593, App |
| C 709 | 29 | 85.3 | 186 | 4 | US-09-270-767-26311 | Sequence 26311, Ap | C 782 | 29 | 85.3 | 384 | 4 | US-09-902-540-1711 | Sequence 1711, Ap |
| C 710 | 29 | 85.3 | 186 | 4 | US-09-270-767-27947 | Sequence 27947, A | 783 | 29 | 85.3 | 390 | 1 | US-08-482-882-79 | Sequence 79, Appl |
| C 711 | 29 | 85.3 | 186 | 4 | US-09-270-767-29227 | Sequence 29227, A | 784 | 29 | 85.3 | 390 | 1 | US-08-483-389-79 | Sequence 79, Appl |
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| C 713 | 29 | 85.3 | 201 | 4 | US-09-248-796A-9277 | Sequence 9277, Ap | 786 | 29 | 85.3 | 390 | 2 | US-08-473-503-79 | Sequence 79, Appl |
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| C 717 | 29 | 85.3 | 222 | 4 | US-09-513-999C-13712 | Sequence 13712, A | 790 | 29 | 85.3 | 390 | 3 | US-08-475-680-79 | Sequence 79, Appl |
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| C 719 | 29 | 85.3 | 231 | 4 | US-09-107-532A-3197 | Sequence 3197, Ap | C 792 | 29 | 85.3 | 391 | 4 | US-09-270-767-3793 | Sequence 3793, Ap |
| C 720 | 29 | 85.3 | 237 | 4 | US-09-270-767-28845 | Sequence 28845, A | C 793 | 29 | 85.3 | 391 | 4 | US-09-270-767-19075 | Sequence 19075, A |
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| C 722 | 29 | 85.3 | 255 | 4 | US-09-902-540-8500 | Sequence 8500, Ap | C 795 | 29 | 85.3 | 393 | 4 | US-09-107-433-943 | Sequence 943, App |
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| C 724 | 29 | 85.3 | 262 | 4 | US-09-313-294A-2014 | Sequence 2014, Ap | C 797 | 29 | 85.3 | 400 | 4 | US-08-956-171E-3726 | Sequence 3726, Ap |
| C 725 | 29 | 85.3 | 267 | 4 | US-09-313-294A-117 | Sequence 117, App | C 798 | 29 | 85.3 | 400 | 4 | US-08-781-986A-3726 | Sequence 3726, Ap |
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| C 732 | 29 | 85.3 | 305 | 3 | US-09-439-313-295 | Sequence 295, App | C 805 | 29 | 85.3 | 411 | 4 | US-09-902-540-8481 | Sequence 8481, Ap |
| C 733 | 29 | 85.3 | 305 | 3 | US-09-352-616A-295 | Sequence 295, App | C 806 | 29 | 85.3 | 412 | 4 | US-09-621-976-623 | Sequence 623, App |
| C 734 | 29 | 85.3 | 305 | 3 | US-09-232-149A-295 | Sequence 295, App | C 807 | 29 | 85.3 | 429 | 4 | US-09-543-681A-3274 | Sequence 3274, Ap |
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| C 740 | 29 | 85.3 | 305 | 4 | US-09-759-143-295 | Sequence 295, App | C 813 | 29 | 85.3 | 446 | 4 | US-09-270-767-12225 | Sequence 12225, A |
| C 741 | 29 | 85.3 | 305 | 4 | US-09-651-236-295 | Sequence 295, App | C 814 | 29 | 85.3 | 447 | 4 | US-09-501-115-17 | Sequence 17, Appl |
| C 742 | 29 | 85.3 | 310 | 4 | US-09-270-767-2772 | Sequence 2772, Ap | 815 | 29 | 85.3 | 450 | 4 | US-09-270-767-5413 | Sequence 5413, Ap |

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| C 820 | 29 | 85.3 | 456 | 3 | US-09-328-352-1362 | Sequence 1362, Ap | C 893 | 29 | 85.3 | 601 | 4 | US-09-949-016-26974 | Sequence 26974, A |
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| C 823 | 29 | 85.3 | 464 | 4 | US-09-270-767-10019 | Sequence 10019, A | C 896 | 29 | 85.3 | 601 | 4 | US-09-949-016-26974 | Sequence 26974, A |
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| C 858 | 29 | 85.3 | 544 | 4 | US-09-621-976-2695 | Sequence 2695, Ap | C 931 | 29 | 85.3 | 601 | 4 | US-09-949-016-26974 | Sequence 26974, A |
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ALIGNMENTS

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; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33466
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-33466
Alignment Scores:
Pred. No.: 19.2 Length: 25
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-396-196G-33466 (1-25)
Qy 1 HisAsnAlaHisHis 5
Db 6 CACAATGCACATCAC 20
RESULT 2
US-09-270-767-8295
; Sequence 8295, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8295
; LENGTH: 82
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-8295
Alignment Scores:
Pred. No.: 71.8 Length: 82
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-270-767-8295 (1-82)
Qy 1 HisAsnAlaHisHis 5
Db 2 CACAACGCCACCAC 16
RESULT 3
US-09-270-767-23577
; Sequence 23577, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23577
; LENGTH: 82
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-23577
Alignment Scores:
Pred. No.: 71.8 Length: 82
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-270-767-23577 (1-82)
Qy 1 HisAsnAlaHisHis 5
Db 2 CACAACGCCACCAC 16
RESULT 4
US-09-270-767-28874

```
; Sequence 28874, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 28874
; LENGTH: 206
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-28874

Alignment Scores:
Pred. No.: 200 Length: 206
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-270-767-28874 (1-206)

Qy 1 HisAenAlaHis 5
Db 183 CACAATGCCACCAT 197

RESULT 5
US-09-556-171E-4362/c
; Sequence 4362, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESS: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 4362:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 206 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-4362

Alignment Scores:
Pred. No.: 322 Length: 316
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-08-781-986A-4362 (1-316)

Qy 1 HisAenAlaHis 5
Db 205 CATAACGCCACATCAT 191

RESULT 6
US-08-781-986A-4362/c
; Sequence 4362, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESS: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 4362:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-4362

Alignment Scores:
Pred. No.: 322 Length: 316
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-08-781-986A-4362 (1-316)
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```
Oy      1 HisaenAlaHisHis 5
      |||||
Db      205 CATACGGCACATCAT 191

RESULT 7
US-09-543-681A-3814/c
; Sequence 3814, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETTON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 3814
; LENGTH: 333
; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-3814

Alignment Scores:
Pred. No.:      341      Length:      333
Score:          34.00    Matches:      5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:      100.00% Indels:      0
DB:              4      Gaps:      0

US-10-029-756-12 (1-5) x US-09-543-681A-3814 (1-333)

Oy      1 HisaenAlaHisHis 5
      |||||
Db      205 CATACGGGCACCAC 191

RESULT 8
US-08-956-171E-4136
; Sequence 4136, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 4136:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-4136

Alignment Scores:
Pred. No.:      358      Length:      348
Score:          34.00    Matches:      5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:      100.00% Indels:      0
DB:              4      Gaps:      0

US-10-029-756-12 (1-5) x US-08-956-171E-4136 (1-348)

Oy      1 HisaenAlaHisHis 5
      |||||
Db      144 CATACGGCACATCAT 158

RESULT 9
US-08-781-986A-4136
; Sequence 4136, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 4136:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 348 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-4136

Alignment Scores:
Pred. No.:      358      Length:      348
Score:          34.00    Matches:      5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:      100.00% Indels:      0
DB:              4      Gaps:      0
```

Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-08-781-986A-4136 (1-348)

Qy 1 HisAenAlaHisHis 5
Db 144 CATAACGCACCAT 158

RESULT 10
US-08-975-316-33/c
; Sequence 33, Application US/08975316
; Patent No. 5952486
; GENERAL INFORMATION:
; APPLICANT: BLOKBERG, Leonard N., HAVUKKALA, Ilkka
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; FILE REFERENCE: 11000.1003C4U
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-SEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,316
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/713,000
; FILING DATE: September 11, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SLEATH, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000/1003C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-975-316-33

Alignment Scores:
Pred. No.: 395 Length: 380
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-12 (1-5) x US-08-975-316-33 (1-380)

Qy 1 HisAenAlaHisHis 5
Db 50 CACAACGCTCACCAT 36

RESULT 11
US-09-615-192A-33/c

; Sequence 33, Application US/09615192A
; Patent No. 6410718
; GENERAL INFORMATION:
; APPLICANT: BLOKBERG, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; FILE REFERENCE: 11000.1003C4U
; CURRENT APPLICATION NUMBER: US/09/615,192A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 08/975,316
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 08/713,000
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: US 09/169,789
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 380
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-615-192A-33

Alignment Scores:
Pred. No.: 395 Length: 380
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x US-09-615-192A-33 (1-380)

Qy 1 HisAenAlaHisHis 5
Db 50 CACAACGCTCACCAT 36

RESULT 12
US-09-169-789-33/c
; Sequence 33, Application US/09169789
; Patent No. 665328
; GENERAL INFORMATION:
; APPLICANT: BLOKBERG, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; FILE REFERENCE: 11000.1003C2
; CURRENT APPLICATION NUMBER: US/09/169,789
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 08/975,316
; EARLIER FILING DATE: 1997-11-21
; EARLIER APPLICATION NUMBER: US 08/713,000
; EARLIER FILING DATE: 1996-09-11
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 380
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-169-789-33

Alignment Scores:
Pred. No.: 395 Length: 380
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-169-789-33 (1-380)

Qy 1 HisAenAlaHisHis 5

```
Db      50 CACAAGGCTCACCAT 36
|||||
RESULT 13
US-08-956-171E-3743
; Sequence 3743, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956.171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 3743:
; LENGTH: 400 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3743:
US-08-956-171E-3743
Alignment Scores:
Pred. No.: 418 Length: 400
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-029-756-12 (1-5) x US-08-956-171E-3743 (1-400)
Qy      1 HisAenAlaHisHis 5
Db      79 CATAACGCACATCAT 93
|||||
RESULT 15
US-09-615-192A-115/c
; Sequence 115, Application US/09615192A
; Patent No. 6410718
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; TITLE OF INVENTION: Modification of Plant Lignin Content
; FILE REFERENCE: 11000.1003C4U
; CURRENT APPLICATION NUMBER: US/09/615,192A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 08/975,316
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 08/713,000
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: US 09/169,789
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 420
; TYPE: DNA
```



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; ORGANISM: Eucalyptus grandis
US-09-615-192A-115

Alignment Scores:
Pred. No.: 441          Length: 420
Score: 34.00           Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3                  Gaps: 0

US-10-029-756-12 (1-5) x US-09-615-192A-115 (1-420)

Qy 1 HisAenAlaHisHis 5
Db 80 CACAACGCTCACCAT 66

RESULT 16
US-09-169-789-115/c
; Sequence 115, Application US/09169789
; Patent No. 6653528
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; FILE REFERENCE: 11000.1003c2
; CURRENT APPLICATION NUMBER: US/09/169,789
; EARLIER FILING DATE: 1998-10-09
; EARLIER FILING DATE: 1997-11-21
; EARLIER FILING DATE: 1996-09-11
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 420
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-169-789-115

Alignment Scores:
Pred. No.: 441          Length: 420
Score: 34.00           Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4                  Gaps: 0

US-10-029-756-12 (1-5) x US-09-169-789-115 (1-420)

Qy 1 HisAenAlaHisHis 5
Db 80 CACAACGCTCACCAT 66

RESULT 17
US-09-513-999C-12497
; Sequence 12497, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 12497

; ORGANISM: Homo sapiens
US-09-593-887-7

Alignment Scores:
Pred. No.: 455          Length: 432
Score: 34.00           Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4                  Gaps: 0

US-10-029-756-12 (1-5) x US-09-593-887-7 (1-432)

Qy 1 HisAenAlaHisHis 5
Db 216 CACAATGCCACCAC 202

RESULT 19
US-09-270-767-4421
; Sequence 4421, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
```

```
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4421
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-4421

Alignment Scores:
Pred. No.: 610 Length: 562
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-270-767-4421 (1-562)

Qy 1 HisAenAlahisHis 5
Db 346 CATAACGGCACCAC 360

RESULT 20
US-09-270-767-19703
; Sequence 19703, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19703
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-19703

Alignment Scores:
Pred. No.: 610 Length: 562
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-270-767-19703 (1-562)

Qy 1 HisAenAlahisHis 5
Db 346 CATAACGGCACCAC 360

RESULT 21
US-09-949-016-94983/c
; Sequence 94983, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95095
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-94983/c

Alignment Scores:
Pred. No.: 657 Length: 601
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-949-016-95095 (1-601)

Qy 1 HisAenAlahisHis 5
Db 381 CACAATGCACATCAC 367

RESULT 22
US-09-949-016-95095/c
; Sequence 95095, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95095
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-95095/c

Alignment Scores:
Pred. No.: 657 Length: 601
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-949-016-95095 (1-601)

Qy 1 HisAenAlahisHis 5
Db 381 CACAATGCACATCAC 367

RESULT 23
US-09-949-016-150166
; Sequence 150166, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
```

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; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94983
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-94983

Alignment Scores:
Pred. No.: 657 Length: 601
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-949-016-94983 (1-601)

Qy 1 HisAenAlahisHis 5
Db 381 CACAATGCACATCAC 367

RESULT 22
US-09-949-016-95095/c
; Sequence 95095, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95095
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-95095/c

Alignment Scores:
Pred. No.: 657 Length: 601
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-949-016-95095 (1-601)

Qy 1 HisAenAlahisHis 5
Db 381 CACAATGCACATCAC 367

RESULT 23
US-09-949-016-150166
; Sequence 150166, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
```

; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150166
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-150166

Alignment Scores:
Pred. No.: 657 Length: 601
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-949-016-150166 (1-601)

Qy 1 HisAenAlaHisHis 5
Db 318 CACAAGGCCACCAC 332

RESULT 24

US-09-949-016-153056/c
; Sequence 153056, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 153056
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-153056

Alignment Scores:
Pred. No.: 657 Length: 601
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-949-016-153056 (1-601)

Qy 1 HisAenAlaHisHis 5
Db 455 CACAATGCCACCAC 441

RESULT 25

US-09-949-016-165560
; Sequence 165560, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165560
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-165560

Alignment Scores:
Pred. No.: 657 Length: 601
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-949-016-165560 (1-601)

Qy 1 HisAenAlaHisHis 5
Db 487 CATAATGCCACCAC 501

RESULT 26

US-09-949-016-181710/c
; Sequence 181710, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 181710
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-181710

Alignment Scores:
Pred. No.: 657 Length: 601
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-949-016-181710 (1-601)

Qy 1 HisAenAlaHisHis 5
Db 381 CACAATGCCACCAC 367

```
RESULT 27
US-09-949-016-181829/c
; Sequence 181829, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 181829
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-181829

Alignment Scores:
Pred. No.:      657      Length:      601
Score:          34.00    Matches:      5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:     100.00% Indels:      0
DB:              4      Gaps:        0

US-10-029-756-12 (1-5) x US-09-949-016-181829 (1-601)

Qy      1 HisAsnAlaHisHis 5
Db      381 CACAATGCACATCAC 367

RESULT 28
US-09-949-016-181948/c
; Sequence 181948, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 181948
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-181948

Alignment Scores:
Pred. No.:      657      Length:      601
Score:          34.00    Matches:      5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:     100.00% Indels:      0
DB:              4      Gaps:        0

US-10-029-756-12 (1-5) x US-09-949-016-181948 (1-601)

Qy      1 HisAsnAlaHisHis 5
Db      381 CACAATGCACATCAC 367

RESULT 29
US-09-702-705-1397
; Sequence 1397, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITL OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1397
; LENGTH: 653
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-702-705-1397

Alignment Scores:
Pred. No.:      721      Length:      653
Score:          34.00    Matches:      5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:     100.00% Indels:      0
DB:              4      Gaps:        0

US-10-029-756-12 (1-5) x US-09-702-705-1397 (1-653)

Qy      1 HisAsnAlaHisHis 5
Db      448 CACAATGCCACCCAC 462

RESULT 30
US-09-736-457-1397
; Sequence 1397, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITL OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1397
; LENGTH: 653
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-1397
```

Alignment Scores:
Pred. No.: 721 Length: 653
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-736-457-1397 (1-653)

Qy 1 HisAenAlaHisHis 5
Db 448 CACAATGCCACCAC 462

RESULT 31

US-09-614-124B-1397
; Sequence 1397, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1397
; LENGTH: 653
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-614-124B-1397

Alignment Scores:
Pred. No.: 721 Length: 653
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-614-124B-1397 (1-653)

Qy 1 HisAenAlaHisHis 5
Db 448 CACAATGCCACCAC 462

RESULT 32

US-09-671-325-1397
; Sequence 1397, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325

; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1397
; LENGTH: 653
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-671-325-1397

Alignment Scores:
Pred. No.: 721 Length: 653
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-671-325-1397 (1-653)

Qy 1 HisAenAlaHisHis 5
Db 448 CACAATGCCACCAC 462

RESULT 33

US-09-658-824-1397
; Sequence 1397, Application US/09658824
; Patent No. 6746846
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C11
; CURRENT APPLICATION NUMBER: US/09/658,824
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 1788
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1397
; LENGTH: 653
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-658-824-1397

Alignment Scores:
Pred. No.: 721 Length: 653
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-658-824-1397 (1-653)

Qy 1 HisAenAlaHisHis 5
Db 448 CACAATGCCACCAC 462

RESULT 34

US-09-495-052-56
; Sequence 56, Application US/09495052
; Patent No. 6479258
; GENERAL INFORMATION:
; APPLICANT: DIVERSA CORPORATION
; APPLICANT: SHORT, Jay
; TITLE OF INVENTION: NON-STOCHASTIC GENERATION OF GENETIC VACCINES
; FILE REFERENCE: DIVER1460-11

; CURRENT APPLICATION NUMBER: US/09/495,052
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: US 09/276,860
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/267,118
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 09/246,178
; PRIOR FILING DATE: 1999-02-04
; PRIOR APPLICATION NUMBER: US 09/185,373
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: US 08/760,489
; PRIOR FILING DATE: 1996-12-05
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 56
; LENGTH: 824
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-495-052-56

Alignment Scores:
Pred. No.: 933 Length: 824
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-495-052-56 (1-824)

Qy 1 HisAenAlaHis 5
Db 523 CACAATGCCACCAC 537

RESULT 35

US-09-270-767-12993
; Sequence 12993, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 12993
; LENGTH: 881
; TYPE: DNA
; ORGANISM: *Drosophila melanogaster*
US-09-270-767-12993

Alignment Scores:
Pred. No.: 1,01e+03 Length: 881
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-270-767-12993 (1-881)

Qy 1 HisAenAlaHis 5
Db 858 CACAATGCCACCAC 872

RESULT 36

US-09-991A-10187
; Sequence 10187, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *PSEUDOMONAS*

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 10187
; LENGTH: 1068
; TYPE: DNA
; ORGANISM: *Pseudomonas aeruginosa*
US-09-252-991A-10187

Alignment Scores:
Pred. No.: 1.25e+03 Length: 1068
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-252-991A-10187 (1-1068)

Qy 1 HisAenAlaHis 5
Db 832 CACAATGCCACCAC 846

RESULT 37

US-09-949-016-5053/c
; Sequence 5053, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5053
; LENGTH: 1081
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5053

Alignment Scores:
Pred. No.: 1.26e+03 Length: 1081
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-949-016-5053 (1-1081)

Qy 1 HisAenAlaHis 5
Db 758 CACAATGCCACCAC 744

RESULT 38

US-09-328-352-1975/c
; Sequence 1975, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 1975
; LENGTH: 1086
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-1975

Alignment Scores:
Pred. No.: 1.27e+03 Length: 1086
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-328-352-1975 (1-1086)

Qy 1 HisAenAlaHisHis 5
|||||
Db 937 CATAATGCCACCAT 923

RESULT 39

US-09-543-681A-1032/c
; Sequence 1032, Application US/09543681A
; Patent No. 6605709

; GENERAL INFORMATION:
; APPLICANT: GARY BRETON

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001

; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05

; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09

; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 1032

; LENGTH: 1179
; TYPE: DNA

; ORGANISM: Proteus mirabilis
US-09-543-681A-1032

Alignment Scores:
Pred. No.: 1.39e+03 Length: 1179
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-543-681A-1032 (1-1179)

Qy 1 HisAenAlaHisHis 5
|||||
Db 663 CATAATGCCACCAT 649

RESULT 40

US-09-857-583B-3

; Sequence 3, Application US/09857583B
; Patent No. 6825017

; GENERAL INFORMATION:
; APPLICANT: WASHINGTON STATE UNIVERSITY RESEARCH FOUNDATION

; APPLICANT: Browne, John A
; APPLICANT: Wallis, James G

; APPLICANT: Watts, Jennifer L
; TITLE OF INVENTION: DESATURASES AND METHODS OF USING THEM FOR SYNTHESIS OF

; FILE REFERENCE: POLYUNSATURATED FATTY ACIDS
; PRIOR FILING DATE: 1998-02-13

; CURRENT APPLICATION NUMBER: US/09/857,583B
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/111,301
; PRIOR FILING DATE: 1998-12-07
; PRIOR APPLICATION NUMBER: PCT/US99/28655
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 1281
; TYPE: DNA
; ORGANISM: Euglena gracilis
US-09-857-583B-3

Alignment Scores:
Pred. No.: 1.52e+03 Length: 1281
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-857-583B-3 (1-1281)

Qy 1 HisAenAlaHisHis 5
|||||
Db 557 CACAATGCATCAT 571

RESULT 41

US-09-540-236-1347/c

; Sequence 1347, Application US/09540236
; Patent No. 6673910

; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAT
; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001

; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04

; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 1347

; LENGTH: 1293
; TYPE: DNA

; ORGANISM: M.catarrhalis
US-09-540-236-1347

Alignment Scores:
Pred. No.: 1.54e+03 Length: 1293
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-540-236-1347 (1-1293)

Qy 1 HisAenAlaHisHis 5
|||||
Db 757 CATAATGCCATCAC 743

RESULT 42

US-09-248-796A-442

; Sequence 442, Application US/09248796A
; Patent No. 6747137

; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 442
; LENGTH: 1323
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-442

Alignment Scores: Length: 1323
Pred. No.: 1.58e+03
Score: 34.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4

US-10-029-756-12 (1-5) x US-09-248-796A-442 (1-1323)

Qy 1 HisAenAlaHis 5
Db 742 CATAATGCATCATC 756

RESULT 43

US-09-540-236-1678/c
; Sequence 1678, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 1678
; LENGTH: 1425
; TYPE: DNA
; ORGANISM: M.catarrhalis
US-09-540-236-1678

Alignment Scores: Length: 1425
Pred. No.: 1.72e+03
Score: 34.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4

US-10-029-756-12 (1-5) x US-09-540-236-1678 (1-1425)

Qy 1 HisAenAlaHis 5
Db 730 CATAACGTCATCAT 716

RESULT 44

US-09-489-039A-4667/c
; Sequence 4667, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 4667
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-4667

Alignment Scores: Length: 1479
Pred. No.: 1.79e+03
Score: 34.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4

US-10-029-756-12 (1-5) x US-09-489-039A-4667 (1-1479)

Qy 1 HisAenAlaHis 5
Db 1119 CATAATGCCACCAC 1105

RESULT 45

US-09-949-016-4296/c
; Sequence 4296, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4296
; LENGTH: 1499
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4296

Alignment Scores: Length: 1499
Pred. No.: 1.82e+03
Score: 34.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4

US-10-029-756-12 (1-5) x US-09-949-016-4296 (1-1499)

Qy 1 HisAenAlaHis 5
Db 1241 CACAATGCCACCAC 1227

RESULT 46

US-09-814-915A-41/c
; Sequence 41, Application US/09814915A
; Patent No. 6750015
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Kathryn
; APPLICANT: Richer, Jennifer
; TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methods Relat
; TITLE OF INVENTION: Theteto
; FILE REFERENCE: 2848-39
; CURRENT APPLICATION NUMBER: US/09/814,915A
; CURRENT FILING DATE: 2002-03-21
; PRIOR APPLICATION NUMBER: 60/214,870
; PRIOR FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 1517

;
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-915A-41

Alignment Scores:
Pred. No.: 1.84e+03 Length: 1517
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-814-915A-41 (1-1517)

QY 1 HisAenAlaHisHis 5
Db 1259 CACAATGCCACCAC 1245

RESULT 47
US-08-815-176-2/c
; Sequence 2, Application US/08815176
; Patent No. 5874224
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Diegidio, Tony
; TITLE OF INVENTION: NOVEL EGF RECEPTOR BINDING PROTEIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,176
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0236 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1661 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: PGNOT03
; CLONE: 1291904
US-08-815-176-2

Alignment Scores:
Pred. No.: 2.03e+03 Length: 1661
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-12 (1-5) x US-08-815-176-2 (1-1661)

QY 1 HisAenAlaHisHis 5
Db 1114 CACAATGCCCATCAT 1100

RESULT 48
US-09-197-344-2/c
; Sequence 2, Application US/09197344
; Patent No. 6417329
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Diegidio, Tony
; TITLE OF INVENTION: NOVEL EGF RECEPTOR BINDING PROTEIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/197,344
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/815,176
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0236 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1661 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: PGNOT03
; CLONE: 1291904
US-09-197-344-2

Alignment Scores:
Pred. No.: 2.03e+03 Length: 1661
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x US-09-197-344-2 (1-1661)

QY 1 HisAenAlaHisHis 5
Db 1114 CACAATGCCCATCAT 1100

RESULT 49
US-08-831-570-1
; Sequence 1, Application US/08831570
; Patent No. 5959175
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; APPLICANT: Nunberg, Andrew N.
; APPLICANT: Beremand, Phillip D.

;; TITLE OF INVENTION: A SUNFLOWER ALBUMIN 5' REGULATORY REGION
;; TITLE OF INVENTION: FOR THE MODIFICATION OF PLANT SEED LIPID
;; TITLE OF INVENTION: COMPOSITION
;; NUMBER OF SEQUENCES: 22
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Scully, Scott, Murphy & Presser
;; STREET: 400 Garden City Plaza
;; CITY: Garden City
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 11530
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/831,570
;; FILING DATE: 09-APR-1997
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Digiglio, Frank S.
;; REGISTRATION NUMBER: 31,346
;; REFERENCE/DOCKET NUMBER: 10545
;; TELEPHONE: (516) 742-4343
;; TELEFAX: (516) 742-4366
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1684 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 43..1387
;;
US-08-831-570-1

Alignment Scores:
Pred. No.: 2.07e+03 Length: 1684
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-12 (1-5) x US-08-831-570-1 (1-1684)

Qy 1 HisaenAlaHisHis 5
Db 628 CATAATGCACATCAC 642

RESULT 50
US-08-831-575-1
; Sequence 1, Application US/08831575
; Patent No. 5977436
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; APPLICANT: Li, Zhongsen
; TITLE OF INVENTION: AN OLBSIN 5' REGULATORY REGION FOR THE
; TITLE OF INVENTION: MODIFICATION OF PLANT SEED LIPID COMPOSITION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/831,575
;; FILING DATE: 09-APR-1997
;; CLASSIFICATION: 800
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Digiglio, Frank S.
;; REGISTRATION NUMBER: 31,346
;; REFERENCE/DOCKET NUMBER: 10203
;; TELEPHONE: (516) 742-4343
;; TELEFAX: (516) 742-4366
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1684 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 43..1387
;;
US-08-831-575-1

Alignment Scores:
Pred. No.: 2.07e+03 Length: 1684
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-12 (1-5) x US-08-831-575-1 (1-1684)

Qy 1 HisaenAlaHisHis 5
Db 628 CATAATGCACATCAC 642

RESULT 51
US-08-366-779-4
; Sequence 4, Application US/08366779
; Patent No. 5614393
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; APPLICANT: Nuccio, Avutu S.
; APPLICANT: Freyssinet, Georges L.
; APPLICANT: Nunberg, Andrew N.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; TITLE OF INVENTION: DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/366,779
; FILING DATE: 30-DEC-1994
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 83832YXW
; TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1685 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-366-779-4

Alignment Scores:
Pred. No.: 2.07e+03 Length: 1685
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-029-756-12 (1-5) x US-08-366-779-4 (1-1685)

Qy 1 HisanAlaHisHis 5
Db 629 CATATGCATCAC 643

RESULT 52
US-08-789-936-4
; Sequence 4, Application US/08789936
; Patent No. 5789220
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; APPLICANT: Reddy, Avutu S.
; APPLICANT: Nuccio, Michael
; APPLICANT: Freyvasinet, Georges L.
; APPLICANT: Nunberg, Andrew N.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 28-JAN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 8383ZYXWU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1685 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

```

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US-08-789-936-4

Alignment Scores:
Pred. No.: 2.07e+03 Length: 1685
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-029-756-12 (1-5) x US-08-789-936-4 (1-1685)

Qy 1 HisanAlaHisHis 5
Db 629 CATATGCATCAC 643

RESULT 53
US-08-934-254-4
; Sequence 4, Application US/08934254
; Patent No. 6355861
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 28-JAN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 8383ZYXWU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1685 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-934-254-4

Alignment Scores:
Pred. No.: 2.07e+03 Length: 1685
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x US-08-934-254-4 (1-1685)

Qy 1 HisanAlaHisHis 5
Db 629 CATATGCATCAC 643

RESULT 54

```

```
US-09-685-775-4
; Sequence 4, Application US/09685775
; Patent No. 6683232
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; DELTA 6-DESATURASE
;
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/685,775
; FILING DATE: 10-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,254
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 8383ZYXWVU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1685 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-685-775-4
Alignment Scores:
Pred. No.: 2.07e+03 Length: 1685
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-029-756-12 (1-5) x US-09-685-775-4 (1-1685)
Qy 1 HisenAlaHisHis 5
Db 629 CATAATGCACATC 643
RESULT 55
US-08-934-254-26
; Sequence 26, Application US/08934254
; Patent No. 635861
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; DELTA 6-DESATURASE
;
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,254
; FILING DATE: 10-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,254
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 8383ZYXWVU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1685 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-685-775-4
Alignment Scores:
Pred. No.: 2.07e+03 Length: 1685
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-029-756-12 (1-5) x US-08-934-254-26 (1-1702)
Qy 1 HisenAlaHisHis 5
Db 636 CACAACGCCACCAC 650
RESULT 56
US-09-685-775-26
; Sequence 26, Application US/09685775
; Patent No. 6683232
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; DELTA 6-DESATURASE
;
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/685,775
; FILING DATE: 10-Oct-2000
; CLASSIFICATION: <Unknown>
```


RESULT 60
US-08-549-515-2
; Sequence 2, Application US/08549515
; Patent No. 6054123
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: Haemophilus Influenzae
; TITLE OF INVENTION: Dimethylsulphoxide Reductase Enzyme
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 Unviersity Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/549,515
; FILING DATE: 27-OCT-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-522
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2418 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-549-515-2

Alignment Scores:
Pred. No.: 3.09e+03 Length: 2418
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x US-08-549-515-2 (1-2418)

Qy 1 HisAsnAlaHisHis 5
| | | | | | | | | |
Db 2351 CACAAGGCCCATCAC 2365

RESULT 61
US-09-023-655-1000/c
; Sequence 1000, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA

; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1000:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2591 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g178083
; US-09-023-655-1000

Alignment Scores:
Pred. No.: 3.34e+03 Length: 2591
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-023-655-1000 (1-2591)

Qy 1 HisAsnAlaHisHis 5
| | | | | | | | | |
Db 1206 CACAATGCCCATCAC 1192

RESULT 62
US-09-540-236-217/c
; Sequence 217, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 217
; LENGTH: 2970
; TYPE: DNA
; ORGANISM: M.catarrhalis
; US-09-540-236-217

Alignment Scores:
Pred. No.: 3.88e+03 Length: 2970
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-540-236-217 (1-2970)

```

1 FILING DATE: 20-Oct-1997
2 CLASSIFICATION: <Unknown>
3 PRIOR APPLICATION DATA:
4 APPLICATION NUMBER: 60/009,861
5 FILING DATE: January 5, 1996
6 APPLICATION NUMBER: 08/781,986
7 FILING DATE: January 3, 1997
8 ATTORNEY/AGENT INFORMATION:
9 NAME: Mark J. Hyman
10 REGISTRATION NUMBER: 46,789
11 REFERENCE/DOCKET NUMBER: PB248P1
12 TELECOMMUNICATION INFORMATION:
13 TELEPHONE: (240) 314-1224
14 TELEFAX: (301) 309-8439
15 INFORMATION FOR SEQ ID NO: 816:
16 SEQUENCE CHARACTERISTICS:
17 TYPE: nucleic acid
18 LENGTH: 3989 base pairs
19 STRANDEDNESS: double
20 TOPOLOGY: linear
21 SEQUENCE DESCRIPTION: SEQ ID NO: 816:
22 US-08-956-171E-816
23
24 Alignment Scores:
25 Pred. No.: 5.39e+03 Length: 3989
26 Score: 34.00 Matches: 5
27 Percent Similarity: 100.00% Conservative: 0
28 Best Local Similarity: 100.00% Mismatches: 0
29 Query Match: 100.00% Indels: 0
30 DB: 4 Gaps: 0
31
32 US-10-029-756-12 (1-5) x US-08-956-171E-816 (1-3989)
33
34 QY 1 HisAsnAlaHisHis 5
35 DB 2089 CATACGCACATCAT 2103
36
37 RESULT 65
38 US-08-781-986A-816
39 ; Sequence 816, Application US/08781986A
40 ; Patent No: 6737248
41 ; GENERAL INFORMATION:
42 ; APPLICANT: Charles Kunsch
43 ; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
44 ; NUMBER OF SEQUENCES: 5255
45 ; CORRESPONDENCE ADDRESS:
46 ; ADDRESSEE: Human Genome Sciences, Inc.
47 ; STREET: 9410 Key West Avenue
48 ; CITY: Rockville
49 ; STATE: Maryland
50 ; COUNTRY: USA
51 ; ZIP: 20850
52 ; COMPUTER READABLE FORM:
53 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
54 ; COMPUTER: HP Vectra 486/33
55 ; OPERATING SYSTEM: MSDOS version 6.2
56 ; SOFTWARE: ASCII Text
57 ; CURRENT APPLICATION DATA:
58 ; APPLICATION NUMBER: US/08/781,986A
59 ; FILING DATE:
60 ; CLASSIFICATION: 435
61 ; PRIOR APPLICATION DATA:
62 ; APPLICATION NUMBER:
63 ; FILING DATE:
64 ; ATTORNEY/AGENT INFORMATION:
65 ; NAME: Benson, Bob
66 ; REGISTRATION NUMBER: 30,446
67 ; REFERENCE/DOCKET NUMBER: PB248PP
68 ; TELECOMMUNICATION INFORMATION:
69 ; TELEPHONE: (301) 309-8504
70 ; TELEFAX: (301) 309-8512
71 ; INFORMATION FOR SEQ ID NO: 816:
72 ; SEQUENCE CHARACTERISTICS:

```

```

; LENGTH: 3989 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-816

Alignment Scores:
Pred. No.: 5.39e+03 Length: 3989
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-08-781-986A-816 (1-3989)

Qy 1 HisAenAlaHisHis 5
Db 2089 CATAACGCACATCAT 2103

RESULT 66
US-08-549-515-1
; Sequence 1, Application US/08549515
; Patent No. 6054123
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: Haemophilus Influenzae
; TITLE OF INVENTION: Dimethylsulphoxide Reductase Enzyme
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/549.515
; FILING DATE: 27-OCT-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-522
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4051 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(65..2482, 2496..3110, 3115..3951)
US-08-549-515-1

Alignment Scores:
Pred. No.: 5.48e+03 Length: 4051
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x US-08-549-515-1 (1-4051)

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```

Qy 1 HisAenAlaHisHis 5
Db 2415 CACAACGCCCATCAC 2429

RESULT 67
US-09-721-480-1
; Sequence 1, Application US/09721480
; Patent No. 6740323
; GENERAL INFORMATION:
; APPLICANT: Selby, Mark
; APPLICANT: Glazer, Edward
; APPLICANT: Houghton, Michael
; TITLE OF INVENTION: HBV/HCV VIRUS-LIKE PARTICLE
; FILE REFERENCE: PP01635.002
; CURRENT APPLICATION NUMBER: US/09/721.480
; CURRENT FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4276
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid pCMVII
US-09-721-480-1

Alignment Scores:
Pred. No.: 5.82e+03 Length: 4276
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-721-480-1 (1-4276)

Qy 1 HisAenAlaHisHis 5
Db 1662 CACAATGCCACAC 1676

RESULT 68
US-08-760-615-7
; Sequence 7, Application US/08760615
; Patent No. 6200959
; GENERAL INFORMATION:
; APPLICANT: Haynes, Joel R
; APPLICANT: Schmaljohn, Connie S
; APPLICANT: Fuller, Deborah L
; APPLICANT: Schmaljohn, Alan
; APPLICANT: Jahrling, Peter B
; TITLE OF INVENTION: GENETIC INDUCTION OF ANTI-VIRAL IMMUNE
; TITLE OF INVENTION: RESPONSE AND GENETIC VACCINE FOR FILOVIRUS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53703
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760.615
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Berson, Bennett J
; REGISTRATION NUMBER: 37094

```


REFERENCE/DOCKET NUMBER: 110229.91241
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4326 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Expression vector
DESCRIPTION: Construct"
CLONE: pWRG7077
FEATURE:
NAME/KEY: promoter
LOCATION: 1250..2062
FEATURE:
NAME/KEY: intron
LOCATION: 2063..2887
OTHER INFORMATION: /function= "Human Cytomegalovirus
OTHER INFORMATION: Intron A"
FEATURE:
NAME/KEY: polyA site
LOCATION: 2912..3314
FEATURE:
NAME/KEY: CDS
LOCATION: complement (299..1114)

Alignment Scores:
Pred. No.: 5.9e+03 Length: 4326
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x US-08-760-615-7 (1-4326)

Qy 1 HisaenAlaHisHis 5
Db 2586 CACAATGCCACCAC 2600

RESULT 69

US-09-132-808-1
Sequence 1, Application US/09132808
Patent No. 6197332
GENERAL INFORMATION:
APPLICANT: Ronald Zuckermann et al.
TITLE OF INVENTION: Lipid-Conjugated Polyamide Compounds and Related
TITLE OF INVENTION: Compositions and Methods Thereof
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESS: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94608-2916
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09132.808
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,459

REFERENCE/DOCKET NUMBER: 1387.002
TELEPHONE: (510) 923-2706
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4328 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-132-808-1
Alignment Scores:
Pred. No.: 5.9e+03 Length: 4328
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x US-09-132-808-1 (1-4328)

Qy 1 HisaenAlaHisHis 5
Db 1333 CACAATGCCACCAC 1347

RESULT 70

US-08-910-647-2
Sequence 2, Application US/08910647
Patent No. 6251433
GENERAL INFORMATION:
APPLICANT: Zuckermann et al.
TITLE OF INVENTION: Compositions and Methods for
TITLE OF INVENTION: Polynucleotide Delivery
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94608-2916
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910.647
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 1218.002
TELEPHONE: (510) 923-2706
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4328 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-910-647-2

Alignment Scores:
Pred. No.: 5.9e+03 Length: 4328
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x US-08-910-647-2 (1-4328)

Qy 1 HisAsnAlaHisHis 5
|||||

Db 1333 CACAATGCCACCAC 1347

RESULT 71

US-09-620-925-2
; Sequence 2, Application US/09620925
; Patent No. 6468986
; GENERAL INFORMATION:
; APPLICANT: Zuckermann et al.
; TITLE OF INVENTION: Compositions and Methods for Polynucleotide Delivery

NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94608-2916

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/620,925
FILING DATE: 21-Jul-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/910,647
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 1218.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2706
TELEFAX: (510) 655-3542

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4328 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (Genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Alignment Scores:
Pred. No.: 5.9e+03 Length: 4328
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x US-09-620-925-2 (1-4328)

Qy 1 HisAsnAlaHisHis 5
|||||

Db 1333 CACAATGCCACCAC 1347

RESULT 72

US-09-620-260-1
; Sequence 1, Application US/09620260
; Patent No. 6569450
; GENERAL INFORMATION:

APPLICANT: Ronald Zuckermann et al.
TITLE OF INVENTION: Lipid-Conjugated Polyamide Compounds and Related Compositions and Methods Thereof

NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94608-2916

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/620,260
FILING DATE: 09-Oct-2001
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 1387.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2706
TELEFAX: (510) 655-3542

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4328 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-620-260-1

Alignment Scores:
Pred. No.: 5.9e+03 Length: 4328
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-620-260-1 (1-4328)

Qy 1 HisAsnAlaHisHis 5
|||||

Db 1333 CACAATGCCACCAC 1347

RESULT 73

US-09-620-259-1
; Sequence 1, Application US/09620259
; Patent No. 6572881
; GENERAL INFORMATION:
; APPLICANT: Ronald Zuckermann et al.
; TITLE OF INVENTION: Lipid-Conjugated Polyamide Compounds and Related Compositions and Methods Thereof

NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94608-2916

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/620,259
FILING DATE: 03-Oct-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 1387,002
TELEPHONE: (510) 923-2706
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4328 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-620-259-1

Alignment Scores:
Pred. No.: 5,9e+03 Length: 4328
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-620-259-1 (1-4328)

Qy 1 HisAenAlaHis 5
Db 1333 CACAATGCCACCAC 1347

RESULT 74

US-08-956-171E-546/c
; Sequence 546, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:

APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 546:
SEQUENCE CHARACTERISTICS:
LENGTH: 4336 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 546:
US-08-956-171E-546

Alignment Scores:
Pred. No.: 5,91e+03 Length: 4336
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-08-956-171E-546 (1-4336)

Qy 1 HisAenAlaHis 5
Db 2081 CATACGCACATCAT 2067

RESULT 75

US-08-781-986A-546/c
; Sequence 546, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:

APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Benson, Bob

REGISTRATION NUMBER: 30,446

REFERENCE/DOCKET NUMBER: PB248PP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 546:

SEQUENCE CHARACTERISTICS:

LENGTH: 4336 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-08-781-986A-546

Alignment Scores:

Pred. No.: 5,91e+03 Length: 4336

Score: 34.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-08-781-986A-546 (1-4336)

Qy 1 HisaAsnAlaHisHis 5
|||||

Db 2081 CATAACGCACATCAT 2067

RESULT 76

US-09-949-016-1943/c
; Sequence 1943, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1943
; LENGTH: 4531
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1943

Alignment Scores:

| | | | |
|------------------------|----------|---------------|------|
| Pred. No.: | 6.21e+03 | Length: | 4531 |
| Score: | 34.00 | Matches: | 5 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 4 | Gaps: | 0 |

US-10-029-756-12 (1-5) x US-09-949-016-1943 (1-4531)

Qy 1 HisaAsnAlaHisHis 5
|||||

Db 3947 CACAATGCCACCAC 3933

RESULT 77

US-08-910-647-4
; Sequence 4, Application US/08910647
; Patent No. 6251433
; GENERAL INFORMATION:
; APPLICANT: Zuckermann et al.
; TITLE OF INVENTION: Compositions and Methods for
; Polynucleotide Delivery
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/910,647
; FILING DATE: 2000-07-21
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/910,647
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Fujita, Sharon M.
; REGISTRATION NUMBER: 38,459
; REFERENCE/DOCKET NUMBER: 1218.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 923-2706
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4818 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-620-925-4

NAME: Fujita, Sharon M.
REGISTRATION NUMBER: 38,459
REFERENCE/DOCKET NUMBER: 1218.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 923-2706
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4818 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-620-925-4

Alignment Scores:

| | | | |
|------------------------|----------|---------------|------|
| Pred. No.: | 6.55e+03 | Length: | 4818 |
| Score: | 34.00 | Matches: | 5 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 3 | Gaps: | 0 |

US-10-029-756-12 (1-5) x US-08-910-647-4 (1-4818)

Qy 1 HisaAsnAlaHisHis 5
|||||

Db 1336 CACAATGCCACCAC 1350

RESULT 78

US-09-620-925-4
; Sequence 4, Application US/09620925
; Patent No. 6468986
; GENERAL INFORMATION:
; APPLICANT: Zuckermann et al.
; TITLE OF INVENTION: Compositions and Methods for
; Polynucleotide Delivery
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/620,925
; FILING DATE: 21-Jul-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/910,647
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Fujita, Sharon M.
; REGISTRATION NUMBER: 38,459
; REFERENCE/DOCKET NUMBER: 1218.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 923-2706
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4818 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-620-925-4

Alignment Scores:
Pred. No.: 6.65e+03 Length: 4818
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x US-09-620-925-4 (1-4818)

Qy 1 HisaenAlaHisHis 5
Db 1336 CACAATGCCACCAC 1350

RESULT 79
US-08-345-913-1
; Sequence 1, Application US/08345913
; Patent No. 5641665
; GENERAL INFORMATION:
; APPLICANT: Hobart, Peter
; APPLICANT: Parker, Suzanne
; APPLICANT: Margalith, Michal
; APPLICANT: Khatibi, Shirin
; TITLE OF INVENTION: PLASMIDS SUITABLE FOR IL-2 EXPRESSION
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESS: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/345,913
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ways Vensko, Nancy
; REGISTRATION NUMBER: 36,298
; REFERENCE/DOCKET NUMBER: VICAL.043A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4928 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1689...2159
; OTHER INFORMATION:
US-08-345-913-1

Alignment Scores:
Pred. No.: 6.81e+03 Length: 4928
Score: 34.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-029-756-12 (1-5) x US-08-345-913-1 (1-4928)

Qy 1 HisaenAlaHisHis 5
Db 1316 CACAATGCCACCAC 1330

RESULT 80
US-08-818-562-1
; Sequence 1, Application US/08018562
; Patent No. 6147055
; GENERAL INFORMATION:
; APPLICANT: Hobart, Peter M.
; APPLICANT: Margalith, Michal
; APPLICANT: Parker, Suzanne E.
; APPLICANT: Khatibi, Shirin
; TITLE OF INVENTION: Plasmids Suitable for IL-2 Expression
; FILE REFERENCE: 1530.0080001
; CURRENT APPLICATION NUMBER: US/08/818,562
; CURRENT FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: US 08/345,913
; EARLIER FILING DATE: 1994-11-28
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4928
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1689)..(2159)
US-08-818-562-1

Alignment Scores:
Pred. No.: 6.81e+03 Length: 4928
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x US-08-818-562-1 (1-4928)

Qy 1 HisaenAlaHisHis 5
Db 1316 CACAATGCCACCAC 1330

RESULT 81
US-09-628-445-1
; Sequence 1, Application US/09628445
; Patent No. 6399588
; GENERAL INFORMATION:
; APPLICANT: Hobart, Peter M.
; APPLICANT: Margalith, Michal
; APPLICANT: Parker, Suzanne E.
; APPLICANT: Khatibi, Shirin
; TITLE OF INVENTION: Cancer Treatment Utilizing Plasmids Suitable for IL-2 Expression
; FILE REFERENCE: 1530.0080002
; CURRENT APPLICATION NUMBER: US/09/628,445
; CURRENT FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 08/818,562
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: US 08/345,913
; PRIOR FILING DATE: 1994-11-28
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 4928
; TYPE: DNA

```
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1689)..(2159)
US-09-628-445-1
Alignment Scores:
Pred. No.: 6.81e+03 Length: 4928
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-029-756-12 (1-5) x US-09-628-445-1 (1-4928)
Qy 1 HisAenAlaHisHis 5
Db 1316 CACAATGCCACCAC 1330
RESULT 82
US-08-910-647-3
; Sequence 3, Application US/08910647
; Patent No. 6251433
; GENERAL INFORMATION:
; APPLICANT: Zuckermann et al.
; TITLE OF INVENTION: Compositions and Methods for
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 21-Jul-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/910,647
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Fujita, Sharon M.
; REGISTRATION NUMBER: 38,459
; REFERENCE/DOCKET NUMBER: 1218.002
; TELEPHONE: (510) 923-2706
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5107 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-910-647-3
Alignment Scores:
Pred. No.: 7.09e+03 Length: 5107
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-029-756-12 (1-5) x US-08-910-647-3 (1-5107)
Qy 1 HisAenAlaHisHis 5
Db 1316 CACAATGCCACCAC 1330
```

```
Db 1336 CACAATGCCACCAC 1350
RESULT 83
US-09-620-925-3
; Sequence 3, Application US/09620925
; Patent No. 6468986
; GENERAL INFORMATION:
; APPLICANT: Zuckermann et al.
; TITLE OF INVENTION: Compositions and Methods for
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/620,925
; FILING DATE: 21-Jul-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/910,647
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Fujita, Sharon M.
; REGISTRATION NUMBER: 38,459
; REFERENCE/DOCKET NUMBER: 1218.002
; TELEPHONE: (510) 923-2706
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5107 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-620-925-3
Alignment Scores:
Pred. No.: 7.09e+03 Length: 5107
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-029-756-12 (1-5) x US-09-620-925-3 (1-5107)
Qy 1 HisAenAlaHisHis 5
Db 1336 CACAATGCCACCAC 1350
RESULT 84
US-09-628-730-51
; Sequence 51, Application US/09628730
; Patent No. 6759393
; GENERAL INFORMATION:
; APPLICANT: Morsey, Mohamad
; TITLE OF INVENTION: GROWTH HORMONE AND GROWTH HORMONE RELEASING HORMONE
; COMPOSITIONS
; FILE REFERENCE: FC10525B
; CURRENT APPLICATION NUMBER: US/09/628,730
; CURRENT FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 67
```

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 5108
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: pGHRH1-29WTCMV construct
US-09-628-730-51
```

```
Alignment Scores:
Pred. No.: 7,09e+03 Length: 5108
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
```

US-10-029-756-12 (1-5) x US-09-628-730-51 (1-5108)

```
QY 1 HisAenAlaHisHis 5
Db 4544 CACAATGCCACCAC 4558
```

RESULT 85

```
US-09-628-730-52
; Sequence 52, Application US/09628730
; Patent No. 6759393
```

GENERAL INFORMATION:

```
; APPLICANT: Morsey, Mohamad
; TITLE OF INVENTION: GROWTH HORMONE AND GROWTH HORMONE RELEASING HORMONE
; FILE REFERENCE: PC10525B
; CURRENT APPLICATION NUMBER: US/09/628,730
; CURRENT FILING DATE: 2000-07-28
```

```
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 52
; LENGTH: 5108
```

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

```
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: pGHRH1-29WTCMV construct
```

US-09-628-730-52

```
Alignment Scores:
Pred. No.: 7,09e+03 Length: 5108
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
```

US-10-029-756-12 (1-5) x US-09-628-730-52 (1-5108)

```
QY 1 HisAenAlaHisHis 5
Db 4544 CACAATGCCACCAC 4558
```

RESULT 86

US-09-628-730-55

```
; Sequence 55, Application US/09628730
; Patent No. 6759393
```

GENERAL INFORMATION:

```
; APPLICANT: Morsey, Mohamad
; TITLE OF INVENTION: GROWTH HORMONE AND GROWTH HORMONE RELEASING HORMONE
; FILE REFERENCE: PC10525B
; CURRENT APPLICATION NUMBER: US/09/628,730
; CURRENT FILING DATE: 2000-07-28
```

```
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 55
; LENGTH: 5111
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: pGHRH1-29fa1a1522CMV construct
US-09-628-730-55
```

```
Alignment Scores:
Pred. No.: 7,1e+03 Length: 5111
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
```

US-10-029-756-12 (1-5) x US-09-628-730-55 (1-5111)

```
QY 1 HisAenAlaHisHis 5
Db 4544 CACAATGCCACCAC 4558
```

RESULT 87

US-09-721-480-2

```
; Sequence 2, Application US/09721480
; Patent No. 6740323
```

GENERAL INFORMATION:

```
; APPLICANT: Selby, Mark
; APPLICANT: Glazer, Edward
; APPLICANT: Houghton, Michael
; FILE REFERENCE: PP01635.002
; CURRENT APPLICATION NUMBER: US/09/721,480
; CURRENT FILING DATE: 2000-11-22
```

```
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
```

```
; SEQ ID NO 2
; LENGTH: 5128
```

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

```
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
; OTHER INFORMATION: PCMVII-ps2-SAG
```

NAME/KEY: CDS

LOCATION: (1988) ..(2830)

US-09-721-480-2

```
Alignment Scores:
Pred. No.: 7,12e+03 Length: 5128
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
```

US-10-029-756-12 (1-5) x US-09-721-480-2 (1-5128)

```
QY 1 HisAenAlaHisHis 5
Db 1662 CACAATGCCACCAC 1676
```

RESULT 88

US-09-628-730-47

```
; Sequence 47, Application US/09628730
; Patent No. 6759393
```

GENERAL INFORMATION:

```
; APPLICANT: Morsey, Mohamad
; TITLE OF INVENTION: GROWTH HORMONE AND GROWTH HORMONE RELEASING HORMONE
; FILE REFERENCE: PC10525B
; CURRENT APPLICATION NUMBER: US/09/628,730
; CURRENT FILING DATE: 2000-07-28
```

; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 5185
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pGHRH-4
; OTHER INFORMATION: construct
US-09-628-730-47

Alignment Scores:
Pred. No.: 7.21e+03 Length: 5185
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-628-730-47 (1-5185)

Qy 1 HisAenAlaHisHis 5
Db 4544 CACAATGCCACCAC 4558

RESULT 89

US-09-628-730-59
; Sequence 59, Application US/09628730
; Patent No. 6759393

GENERAL INFORMATION:

; APPLICANT: Morsey, Mohamad
; TITLE OF INVENTION: GROWTH HORMONE AND GROWTH HORMONE RELEASING HORMONE
; FILE REFERENCE: PC10525B

; CURRENT APPLICATION NUMBER: US/09/628,730

; CURRENT FILING DATE: 2000-07-28

; NUMBER OF SEQ ID NOS: 67

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 59

; LENGTH: 5188

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:

; OTHER INFORMATION: pGHRH-44YTCMV construct

US-09-628-730-59

Alignment Scores:
Pred. No.: 7.22e+03 Length: 5188
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-628-730-59 (1-5188)

Qy 1 HisAenAlaHisHis 5
Db 4544 CACAATGCCACCAC 4558

RESULT 90

US-09-173-053-8

; Sequence 8, Application US/09173053

; Patent No. 6451769

GENERAL INFORMATION:

; APPLICANT: HUEBNER, Robert C.

; APPLICANT: NORMAN, Jon A.

; APPLICANT: LIANG, Xisowu

; APPLICANT: CARNER, Kristin R.

; APPLICANT: BARBOUR, Alan G.

; APPLICANT: LUKE, Catherine J.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ADMINISTERING BORRELIA DNA

; FILE REFERENCE: 454312-2440.1
; CURRENT APPLICATION NUMBER: US/09/173,053
; CURRENT FILING DATE: 1998-10-15
; PRIOR APPLICATION NUMBER: 08/663,998
; PRIOR FILING DATE: 1996-06-14
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 5215
; TYPE: DNA
; ORGANISM: Borrelia burgdorferi
US-09-173-053-8

Alignment Scores:
Pred. No.: 7.26e+03 Length: 5215
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x US-09-173-053-8 (1-5215)

Qy 1 HisAenAlaHisHis 5
Db 1500 CACAATGCCACCAC 1514

RESULT 91

US-09-628-730-60

; Sequence 60, Application US/09628730

; Patent No. 6759393

GENERAL INFORMATION:

; APPLICANT: Morsey, Mohamad

; TITLE OF INVENTION: GROWTH HORMONE AND GROWTH HORMONE RELEASING HORMONE

; FILE REFERENCE: PC10525B

; CURRENT APPLICATION NUMBER: US/09/628,730

; CURRENT FILING DATE: 2000-07-28

; NUMBER OF SEQ ID NOS: 67

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 60

; LENGTH: 5254

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:

; OTHER INFORMATION: pGHRH-44WTGHPep construct

US-09-628-730-60

Alignment Scores:
Pred. No.: 7.32e+03 Length: 5254
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-628-730-60 (1-5254)

Qy 1 HisAenAlaHisHis 5
Db 4544 CACAATGCCACCAC 4558

RESULT 92

US-09-721-480-4

; Sequence 4, Application US/09721480

; Patent No. 6740323

GENERAL INFORMATION:

; APPLICANT: Selby, Mark

; APPLICANT: Glazer, Edward

; APPLICANT: Houghton, Michael

; TITLE OF INVENTION: HBV/HCV VIRUS-LIKE PARTICLE

; FILE REFERENCE: PP01635.002


```
; CURRENT APPLICATION NUMBER: US/09/721,480
; CURRENT FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 5459
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pCMVII opti
; NAME/KEY: CDS
; LOCATION: (1992)..(3161)
US-09-721-480-4

Alignment Scores:
Pred. No.: 7,64e+03 Length: 5459
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-721-480-4 (1-5459)

Qy 1 HisAenAlaHisHis 5
Db 1662 CACAATGCCACCAC 1676

RESULT 93
US-09-721-480-6
; Sequence 6, Application US/09721480
; Patent No. 6740323
; GENERAL INFORMATION:
; APPLICANT: Selby, Mark
; APPLICANT: Glazer, Edward
; APPLICANT: Houghton, Michael
; FILE OF INVENTION: HBV/HCV VIRUS-LIKE PARTICLE
; TITLE OF INVENTION: PP01635.002
; CURRENT APPLICATION NUMBER: US/09/721,480
; CURRENT FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 5882
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
; NAME/KEY: CDS
; LOCATION: (1992)..(3584)
US-09-721-480-6

Alignment Scores:
Pred. No.: 8.3e+03 Length: 5882
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-721-480-6 (1-5882)

Qy 1 HisAenAlaHisHis 5
Db 1662 CACAATGCCACCAC 1676

RESULT 94
US-09-770-315-1
; Sequence 1, Application US/09770315
; Patent No. 6429001
; GENERAL INFORMATION:
```

```
; APPLICANT: Chiron Corporation
; TITLE OF INVENTION: Recombinant AAV Packaging Systems
; FILE REFERENCE: 20263-501
; CURRENT APPLICATION NUMBER: US/09/770,315
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,536
; PRIOR FILING DATE: 2000-01-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 7015
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: recombinant DNA
US-09-770-315-1

Alignment Scores:
Pred. No.: 1.01e+04 Length: 7015
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x US-09-770-315-1 (1-7015)

Qy 1 HisAenAlaHisHis 5
Db 2821 CACAATGCCACCAC 2835

RESULT 95
US-08-910-647-1
; Sequence 1, Application US/08910647
; Patent No. 6251433
; GENERAL INFORMATION:
; APPLICANT: Zuckermann et al.
; TITLE OF INVENTION: Compositions and Methods for
; TITLE OF INVENTION: Polynucleotide Delivery
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/910,647
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fujita, Sharon M.
; REGISTRATION NUMBER: 38,459
; REFERENCE/DOCKET NUMBER: 1218.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 923-2706
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9600 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-910-647-1

Alignment Scores:
```

Pred. No.: 1.43e+04 Length: 9600
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-12 (1-5) x US-08-910-647-1 (1-9600)

Qy 1 HisAenAlaHis 5

Db 6438 CACAATGCCACCAC 6452

RESULT 96

US-09-620-925-1

; Sequence 1, Application US/09620925

; Patent No. 6468986

; GENERAL INFORMATION:

; APPLICANT: Zuckermann et al.

; TITLE OF INVENTION: Compositions and Methods for

; POLYNUCLEOTIDE DELIVERY

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Chiron Corporation

; STREET: 4560 Horton Street

; CITY: Emeryville

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 94608-2916

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/620,925

; FILING DATE: 21-Jul-2000

; CLASSIFICATION: <unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/910,647

; FILING DATE: <unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Fujita, Sharon M.

; REGISTRATION NUMBER: 38,459

; REFERENCE/DOCKET NUMBER: 1218.002

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (510) 923-2706

; TELEFAX: (510) 655-3542

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9600 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (Genomic)

; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-620-925-1

Alignment Scores:

Pred. No.: 1.43e+04

Score: 34.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 3

US-10-029-756-12 (1-5) x US-09-620-925-1 (1-9600)

Qy 1 HisAenAlaHis 5

Db 6438 CACAATGCCACCAC 6452

RESULT 97

US-09-554-337-1
; Sequence 1, Application US/09554337
; Patent No. 6475780
; GENERAL INFORMATION:
; APPLICANT: Parrington, Mark
; APPLICANT: Li, Xiaomao
; APPLICANT: Klein, Michel H.
; TITLE OF INVENTION: ALPHAVIRUS VECTORS FOR PARAMYXOVIRUS VACCINES
; FILE REFERENCE: 1038-1042 MTS
; CURRENT APPLICATION NUMBER: US/09/554,337
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/065,791
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: PCT/CA98/01064
; PRIOR FILING DATE: 1998-11-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 15538
; TYPE: DNA
; ORGANISM: respiratory syncytial virus
US-09-554-337-1

Alignment Scores:
Pred. No.: 2.43e+04 Length: 15538
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-554-337-1 (1-15538)

Qy 1 HisAenAlaHis 5

Db 1563 CACAATGCCACCAC 1577

RESULT 98

US-09-949-016-16407/C

; Sequence 16407, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: Fast-Seq for Windows Version 4.0

; SEQ ID NO 16407

; LENGTH: 21893

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(21893)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-16407

Alignment Scores:

Pred. No.: 3.55e+04

Score: 34.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 4

US-10-029-756-12 (1-5) x US-09-949-016-16407 (1-21893)
Length: 21893
Matches: 5
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-029-756-12 (1-5) x US-09-949-016-16407 (1-21893)

Qy 1 HisAsnAlaHisHis 5
DB 8335 CATATGACACAC 8321

RESULT 99

US-09-949-016-14958/c
; Sequence 14958, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14958
; LENGTH: 23406
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14958

Alignment Scores:

| Pred. No.: | 3.82e+04 | Length: | 23406 |
|------------------------|----------|---------------|-------|
| Score: | 34.00 | Matches: | 5 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 4 | Gaps: | 0 |

US-10-029-756-12 (1-5) x US-09-949-016-14958 (1-23406)

Qy 1 HisAsnAlaHisHis 5
DB 13430 CATATGCCCATCAT 13416

RESULT 100

US-09-949-016-14320
; Sequence 14320, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14320
; LENGTH: 24056
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14320

Alignment Scores:

| Pred. No.: | 3.94e+04 | Length: | 24056 |
|------------|----------|---------|-------|
|------------|----------|---------|-------|

Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-12 (1-5) x US-09-949-016-14320 (1-24056)

Qy 1 HisAsnAlaHisHis 5
DB 19415 CACAATGCCCATCAT 19429

Search completed: June 8, 2005, 15:29:24
Job time : 152.316 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 8, 2005, 09:39:06 ; Search time 1236.32 Seconds
(without alignments)
235.159 Million cell updates/sec

Title: US-10-029-756-20

Perfect score: 36

Sequence: 1 FQIRHH 6

Scoring table: BLOSUM62

Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp
-Q=/cgn2.1/USPTO.spool_p/US10029756/runat_07062005.122750.28779/app_query.fasta.1.597
-DB=GenEmbl -QFMT=fascap -SUPFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=1000
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=100 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10029756 @CGN 1.1.5965 @runat_07062005.122750.28779 -NCPU=6 -ICPU=3
-NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sv.*
13: gb.un.*
14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------|
| ----- | | | | | |
| C 1 | 36 | 100.0 | 20 | 6 | AX253333 Sequence |
| 2 | 36 | 100.0 | 266 | 6 | AR247897 Sequence |
| 3 | 36 | 100.0 | 291 | 6 | AR246607 Sequence |
| C 4 | 36 | 100.0 | 347 | 6 | AR272626 Sequence |

| | | | | | | |
|---|----|----|-------|------|----|----------------------|
| C | 5 | 36 | 100.0 | 347 | 6 | AR276207 Sequence |
| C | 6 | 36 | 100.0 | 347 | 6 | AR406482 Sequence |
| C | 7 | 36 | 100.0 | 347 | 6 | AR440332 Sequence |
| C | 8 | 36 | 100.0 | 347 | 6 | AR472490 Sequence |
| C | 9 | 36 | 100.0 | 347 | 6 | AR543143 Sequence |
| C | 10 | 36 | 100.0 | 347 | 6 | AX062728 Sequence |
| C | 11 | 36 | 100.0 | 347 | 6 | AX367645 Sequence |
| C | 12 | 36 | 100.0 | 372 | 6 | AR484509 Sequence |
| C | 13 | 36 | 100.0 | 372 | 6 | AX143133 Sequence |
| C | 14 | 36 | 100.0 | 372 | 6 | AR221976 Sequence |
| C | 15 | 36 | 100.0 | 473 | 6 | AR221975 Sequence |
| C | 16 | 36 | 100.0 | 480 | 6 | AX840703 Sequence |
| C | 17 | 36 | 100.0 | 520 | 6 | BD082632 Methods a |
| C | 18 | 36 | 100.0 | 520 | 6 | BD082647 Methods a |
| C | 19 | 36 | 100.0 | 520 | 6 | BD092937 Methods a |
| C | 20 | 36 | 100.0 | 560 | 6 | BD147335 Primer fo |
| C | 21 | 36 | 100.0 | 560 | 6 | AX867273 Sequence |
| C | 22 | 36 | 100.0 | 655 | 6 | AR221955 Sequence |
| C | 23 | 36 | 100.0 | 655 | 6 | BD082635 Methods a |
| C | 24 | 36 | 100.0 | 655 | 6 | BD082650 Methods a |
| C | 25 | 36 | 100.0 | 655 | 6 | BD092929 Methods a |
| C | 26 | 36 | 100.0 | 739 | 6 | BD148047 Primer fo |
| C | 27 | 36 | 100.0 | 739 | 6 | AX867985 Sequence |
| C | 28 | 36 | 100.0 | 808 | 6 | CQ780299 Sequence |
| C | 29 | 36 | 100.0 | 808 | 6 | CQ781966 Sequence |
| C | 30 | 36 | 100.0 | 808 | 6 | BD125008 Primer fo |
| C | 31 | 36 | 100.0 | 808 | 6 | BD126675 Primer fo |
| C | 32 | 36 | 100.0 | 864 | 6 | AR221961 Sequence |
| C | 33 | 36 | 100.0 | 876 | 6 | AR547128 Sequence |
| C | 34 | 36 | 100.0 | 1132 | 1 | AF270385 Sequence |
| C | 35 | 36 | 100.0 | 1132 | 6 | AX486339 Sequence |
| C | 36 | 36 | 100.0 | 1132 | 6 | AX145703 Sequence |
| C | 37 | 36 | 100.0 | 1320 | 6 | AR410208 Sequence |
| C | 38 | 36 | 100.0 | 1320 | 6 | AX467713 Sequence |
| C | 39 | 36 | 100.0 | 1320 | 6 | AX577003 Sequence |
| C | 40 | 36 | 100.0 | 1320 | 6 | AX951587 Sequence |
| C | 41 | 36 | 100.0 | 1320 | 8 | AF489588 Thraustoc |
| C | 42 | 36 | 100.0 | 1329 | 6 | AX577009 Sequence |
| C | 43 | 36 | 100.0 | 1335 | 6 | CQ729637 Sequence |
| C | 44 | 36 | 100.0 | 1335 | 6 | AR221953 Sequence |
| C | 45 | 36 | 100.0 | 1335 | 6 | AX253297 Sequence |
| C | 46 | 36 | 100.0 | 1335 | 6 | AX253298 Sequence |
| C | 47 | 36 | 100.0 | 1335 | 6 | BD091695 Processes f |
| C | 48 | 36 | 100.0 | 1335 | 9 | AF199596 Homo sapi |
| C | 49 | 36 | 100.0 | 1335 | 9 | AF226273 Homo sapi |
| C | 50 | 36 | 100.0 | 1338 | 6 | AX577005 Sequence |
| C | 51 | 36 | 100.0 | 1341 | 8 | AF536525 Anemone 1 |
| C | 52 | 36 | 100.0 | 1347 | 8 | AY131238 Argania a |
| C | 53 | 36 | 100.0 | 1347 | 9 | HS4325501 Homo sapi |
| C | 54 | 36 | 100.0 | 1365 | 5 | AF478472 Salmo sal |
| C | 55 | 36 | 100.0 | 1385 | 8 | AY234126 Primula v |
| C | 56 | 36 | 100.0 | 1442 | 10 | RNO494720 Rattus no |
| C | 57 | 36 | 100.0 | 1478 | 6 | BD195601 70 human |
| C | 58 | 36 | 100.0 | 1478 | 6 | CQ775646 Sequence |
| C | 59 | 36 | 100.0 | 1478 | 6 | AR352656 Sequence |
| C | 60 | 36 | 100.0 | 1498 | 5 | AB074149 Oncothym |
| C | 61 | 36 | 100.0 | 1508 | 10 | AF126798 Mus muscu |
| C | 62 | 36 | 100.0 | 1539 | 10 | BC055950 Mus muscu |
| C | 63 | 36 | 100.0 | 1546 | 10 | AB021980 Rattus no |
| C | 64 | 36 | 100.0 | 1576 | 5 | AB069727 Oreochrom |
| C | 65 | 36 | 100.0 | 1590 | 5 | AF309556 Danio rer |
| C | 66 | 36 | 100.0 | 1608 | 10 | BC057189 Mus muscu |
| C | 67 | 36 | 100.0 | 1619 | 8 | AY332747 Pavlova 1 |
| C | 68 | 36 | 100.0 | 1681 | 8 | AY234124 Primula f |
| C | 69 | 36 | 100.0 | 1684 | 6 | AR076814 Sequence |
| C | 70 | 36 | 100.0 | 1684 | 6 | AR084177 Sequence |
| C | 71 | 36 | 100.0 | 1684 | 6 | BD062571 A sunflow |
| C | 72 | 36 | 100.0 | 1684 | 6 | BD070919 An oleos |
| C | 73 | 36 | 100.0 | 1685 | 6 | AR020904 Sequence |
| C | 74 | 36 | 100.0 | 1685 | 6 | I38430 Sequence 4 |
| C | 75 | 36 | 100.0 | 1685 | 6 | AR200408 Sequence |
| C | 76 | 36 | 100.0 | 1685 | 6 | AR455421 Sequence |
| C | 77 | 36 | 100.0 | 1685 | 8 | AF007561 Borago of |

| | | | | | | | | | | | | | |
|-----|----|-------|------|----|------------|----------------------|-------|----|-------|--------|----|-----------|--------------------|
| 78 | 36 | 100.0 | 1686 | 6 | AR221958 | Sequence | 151 | 36 | 100.0 | 3131 | 6 | AX416639 | Sequence |
| 79 | 36 | 100.0 | 1686 | 6 | BD082638 | Methods a | 152 | 36 | 100.0 | 3149 | 9 | AF084559 | Homo sapi |
| 80 | 36 | 100.0 | 1686 | 6 | BD082653 | Methods a | 153 | 36 | 100.0 | 3184 | 6 | BD243025 | Human oxi |
| 81 | 36 | 100.0 | 1686 | 6 | BD092932 | Methods a | 154 | 36 | 100.0 | 3334 | 10 | BC063053 | Mus muscu |
| 82 | 36 | 100.0 | 1687 | 6 | AX951561 | Sequence | 155 | 36 | 100.0 | 3349 | 10 | AF061504 | Mus muscu |
| 83 | 36 | 100.0 | 1687 | 8 | BD079010 | Sequence | 156 | 36 | 100.0 | 3380 | 10 | AB052085 | Rattus no |
| 84 | 36 | 100.0 | 1692 | 5 | AB070444 | Oncorhync | 157 | 36 | 100.0 | 3403 | 5 | BC077556 | Xenopus l |
| 85 | 36 | 100.0 | 1700 | 6 | BD228694 | Delta 6 f | 158 | 36 | 100.0 | 3408 | 10 | AB072976 | Mus muscu |
| 86 | 36 | 100.0 | 1705 | 9 | AF134404 | Homo sapi | 159 | 36 | 100.0 | 3413 | 10 | AF320509 | Rattus no |
| 87 | 36 | 100.0 | 1706 | 10 | BC081776 | BC081776 Rattus no | 160 | 36 | 100.0 | 3415 | 10 | AF320509 | Rattus no |
| 88 | 36 | 100.0 | 1708 | 5 | BC049438 | Danio rer | 161 | 36 | 100.0 | 3416 | 10 | BC022139 | Mus muscu |
| 89 | 36 | 100.0 | 1717 | 5 | AR264713 | Sequence | 162 | 36 | 100.0 | 3437 | 10 | BC026831 | Mus muscu |
| 90 | 36 | 100.0 | 1745 | 5 | AY055749 | Sparus au | c 163 | 36 | 100.0 | 3765 | 8 | AF481861 | Candida a |
| 91 | 36 | 100.0 | 1757 | 6 | AX035942 | Sequence | c 164 | 36 | 100.0 | 4089 | 6 | AX035941 | Sequence |
| 92 | 36 | 100.0 | 1757 | 9 | AF084560 | Homo sapi | 165 | 36 | 100.0 | 4103 | 1 | AF270140 | Staphyloc |
| 93 | 36 | 100.0 | 1781 | 5 | BC063726 | BC063726 xenopus l | 166 | 36 | 100.0 | 4103 | 6 | AR486094 | Sequence |
| 94 | 36 | 100.0 | 1798 | 5 | AF309557 | Cyprinus | 167 | 36 | 100.0 | 4103 | 6 | AX145458 | Sequence |
| 95 | 36 | 100.0 | 1798 | 8 | AK058543 | Oryza sat | 168 | 36 | 100.0 | 4205 | 6 | AX035940 | Sequence |
| 96 | 36 | 100.0 | 1807 | 9 | BC004901 | Homo sapi | 169 | 36 | 100.0 | 4205 | 9 | AF084558 | Homo sapi |
| 97 | 36 | 100.0 | 1816 | 6 | CQ776468 | CQ776468 | 170 | 36 | 100.0 | 4327 | 3 | ACU13191 | Angiostrong |
| 98 | 36 | 100.0 | 1818 | 6 | CQ777377 | Sequence | 171 | 36 | 100.0 | 8185 | 9 | BSM807094 | Homo sapi |
| 99 | 36 | 100.0 | 1818 | 10 | AB041560 | AB041560 Mus muscu | c 172 | 36 | 100.0 | 12204 | 1 | AY510074 | Listeria |
| 100 | 36 | 100.0 | 1838 | 5 | AY458652 | AY458652 Salmo sal | c 173 | 36 | 100.0 | 16349 | 1 | AF498420 | Pseudomon |
| 101 | 36 | 100.0 | 1843 | 6 | AR221959 | Sequence | 174 | 36 | 100.0 | 27035 | 9 | AY191837 | Homo sapi |
| 102 | 36 | 100.0 | 1843 | 6 | BD082639 | Methods a | 175 | 36 | 100.0 | 38060 | 3 | CET13F2 | Caenorhabdi |
| 103 | 36 | 100.0 | 1843 | 6 | BD082654 | Methods a | c 176 | 36 | 100.0 | 65237 | 9 | AC117450 | Homo sapi |
| 104 | 36 | 100.0 | 1843 | 6 | BD092933 | Methods a | c 177 | 36 | 100.0 | 67665 | 2 | AC101324 | Mus muscu |
| 105 | 36 | 100.0 | 1856 | 6 | BD157758 | Primer fo | c 178 | 36 | 100.0 | 79914 | 9 | AC005159 | Homo sapi |
| 106 | 36 | 100.0 | 1856 | 6 | AX879291 | Sequence | c 179 | 36 | 100.0 | 89421 | 9 | AP001965 | Homo sapi |
| 107 | 36 | 100.0 | 1856 | 9 | AK027427 | AK027427 | c 180 | 36 | 100.0 | 91859 | 9 | AL358133 | Human DNA |
| 108 | 36 | 100.0 | 1866 | 5 | AF301910 | Oncorhync | 181 | 36 | 100.0 | 95161 | 8 | AP005554 | Oryza sat |
| 109 | 36 | 100.0 | 1866 | 10 | BC071266 | BC071266 Mus muscu | c 182 | 36 | 100.0 | 101684 | 8 | AP005847 | Oryza sat |
| 110 | 36 | 100.0 | 1887 | 9 | BC007846 | BC007846 Homo sapi | c 183 | 36 | 100.0 | 108205 | 3 | AC102213 | Mus muscu |
| 111 | 36 | 100.0 | 1928 | 6 | BD264714 | BD264714 Sequence | c 184 | 36 | 100.0 | 109041 | 2 | LMFP1408 | Leishmani |
| 112 | 36 | 100.0 | 1946 | 6 | BD159641 | Primer fo | 185 | 36 | 100.0 | 110000 | 2 | AC129052 | Continuation (3 of |
| 113 | 36 | 100.0 | 1946 | 6 | AX882292 | Sequence | 186 | 36 | 100.0 | 110207 | 2 | AC145157 | Medicago |
| 114 | 36 | 100.0 | 1946 | 9 | AK027522 | Homo sapi | 187 | 36 | 100.0 | 111911 | 2 | AC145470 | Medicago |
| 115 | 36 | 100.0 | 1987 | 5 | AY546094 | Scophthal | c 188 | 36 | 100.0 | 114285 | 9 | AP001870 | Homo sapi |
| 116 | 36 | 100.0 | 2016 | 6 | BD195657 | BD195657 70 human | c 189 | 36 | 100.0 | 119945 | 9 | BSA218J18 | Human DNA |
| 117 | 36 | 100.0 | 2016 | 6 | CQ775702 | Sequence | c 190 | 36 | 100.0 | 122499 | 8 | OSJN00205 | Oryza sat |
| 118 | 36 | 100.0 | 2016 | 9 | AK096275 | AK096275 Homo sapi | c 191 | 36 | 100.0 | 122900 | 9 | HSJ0526F5 | Human DNA |
| 119 | 36 | 100.0 | 2079 | 9 | AK096275 | AK096275 Homo sapi | c 192 | 36 | 100.0 | 133445 | 2 | AC073440 | Homo sapi |
| 120 | 36 | 100.0 | 2146 | 6 | BD157807 | Primer fo | c 193 | 36 | 100.0 | 140681 | 8 | AC078894 | Oryza sat |
| 121 | 36 | 100.0 | 2146 | 6 | AX879386 | AX879386 Sequence | c 194 | 36 | 100.0 | 143608 | 9 | AC145752 | Oryza sat |
| 122 | 36 | 100.0 | 2146 | 9 | AK027459 | AK027459 Homo sapi | c 195 | 36 | 100.0 | 144108 | 10 | BSX936355 | Mouse DNA |
| 123 | 36 | 100.0 | 2190 | 6 | BD158110 | BD158110 Primer fo | c 196 | 36 | 100.0 | 144201 | 10 | AC087218 | Rattus no |
| 124 | 36 | 100.0 | 2190 | 6 | AX879945 | AX879945 Sequence | 197 | 36 | 100.0 | 144717 | 2 | AC108901 | Felis cat |
| 125 | 36 | 100.0 | 2190 | 9 | AK027577 | AK027577 Homo sapi | 198 | 36 | 100.0 | 152135 | 9 | AC011199 | Homo sapi |
| 126 | 36 | 100.0 | 2236 | 6 | CQ782686 | CQ782686 Sequence | c 200 | 36 | 100.0 | 161624 | 2 | AP001493 | Homo sapi |
| 127 | 36 | 100.0 | 2236 | 9 | BD127263 | BD127263 Primer fo | c 201 | 36 | 100.0 | 162409 | 2 | AC022184 | Homo sapi |
| 128 | 36 | 100.0 | 2236 | 9 | AK074754 | AK074754 Homo sapi | c 202 | 36 | 100.0 | 162696 | 2 | AC090417 | Homo sapi |
| 129 | 36 | 100.0 | 2257 | 6 | AR221960 | AR221960 Sequence | c 203 | 36 | 100.0 | 163330 | 10 | AL713390 | Mouse DNA |
| 130 | 36 | 100.0 | 2257 | 6 | BD082640 | BD082640 Methods a | c 204 | 36 | 100.0 | 164229 | 9 | AC092671 | Homo sapi |
| 131 | 36 | 100.0 | 2257 | 6 | BD082655 | BD082655 Methods a | c 205 | 36 | 100.0 | 165201 | 2 | AC149902 | Strongylo |
| 132 | 36 | 100.0 | 2257 | 6 | BD092934 | BD092934 Methods a | c 206 | 36 | 100.0 | 166410 | 8 | OSJN00240 | Oryza sat |
| 133 | 36 | 100.0 | 2540 | 6 | AX379750 | AX379750 Sequence | c 207 | 36 | 100.0 | 167429 | 9 | AC110771 | Homo sapi |
| 134 | 36 | 100.0 | 2558 | 6 | CQ783754 | CQ783754 Sequence | c 208 | 36 | 100.0 | 168608 | 2 | AC090464 | Homo sapi |
| 135 | 36 | 100.0 | 2558 | 9 | BD127815 | BD127815 Primer fo | c 209 | 36 | 100.0 | 168862 | 2 | AC092527 | Homo sapi |
| 136 | 36 | 100.0 | 2558 | 9 | AK074925 | AK074925 Homo sapi | c 210 | 36 | 100.0 | 170270 | 2 | AP001548 | Homo sapi |
| 137 | 36 | 100.0 | 2621 | 6 | AX770523 | AX770523 Sequence | c 211 | 36 | 100.0 | 170413 | 2 | AC090405 | Homo sapi |
| 138 | 36 | 100.0 | 2621 | 9 | BSM800210 | BSM800210 Homo sapi | c 212 | 36 | 100.0 | 170862 | 9 | AC015795 | Homo sapi |
| 139 | 36 | 100.0 | 2825 | 6 | CQ782971 | CQ782971 Sequence | c 213 | 36 | 100.0 | 174645 | 9 | AC091111 | Homo sapi |
| 140 | 36 | 100.0 | 2825 | 6 | BD127406 | BD127406 Primer fo | c 214 | 36 | 100.0 | 175850 | 2 | AP001399 | Homo sapi |
| 141 | 36 | 100.0 | 2825 | 9 | AK074991 | AK074991 Homo sapi | c 215 | 36 | 100.0 | 177382 | 2 | AC125953 | Rattus no |
| 142 | 36 | 100.0 | 2872 | 9 | AF486577 | AF486577 Homo sapi | c 216 | 36 | 100.0 | 178148 | 2 | AC149725 | Bos tauru |
| 143 | 36 | 100.0 | 2974 | 9 | AF108658 | AF108658 Homo sapi | c 217 | 36 | 100.0 | 179169 | 2 | AC092759 | Papilo ann |
| 144 | 36 | 100.0 | 2980 | 9 | AK123340 | AK123340 Homo sapi | c 218 | 36 | 100.0 | 183165 | 9 | AP000802 | Homo sapi |
| 145 | 36 | 100.0 | 3007 | 6 | CQ728125 | CQ728125 Sequence | c 219 | 36 | 100.0 | 184841 | 9 | AC016902 | Homo sapi |
| 146 | 36 | 100.0 | 3016 | 9 | AF126799 | AF126799 Homo sapi | c 220 | 36 | 100.0 | 185569 | 2 | AP003099 | Homo sapi |
| 147 | 36 | 100.0 | 3075 | 9 | BSM8005582 | BSM8005582 Homo sapi | c 221 | 36 | 100.0 | 188414 | 2 | CH388091 | Danio rer |
| 148 | 36 | 100.0 | 3083 | 6 | CQ782909 | CQ782909 Sequence | c 222 | 36 | 100.0 | 188736 | 9 | CNS0008M | Human chr |
| 149 | 36 | 100.0 | 3083 | 6 | BD127375 | BD127375 Primer fo | c 223 | 36 | 100.0 | 193917 | 10 | AL844153 | Mouse DNA |
| 150 | 36 | 100.0 | 3083 | 9 | AK074939 | AK074939 Homo sapi | | 36 | 100.0 | 194487 | 2 | AP002896 | Homo sapi |

| | | | | | | | | | | | | | |
|-------|----|-------|--------|----|-----------|--------------------|-------|----|------|--------|----|-------------|---------------------|
| 224 | 36 | 100.0 | 196993 | 9 | CNS01DDT | AL132985 Human chr | c 297 | 35 | 97.2 | 80664 | 2 | AC027592 | AC027592 Homo sapi |
| 225 | 36 | 100.0 | 198990 | 10 | AC131679 | AC131679 Mus muscu | c 298 | 35 | 97.2 | 86820 | 5 | BX890573 | BX890573 Zebrafish |
| c 226 | 36 | 100.0 | 198935 | 9 | AC034268 | AC034268 Homo sapi | c 299 | 35 | 97.2 | 88966 | 5 | AP001943 | AP001943 Homo sapi |
| c 227 | 36 | 100.0 | 204340 | 9 | AC091103 | AC091103 Homo sapi | c 300 | 35 | 97.2 | 96678 | 9 | HS477010A | AL096755 Human DNA |
| c 228 | 36 | 100.0 | 206191 | 10 | AC124535 | AC124535 Mus muscu | c 301 | 35 | 97.2 | 110000 | 1 | AE017332_4 | Continuation (5 of |
| c 229 | 36 | 100.0 | 206454 | 9 | AC018737 | AC018737 Homo sapi | c 302 | 35 | 97.2 | 110000 | 1 | AE017332_5 | Continuation (6 of |
| c 230 | 36 | 100.0 | 208059 | 2 | AC114192 | AC114192 Rattus no | c 303 | 35 | 97.2 | 110000 | 8 | CR382125_08 | Continuation (9 of |
| c 231 | 36 | 100.0 | 208492 | 9 | AC062203 | AC062203 Homo sapi | c 304 | 35 | 97.2 | 110000 | 8 | CR382126_05 | Continuation (6 of |
| c 232 | 36 | 100.0 | 210474 | 9 | AC148447 | AC148447 Pan trogl | c 305 | 35 | 97.2 | 110000 | 8 | CR382126_06 | Continuation (7 of |
| c 233 | 36 | 100.0 | 213989 | 5 | AC145509 | AC145509 Gasterost | c 306 | 35 | 97.2 | 110000 | 8 | AE016820_10 | Continuation (11 of |
| c 234 | 36 | 100.0 | 220219 | 9 | AC021019 | AC021019 Homo sapi | c 307 | 35 | 97.2 | 119774 | 10 | AL731705 | AL731705 Mouse DNA |
| c 235 | 36 | 100.0 | 222858 | 2 | BX248107 | BX248107 Homo sapi | c 308 | 35 | 97.2 | 123236 | 2 | CR384099 | CR384099 Danio rer |
| c 236 | 36 | 100.0 | 224887 | 2 | BX470169 | BX470169 Danio rer | c 309 | 35 | 97.2 | 124895 | 8 | AC135288 | AC135288 Solanum d |
| c 237 | 36 | 100.0 | 227796 | 2 | AC131418 | AC131418 Rattus no | c 310 | 35 | 97.2 | 131385 | 8 | AL591417 | AL591417 Mouse DNA |
| c 238 | 36 | 100.0 | 229784 | 10 | AL845171 | AL845171 Mouse DNA | c 311 | 35 | 97.2 | 137995 | 8 | AP004688 | AP004688 Oryza sat |
| c 239 | 36 | 100.0 | 230610 | 5 | BX248108 | BX248108 Zebrafish | c 312 | 35 | 97.2 | 145293 | 2 | AP003519 | CR023519 Oryza sat |
| c 240 | 36 | 100.0 | 235474 | 2 | AC094786 | AC094786 Rattus no | c 313 | 35 | 97.2 | 145293 | 2 | AP003519 | CR628326 Danio rer |
| c 241 | 36 | 100.0 | 235474 | 2 | AC094786 | AC094786 Rattus no | c 314 | 35 | 97.2 | 146443 | 9 | AC007488 | AC007488 Homo sapi |
| c 242 | 36 | 100.0 | 238527 | 10 | AC129700 | AC129700 Rattus no | c 315 | 35 | 97.2 | 157362 | 2 | CR388035 | CR388035 Danio rer |
| c 243 | 36 | 100.0 | 240000 | 2 | AC012525 | AC012525 Homo sapi | c 316 | 35 | 97.2 | 157362 | 2 | CR388035 | CR388035 Danio rer |
| c 244 | 36 | 100.0 | 241623 | 2 | AC103008 | AC103008 Rattus no | c 317 | 35 | 97.2 | 157362 | 2 | CR388035 | CR388035 Danio rer |
| c 245 | 36 | 100.0 | 243360 | 2 | AC109684 | AC109684 Rattus no | c 318 | 35 | 97.2 | 157362 | 2 | CR388035 | CR388035 Danio rer |
| c 246 | 36 | 100.0 | 250880 | 10 | AC102040 | AC102040 Mus muscu | c 319 | 35 | 97.2 | 157362 | 2 | CR388035 | CR388035 Danio rer |
| c 247 | 36 | 100.0 | 256233 | 2 | AC096530 | AC096530 Rattus no | c 320 | 35 | 97.2 | 157362 | 2 | CR388035 | CR388035 Danio rer |
| c 248 | 36 | 100.0 | 261824 | 2 | AC128390 | AC128390 Rattus no | c 321 | 35 | 97.2 | 157362 | 2 | CR388035 | CR388035 Danio rer |
| c 249 | 36 | 100.0 | 291954 | 1 | AE017328 | AE017328 Listeria | c 322 | 35 | 97.2 | 157362 | 2 | CR388035 | CR388035 Danio rer |
| c 250 | 36 | 100.0 | 294415 | 8 | AE017113 | AE017113 Rattus no | c 323 | 35 | 97.2 | 157362 | 2 | CR388035 | CR388035 Danio rer |
| c 251 | 36 | 100.0 | 300029 | 8 | AE017113 | AE017113 Oryza sat | c 324 | 35 | 97.2 | 157362 | 2 | CR388035 | CR388035 Danio rer |
| c 252 | 36 | 100.0 | 300275 | 1 | AE016751 | AE016751 Staphyloc | c 325 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 253 | 35 | 97.2 | 343529 | 1 | CR378676 | CR378676 Photobact | c 326 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 254 | 35 | 97.2 | 593 | 11 | BV023869 | BV023869 S212P6866 | c 327 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 255 | 35 | 97.2 | 638 | 11 | BV016402 | BV016402 S212P6380 | c 328 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 256 | 35 | 97.2 | 661 | 11 | CNS06E9T | AL395539 T3 end of | c 329 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 257 | 35 | 97.2 | 799 | 11 | CNS06E9M | AL395528 T7 end of | c 330 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 258 | 35 | 97.2 | 889 | 11 | CNS06E9M | AL395528 T7 end of | c 331 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 259 | 35 | 97.2 | 1341 | 8 | AF406816 | AF406816 Aquilegia | c 332 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 260 | 35 | 97.2 | 1341 | 8 | AF536526 | AF536526 Anemone l | c 333 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 261 | 35 | 97.2 | 1362 | 6 | AX824969 | AX824969 Sequence | c 334 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 262 | 35 | 97.2 | 1362 | 6 | AX824971 | AX824971 Sequence | c 335 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 263 | 35 | 97.2 | 1410 | 6 | Q0831424 | Q0831424 Sequence | c 336 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 264 | 35 | 97.2 | 1410 | 6 | Q0874958 | Q0874958 Sequence | c 337 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 265 | 35 | 97.2 | 1410 | 6 | AX951581 | AX951581 Sequence | c 338 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 266 | 35 | 97.2 | 1410 | 8 | AY234125 | AY234125 Primula f | c 339 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 267 | 35 | 97.2 | 1450 | 8 | AY055117 | AY055117 Echium pi | c 340 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 268 | 35 | 97.2 | 1478 | 8 | AY055117 | AY055117 Echium ge | c 341 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 269 | 35 | 97.2 | 1559 | 8 | AY603475 | AY603475 Nitzschia | c 342 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 270 | 35 | 97.2 | 1618 | 8 | AY234127 | AY234127 Primula v | c 343 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 271 | 35 | 97.2 | 1652 | 6 | AX481611 | AX481611 Sequence | c 344 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 272 | 35 | 97.2 | 1652 | 6 | AX481940 | AX481940 Sequence | c 345 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 273 | 35 | 97.2 | 1652 | 8 | AY082392 | AY082392 Phaeodact | c 346 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 274 | 35 | 97.2 | 1671 | 10 | MSAXPEM1 | AF189308 Mus carol | c 347 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 275 | 35 | 97.2 | 1686 | 10 | MSAXPEM1 | AF189310 Mus saxic | c 348 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 276 | 35 | 97.2 | 1782 | 8 | AF031194 | AF031194 Tricium | c 349 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 277 | 35 | 97.2 | 1972 | 8 | BT009556 | BT009556 Tricium | c 350 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 278 | 35 | 97.2 | 1994 | 10 | AL954862 | AL954862 Mouse DNA | c 351 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 279 | 35 | 97.2 | 5593 | 6 | AX137631 | AX137631 Sequence | c 352 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 280 | 35 | 97.2 | 5593 | 6 | AX137856 | AX137856 Sequence | c 353 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 281 | 35 | 97.2 | 5593 | 6 | BD014134 | BD014134 Process o | c 354 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 282 | 35 | 97.2 | 6216 | 6 | AR170533 | AR170533 Sequence | c 355 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 283 | 35 | 97.2 | 9437 | 8 | AF195007 | AF195007 Brenothec | c 356 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 284 | 35 | 97.2 | 10961 | 1 | AE001939 | AE001939 Deinococc | c 357 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 285 | 35 | 97.2 | 17752 | 6 | AX481638 | AX481638 Sequence | c 358 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 286 | 35 | 97.2 | 17752 | 6 | AX481638 | AX481638 Sequence | c 359 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 287 | 35 | 97.2 | 17752 | 6 | AX481967 | AX481967 Sequence | c 360 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 288 | 35 | 97.2 | 17752 | 6 | AX951606 | AX951606 Sequence | c 361 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 289 | 35 | 97.2 | 25002 | 3 | CEC1364 | Z92825 Caenorhabdi | c 362 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 290 | 35 | 97.2 | 25002 | 6 | AX481773 | AX481773 Sequence | c 363 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 291 | 35 | 97.2 | 25621 | 1 | PSY548826 | AJ548826 Pseudomon | c 364 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 292 | 35 | 97.2 | 38608 | 3 | CEP36H1 | Z68760 Caenorhabdi | c 365 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 293 | 35 | 97.2 | 47163 | 10 | AL954297 | AL954297 Mouse DNA | c 366 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 294 | 35 | 97.2 | 56098 | 5 | BX578772 | BX578772 Zebrafish | c 367 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 295 | 35 | 97.2 | 63348 | 2 | AC135176 | AC135176 Homo sapi | c 368 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |
| c 296 | 35 | 97.2 | 63750 | 8 | AP004936 | AP004936 Lotus cor | c 369 | 35 | 97.2 | 162074 | 2 | CR388035 | CR388035 Danio rer |

| | | | | | | | | | | | | |
|-----|----|------|--------|----|------------|-------------------------------|-------|----|------|---------|----|--------------------|
| 370 | 35 | 97.2 | 209484 | 2 | AC024116 | AC024116 Mus muscu | C 443 | 34 | 94.4 | 1528 | 6 | AX166353 Sequence |
| 371 | 35 | 97.2 | 209705 | 10 | AC101931 | AC101931 Mus muscu | 444 | 34 | 94.4 | 1591 | 8 | HACV7B5RN |
| 372 | 35 | 97.2 | 209730 | 2 | AL844860 | AL844860 Mus muscu | 445 | 34 | 94.4 | 1594 | 6 | AX007239 Sequence |
| 373 | 35 | 97.2 | 211178 | 10 | AC139209 | AC139209 Mus muscu | 446 | 34 | 94.4 | 1606 | 6 | AX007273 Sequence |
| 374 | 35 | 97.2 | 211999 | 2 | AC087039 | AC087039 Mus muscu | 447 | 34 | 94.4 | 1610 | 8 | ENAJ4160 |
| 375 | 35 | 97.2 | 212101 | 2 | AC148782 | AC148782 Otleumur | 448 | 34 | 94.4 | 1633 | 8 | AF001394 |
| 376 | 35 | 97.2 | 213050 | 1 | AL646079 | AL646079 Ralstonia | 449 | 34 | 94.4 | 1652 | 8 | AX087345 Arabidops |
| 377 | 35 | 97.2 | 213438 | 2 | AC125903 | AC125903 Rattus no | 450 | 34 | 94.4 | 1678 | 6 | AX007241 Arabidops |
| 378 | 35 | 97.2 | 213524 | 2 | AL390792 | AL390792 Homo sapi | 451 | 34 | 94.4 | 1702 | 6 | AR200409 Sequence |
| 379 | 35 | 97.2 | 218410 | 2 | AC140457 | AC140457 Mus muscu | 452 | 34 | 94.4 | 1702 | 6 | AR455422 Sequence |
| 380 | 35 | 97.2 | 216609 | 2 | AC142133 | AC142133 Rattus no | 453 | 34 | 94.4 | 1704 | 8 | AF428420 Arabidops |
| 381 | 35 | 97.2 | 220823 | 10 | AC108827 | AC108827 Mus muscu | 454 | 34 | 94.4 | 1705 | 8 | ATAJ4161 |
| 382 | 35 | 97.2 | 223392 | 10 | AL670238 | AL670238 Mouse DNA | 455 | 34 | 94.4 | 1743 | 8 | BT000442 Arabidops |
| 383 | 35 | 97.2 | 224402 | 2 | AC096500 | AC096500 Rattus no | C 456 | 34 | 94.4 | 1840 | 6 | AX166371 Sequence |
| 384 | 35 | 97.2 | 224607 | 2 | AC103716 | AC103716 Mus muscu | 457 | 34 | 94.4 | 1857 | 5 | AX398379 |
| 385 | 35 | 97.2 | 224740 | 2 | AC018986 | AC018986 Mus muscu | 458 | 34 | 94.4 | 1869 | 8 | AF133728 |
| 386 | 35 | 97.2 | 225065 | 2 | AC127370 | AC127370 Mus muscu | 459 | 34 | 94.4 | 1924 | 6 | AX166373 Sequence |
| 387 | 35 | 97.2 | 225654 | 5 | AL953842 | AL953842 Zebrafish | C 460 | 34 | 94.4 | 1924 | 6 | AX166385 Sequence |
| 388 | 35 | 97.2 | 227922 | 10 | AC120547 | AC120547 Mus muscu | C 461 | 34 | 94.4 | 1980 | 6 | AR564554 Sequence |
| 389 | 35 | 97.2 | 229678 | 2 | AC103232 | AC103232 Rattus no | C 462 | 34 | 94.4 | 2034 | 8 | AB080193 |
| 390 | 35 | 97.2 | 231755 | 2 | AC109091 | AC109091 Rattus no | C 463 | 34 | 94.4 | 2688 | 6 | AR388599 Sequence |
| 391 | 35 | 97.2 | 232552 | 2 | AC103111 | AC103111 Rattus no | C 464 | 34 | 94.4 | 2762 | 9 | AF222985 |
| 392 | 35 | 97.2 | 233168 | 2 | AC099164 | AC099164 Rattus no | C 465 | 34 | 94.4 | 6876 | 6 | AR354068 Sequence |
| 393 | 35 | 97.2 | 234724 | 10 | AL683854 | AL683854 Mouse DNA | C 466 | 34 | 94.4 | 6876 | 6 | AR535624 Sequence |
| 394 | 35 | 97.2 | 235133 | 2 | AC115375 | AC115375 Rattus no | C 467 | 34 | 94.4 | 7291 | 9 | AF222983 Homo sapi |
| 395 | 35 | 97.2 | 235198 | 10 | AL645571 | AL645571 Mouse DNA | C 468 | 34 | 94.4 | 9466 | 6 | CQ574109 Sequence |
| 396 | 35 | 97.2 | 235915 | 2 | AC134944 | AC134944 Rattus no | C 469 | 34 | 94.4 | 10029 | 1 | AE009551 Brucella |
| 397 | 35 | 97.2 | 241385 | 2 | AC128785 | AC128785 Rattus no | 470 | 34 | 94.4 | 12145 | 1 | AE014388 Brucella |
| 398 | 35 | 97.2 | 243282 | 2 | AC096473 | AC096473 Rattus no | 471 | 34 | 94.4 | 15002 | 9 | AF222981 Homo sapi |
| 399 | 35 | 97.2 | 244677 | 2 | AC129545 | AC129545 Mus muscu | 472 | 34 | 94.4 | 13048 | 3 | U80447 |
| 400 | 35 | 97.2 | 246322 | 2 | AC133966 | AC133966 Homo sapi | C 473 | 34 | 94.4 | 33376 | 9 | AF222987 |
| 401 | 35 | 97.2 | 247984 | 2 | AC130984 | AC130984 Rattus no | C 474 | 34 | 94.4 | 33780 | 6 | AX151213 Sequence |
| 402 | 35 | 97.2 | 248864 | 2 | AC129403 | AC129403 Rattus no | C 475 | 34 | 94.4 | 35660 | 8 | SPBC16H5 |
| 403 | 35 | 97.2 | 249942 | 2 | AC111088 | AC111088 Mus muscu | C 476 | 34 | 94.4 | 39964 | 2 | AC145671 |
| 404 | 35 | 97.2 | 250510 | 2 | AC110837 | AC110837 Rattus no | 477 | 34 | 94.4 | 40400 | 3 | CEF268E4 |
| 405 | 35 | 97.2 | 251228 | 2 | AC097036 | AC097036 Rattus no | 478 | 34 | 94.4 | 41564 | 3 | AF067937 |
| 406 | 35 | 97.2 | 253701 | 2 | AC106658 | AC106658 Rattus no | C 479 | 34 | 94.4 | 41564 | 3 | AF067937 Caenorhab |
| 407 | 35 | 97.2 | 254057 | 2 | AC094747 | AC094747 Rattus no | C 480 | 34 | 94.4 | 57250 | 2 | AC083997 Homo sapi |
| 408 | 35 | 97.2 | 254581 | 2 | AC130626 | AC130626 Rattus no | C 481 | 34 | 94.4 | 59777 | 3 | AC084454 Caenorhab |
| 409 | 35 | 97.2 | 260967 | 2 | AC091771 | AC091771 Mus muscu | 482 | 34 | 94.4 | 61246 | 2 | AL359032_4 |
| 410 | 35 | 97.2 | 262895 | 2 | CR387980 | CR387980 Danio rer | C 483 | 34 | 94.4 | 65283 | 2 | AC101475 Mus muscu |
| 411 | 35 | 97.2 | 272577 | 2 | AC097684 | AC097684 Rattus no | C 484 | 34 | 94.4 | 71302 | 2 | AC087760 Homo sapi |
| 412 | 35 | 97.2 | 301042 | 1 | AS016967 | AS016967 Mycoplasma | C 485 | 34 | 94.4 | 72281 | 2 | HSF20148 Homo sapi |
| 413 | 35 | 97.2 | 308147 | 1 | AS016915 | AS016915 Chromobac | 486 | 34 | 94.4 | 73078 | 9 | AC122132 Homo sapi |
| 414 | 35 | 97.2 | 349980 | 6 | CQ870463 | CQ870463 Sequence | 487 | 34 | 94.4 | 77728 | 9 | AP000146 Homo sapi |
| 415 | 34 | 94.4 | 33 | 6 | AR080602 | AR080602 Sequence | C 488 | 34 | 94.4 | 77728 | 9 | AP000231 Homo sapi |
| 416 | 34 | 94.4 | 33 | 6 | AR098445 | AR098445 Sequence | C 489 | 34 | 94.4 | 79442 | 9 | AL139037 Human DNA |
| 417 | 34 | 94.4 | 33 | 6 | AR136022 | AR136022 Sequence | C 490 | 34 | 94.4 | 86516 | 9 | AC009493 Homo sapi |
| 418 | 34 | 94.4 | 33 | 6 | AR215240 | AR215240 Sequence | 491 | 34 | 94.4 | 86894 | 2 | AL390319 Homo sapi |
| 419 | 34 | 94.4 | 33 | 6 | B0082625 | B0082625 Methods a | C 492 | 34 | 94.4 | 87577 | 2 | BX640459 Danio rer |
| 420 | 34 | 94.4 | 33 | 6 | B0092921 | B0092921 Methods a | C 493 | 34 | 94.4 | 87960 | 2 | AC017906 Drosophil |
| 421 | 34 | 94.4 | 315 | 6 | AR388367 | AR388367 Sequence | 494 | 34 | 94.4 | 90019 | 8 | TM021B04 Arabidops |
| 422 | 34 | 94.4 | 317 | 11 | BX640487 | BX640487 Arabidops | 495 | 34 | 94.4 | 95993 | 8 | ATF2A19 |
| 423 | 34 | 94.4 | 447 | 6 | AS0348 | AS0348 Sequence 7 | C 496 | 34 | 94.4 | 97375 | 9 | AL353898 Human DNA |
| 424 | 34 | 94.4 | 447 | 6 | AS0352 | AS0352 Sequence | C 497 | 34 | 94.4 | 98476 | 8 | AP003706 Oryza sat |
| 425 | 34 | 94.4 | 447 | 6 | AR127512 | AR127512 Sequence | 498 | 34 | 94.4 | 101033 | 9 | AC104090 Homo sapi |
| 426 | 34 | 94.4 | 447 | 6 | AR127514 | AR127514 Sequence | 499 | 34 | 94.4 | 109321 | 9 | AC021079 Homo sapi |
| 427 | 34 | 94.4 | 447 | 14 | HPCCOREE1T | HPCCOREE1T L39302 Hepatitis C | 500 | 34 | 94.4 | 109864 | 9 | AF096876 Homo sapi |
| 428 | 34 | 94.4 | 447 | 14 | HPCCOREE1W | HPCCOREE1W L39302 Hepatitis C | C 501 | 34 | 94.4 | 110000 | 1 | BX571856_05 |
| 429 | 34 | 94.4 | 488 | 9 | BC062656 | BC062656 Homo sapi | C 502 | 34 | 94.4 | 110000 | 1 | BX571857_05 |
| 430 | 34 | 94.4 | 609 | 6 | AX620466 | AX620466 Sequence | C 503 | 34 | 94.4 | 110000 | 2 | AC150872_2 |
| 431 | 34 | 94.4 | 634 | 11 | G40519 | G40519 Z7223 Zebra | C 504 | 34 | 94.4 | 110000 | 2 | AP006497_4 |
| 432 | 34 | 94.4 | 662 | 6 | AX166383 | AX166383 Sequence | C 505 | 34 | 94.4 | 110000 | 2 | AP006497_5 |
| 433 | 34 | 94.4 | 702 | 7 | AF536823 | AF536823 Bacteriop | C 506 | 34 | 94.4 | 110000 | 8 | CR382124_10 |
| 434 | 34 | 94.4 | 1051 | 3 | AY057996 | AY057996 Entamoeba | C 507 | 34 | 94.4 | 110149 | 8 | CR382134_01 |
| 435 | 34 | 94.4 | 1238 | 6 | AX166375 | AX166375 Sequence | C 508 | 34 | 94.4 | 111255 | 8 | AC125478 Medicago |
| 436 | 34 | 94.4 | 1350 | 6 | AX505863 | AX505863 Sequence | 509 | 34 | 94.4 | 1125478 | 9 | AC125478 Homo sapi |
| 437 | 34 | 94.4 | 1365 | 6 | AR564555 | AR564555 Sequence | 510 | 34 | 94.4 | 113282 | 9 | AC120778 Homo sapi |
| 438 | 34 | 94.4 | 1428 | 6 | AX166358 | AX166358 Sequence | C 511 | 34 | 94.4 | 113345 | 8 | AC141110 Medicago |
| 439 | 34 | 94.4 | 1428 | 6 | AX166359 | AX166359 Sequence | 512 | 34 | 94.4 | 114078 | 2 | BX640498 Danio rer |
| 440 | 34 | 94.4 | 1464 | 6 | AX166350 | AX166350 Sequence | C 513 | 34 | 94.4 | 114504 | 9 | AC094080 Homo sapi |
| 441 | 34 | 94.4 | 1491 | 8 | BT003379 | BT003379 Arabidops | C 514 | 34 | 94.4 | 119427 | 5 | BX649415 Zebrafish |
| 442 | 34 | 94.4 | 1524 | 9 | AF465766 | AF465766 Homo sapi | 515 | 34 | 94.4 | 120359 | 10 | BX890584 Mouse DNA |

| | | | | | | | | | | | | | |
|-----|----|------|--------|----|-----------|--------------------|-----|----|------|--------|----|-----------|--------------------|
| 516 | 34 | 94.4 | 122223 | 9 | AC007880 | AC007880 Homo sapi | 589 | 34 | 94.4 | 182140 | 10 | AC137128 | AC137128 Mus muscu |
| 517 | 34 | 94.4 | 124531 | 9 | HSJ633H17 | AL049710 Human DNA | 590 | 34 | 94.4 | 182366 | 9 | AC017014 | AC017014 Homo sapi |
| 518 | 34 | 94.4 | 126087 | 8 | T3E15 | AF147264 Arabidops | 591 | 34 | 94.4 | 182577 | 5 | BX640466 | BX640466 Zebrafish |
| 519 | 34 | 94.4 | 129271 | 8 | AC005687 | AC005687 Arabidops | 592 | 34 | 94.4 | 182591 | 10 | AC127272 | AC127272 Mus muscu |
| 520 | 34 | 94.4 | 129921 | 8 | AC146568 | AC146568 Medicago | 593 | 34 | 94.4 | 182838 | 2 | AC115855 | AC115855 Mus muscu |
| 521 | 34 | 94.4 | 131414 | 9 | HSPI0238 | AL109763 Homo sapi | 594 | 34 | 94.4 | 183604 | 9 | AC022022 | AC022022 Homo sapi |
| 522 | 34 | 94.4 | 132072 | 9 | AC004841 | AC004841 Homo sapi | 595 | 34 | 94.4 | 183779 | 9 | AC123023 | AC123023 Homo sapi |
| 523 | 34 | 94.4 | 133968 | 9 | ALJ36171 | AL136171 Human DNA | 596 | 34 | 94.4 | 184362 | 2 | AL450268 | AL450268 Homo sapi |
| 524 | 34 | 94.4 | 134804 | 8 | AP004888 | AP004888 Oryza sat | 597 | 34 | 94.4 | 184985 | 2 | AC149673 | AC149673 Bos tauru |
| 525 | 34 | 94.4 | 137408 | 2 | AC151098 | AC151098 Bos tauru | 598 | 34 | 94.4 | 185132 | 9 | CNS01DUB | AL133238 Human chr |
| 526 | 34 | 94.4 | 139292 | 2 | AC149664 | AC149664 Bos tauru | 599 | 34 | 94.4 | 185324 | 9 | AC087828 | AC087828 Homo sapi |
| 527 | 34 | 94.4 | 139966 | 9 | AC004820 | AC004820 Homo sapi | 600 | 34 | 94.4 | 185947 | 9 | AC092630 | AC092630 Homo sapi |
| 528 | 34 | 94.4 | 141944 | 9 | AC122108 | AC122108 Homo sapi | 601 | 34 | 94.4 | 186084 | 9 | AP002768 | AP002768 Homo sapi |
| 529 | 34 | 94.4 | 142836 | 2 | AC140695 | AC140695 Rattus no | 602 | 34 | 94.4 | 186834 | 5 | BX004887 | BX004887 Zebrafish |
| 530 | 34 | 94.4 | 143220 | 2 | AL389887 | AL389887 Human DNA | 603 | 34 | 94.4 | 187752 | 10 | AC124689 | AC124689 Mus muscu |
| 531 | 34 | 94.4 | 143398 | 2 | AC141659 | AC141659 Apis mell | 604 | 34 | 94.4 | 187931 | 8 | AP005319 | AP005319 Oryza sat |
| 532 | 34 | 94.4 | 144075 | 2 | AC013763 | AC013763 Homo sapi | 605 | 34 | 94.4 | 188037 | 2 | AC147929 | AC147929 Ovis arie |
| 533 | 34 | 94.4 | 144590 | 8 | AP006452 | AP006452 Oryza sat | 606 | 34 | 94.4 | 188320 | 2 | AC092085 | AC092085 Bos tauru |
| 534 | 34 | 94.4 | 144610 | 2 | CR387981 | CR387981 Danio rer | 607 | 34 | 94.4 | 188907 | 2 | AC150945 | AC150945 Bos tauru |
| 535 | 34 | 94.4 | 148123 | 2 | AC151083 | AC151083 Bos tauru | 608 | 34 | 94.4 | 189421 | 9 | BS000043 | BS000043 Pan trogl |
| 536 | 34 | 94.4 | 148344 | 10 | AC090432 | AC090432 Mus muscu | 609 | 34 | 94.4 | 189502 | 2 | AC119087 | AC119087 Rattus no |
| 537 | 34 | 94.4 | 148555 | 2 | AC126921 | AC126921 Bos tauru | 610 | 34 | 94.4 | 191923 | 2 | AP001846 | AP001846 Homo sapi |
| 538 | 34 | 94.4 | 150052 | 9 | AC006481 | AC006481 Homo sapi | 611 | 34 | 94.4 | 193554 | 2 | AC151137 | AC151137 Bos tauru |
| 539 | 34 | 94.4 | 150325 | 2 | AC018535 | AC018535 Homo sapi | 612 | 34 | 94.4 | 193593 | 10 | AC111008 | AC111008 Mus muscu |
| 540 | 34 | 94.4 | 150817 | 8 | AP003223 | AP003223 Oryza sat | 613 | 34 | 94.4 | 194068 | 2 | AC115327 | AC115327 Rattus no |
| 541 | 34 | 94.4 | 151959 | 2 | AC036192 | AC036192 Homo sapi | 614 | 34 | 94.4 | 194311 | 9 | AC091245 | AC091245 Homo sapi |
| 542 | 34 | 94.4 | 152838 | 2 | AC011589 | AC011589 Homo sapi | 615 | 34 | 94.4 | 194546 | 9 | AC142286 | AC142286 Pan trogl |
| 543 | 34 | 94.4 | 154862 | 2 | AC139310 | AC139310 Bos tauru | 616 | 34 | 94.4 | 194641 | 2 | AC150690 | AC150690 Bos tauru |
| 544 | 34 | 94.4 | 156195 | 9 | AC093799 | AC093799 Homo sapi | 617 | 34 | 94.4 | 194721 | 5 | BX470232 | BX470232 Zebrafish |
| 545 | 34 | 94.4 | 156337 | 2 | AC009938 | AC009938 Homo sapi | 618 | 34 | 94.4 | 196301 | 10 | AC109217 | AC109217 Mus muscu |
| 546 | 34 | 94.4 | 156813 | 9 | HSJ633H13 | AL117333 Human DNA | 619 | 34 | 94.4 | 196455 | 2 | AC151138 | AC151138 Bos tauru |
| 547 | 34 | 94.4 | 156870 | 2 | AC149695 | AC149695 Bos tauru | 620 | 34 | 94.4 | 197064 | 8 | ATCHRIV18 | AL161506 Arabidops |
| 548 | 34 | 94.4 | 157174 | 2 | AC151222 | AC151222 Bos tauru | 621 | 34 | 94.4 | 197646 | 2 | AC011041 | AC011041 Homo sapi |
| 549 | 34 | 94.4 | 157371 | 2 | AC147844 | AC147844 Ovis arie | 622 | 34 | 94.4 | 198160 | 2 | AC013569 | AC013569 Homo sapi |
| 550 | 34 | 94.4 | 157701 | 2 | AC058814 | AC058814 Homo sapi | 623 | 34 | 94.4 | 198503 | 9 | AC107734 | AC107734 Mus muscu |
| 551 | 34 | 94.4 | 157857 | 2 | AC072032 | AC072032 Homo sapi | 624 | 34 | 94.4 | 199503 | 2 | AC018901 | AC018901 Homo sapi |
| 552 | 34 | 94.4 | 159222 | 9 | AC108130 | AC108130 Homo sapi | 625 | 34 | 94.4 | 201673 | 2 | AC099747 | AC099747 Bos tauru |
| 553 | 34 | 94.4 | 161346 | 5 | BX511013 | BX511013 Zebrafish | 626 | 34 | 94.4 | 201673 | 2 | AC099747 | AC099747 Bos tauru |
| 554 | 34 | 94.4 | 162591 | 2 | AC151214 | AC151214 Bos tauru | 627 | 34 | 94.4 | 204617 | 3 | AC006074 | AC006074 Drosophil |
| 555 | 34 | 94.4 | 162739 | 9 | AL353788 | AL353788 Human DNA | 628 | 34 | 94.4 | 205011 | 5 | AL954168 | AL954168 Zebrafish |
| 556 | 34 | 94.4 | 163056 | 2 | AL359968 | AL359968 Homo sapi | 629 | 34 | 94.4 | 206352 | 2 | AC139238 | AC139238 Mus muscu |
| 557 | 34 | 94.4 | 163461 | 2 | AC150853 | AC150853 Bos tauru | 630 | 34 | 94.4 | 206383 | 10 | AC008160 | AC008160 Mus muscu |
| 558 | 34 | 94.4 | 164866 | 4 | AC098686 | AC098686 Bos tauru | 631 | 34 | 94.4 | 208569 | 10 | AC133968 | AC133968 Mus muscu |
| 559 | 34 | 94.4 | 164792 | 2 | AC119551 | AC119551 Rattus no | 632 | 34 | 94.4 | 207555 | 2 | AC104557 | AC104557 Mus muscu |
| 560 | 34 | 94.4 | 164950 | 2 | BX088696 | BX088696 Danio rer | 633 | 34 | 94.4 | 210675 | 2 | AC026272 | AC026272 Homo sapi |
| 561 | 34 | 94.4 | 165067 | 9 | AL138927 | AL138927 Human DNA | 634 | 34 | 94.4 | 211084 | 2 | AC092084 | AC092084 Bos tauru |
| 562 | 34 | 94.4 | 165095 | 2 | AC138665 | AC138665 Mus muscu | 635 | 34 | 94.4 | 211542 | 2 | AC073206 | AC073206 Homo sapi |
| 563 | 34 | 94.4 | 165363 | 9 | HS45914 | AL031120 Human DNA | 636 | 34 | 94.4 | 213974 | 2 | AC121452 | AC121452 Rattus no |
| 564 | 34 | 94.4 | 165765 | 2 | AC117979 | AC117979 Rattus no | 637 | 34 | 94.4 | 213599 | 2 | AC140764 | AC140764 Rattus no |
| 565 | 34 | 94.4 | 165807 | 2 | AL391810 | AL391810 Homo sapi | 638 | 34 | 94.4 | 215399 | 2 | AC116268 | AC116268 Rattus no |
| 566 | 34 | 94.4 | 166655 | 5 | BX537129 | BX537129 Zebrafish | 639 | 34 | 94.4 | 216877 | 9 | AC106791 | AC106791 Homo sapi |
| 567 | 34 | 94.4 | 169947 | 2 | AC130631 | AC130631 Rattus no | 640 | 34 | 94.4 | 216887 | 2 | AC113676 | AC113676 Rattus no |
| 568 | 34 | 94.4 | 169968 | 2 | AC099745 | AC099745 Bos tauru | 641 | 34 | 94.4 | 216958 | 2 | AC115959 | AC115959 Mus muscu |
| 569 | 34 | 94.4 | 170156 | 2 | AP002412 | AP002412 Homo sapi | 642 | 34 | 94.4 | 217844 | 2 | BX927392 | BX927392 Danio rer |
| 570 | 34 | 94.4 | 170365 | 9 | AL390920 | AL390920 Human DNA | 643 | 34 | 94.4 | 218080 | 10 | AC125208 | AC125208 Mus muscu |
| 571 | 34 | 94.4 | 170770 | 9 | AP240627 | AP240627 Homo sapi | 644 | 34 | 94.4 | 218729 | 2 | AC111863 | AC111863 Rattus no |
| 572 | 34 | 94.4 | 172072 | 9 | AC004664 | AC004664 Homo sapi | 645 | 34 | 94.4 | 222632 | 2 | AC106165 | AC106165 Rattus no |
| 573 | 34 | 94.4 | 172456 | 2 | AC151080 | AC151080 Bos tauru | 646 | 34 | 94.4 | 223526 | 2 | AC150549 | AC150549 Bos tauru |
| 574 | 34 | 94.4 | 172579 | 9 | AC008064 | AC008064 Homo sapi | 647 | 34 | 94.4 | 225165 | 2 | AC149666 | AC149666 Bos tauru |
| 575 | 34 | 94.4 | 172641 | 2 | AC150489 | AC150489 Bos tauru | 648 | 34 | 94.4 | 225658 | 10 | AC127353 | AC127353 Mus muscu |
| 576 | 34 | 94.4 | 172688 | 9 | AL512641 | AL512641 Human DNA | 649 | 34 | 94.4 | 226674 | 2 | AC131171 | AC131171 Rattus no |
| 577 | 34 | 94.4 | 173660 | 2 | AC150576 | AC150576 Bos tauru | 650 | 34 | 94.4 | 226924 | 10 | AC113490 | AC113490 Mus muscu |
| 578 | 34 | 94.4 | 175092 | 2 | AC150576 | AC150576 Bos tauru | 651 | 34 | 94.4 | 227340 | 2 | AC095000 | AC095000 Rattus no |
| 579 | 34 | 94.4 | 175177 | 10 | AC124383 | AC124383 Mus muscu | 652 | 34 | 94.4 | 228826 | 2 | AC135589 | AC135589 Rattus no |
| 580 | 34 | 94.4 | 175590 | 9 | AC027119 | AC027119 Homo sapi | 653 | 34 | 94.4 | 228950 | 2 | AC111512 | AC111512 Rattus no |
| 581 | 34 | 94.4 | 176245 | 2 | AC016197 | AC016197 Homo sapi | 654 | 34 | 94.4 | 228231 | 2 | AC096139 | AC096139 Rattus no |
| 582 | 34 | 94.4 | 176551 | 2 | BX537283 | BX537283 Danio rer | 655 | 34 | 94.4 | 233345 | 4 | AJ421481 | AJ421481 Bos tauru |
| 583 | 34 | 94.4 | 178095 | 2 | CR753874 | CR753874 Danio rer | 656 | 34 | 94.4 | 233345 | 4 | AJ421481 | AJ421481 Bos tauru |
| 584 | 34 | 94.4 | 178262 | 3 | AC093049 | AC093049 Drosophil | 657 | 34 | 94.4 | 234844 | 2 | AC111734 | AC111734 Rattus no |
| 585 | 34 | 94.4 | 179779 | 2 | AP005315 | AP005315 Oryza sat | 658 | 34 | 94.4 | 236612 | 2 | AC109678 | AC109678 Rattus no |
| 586 | 34 | 94.4 | 180574 | 9 | AC092807 | AC092807 Homo sapi | 659 | 34 | 94.4 | 240664 | 2 | AC094875 | AC094875 Rattus no |
| 587 | 34 | 94.4 | 181817 | 2 | AL141133 | AL141133 Rattus no | 660 | 34 | 94.4 | 240741 | 2 | AC126133 | AC126133 Rattus no |
| 588 | 34 | 94.4 | 181842 | 2 | AL391823 | AL391823 Homo sapi | 661 | 34 | 94.4 | 243313 | 3 | AE003834 | AE003834 Drosophil |

| | | | | | | | | | | | | | |
|-----|----|------|--------|----|----------|--------------------|-------|----|------|------|----|-------------|--------------|
| 662 | 34 | 94.4 | 243510 | 5 | BX005415 | Zebrafish | 735 | 33 | 91.7 | 1374 | 8 | AF465282 | Mortierel |
| 663 | 34 | 94.4 | 244170 | 2 | AC130152 | Rattus no | 736 | 33 | 91.7 | 1404 | 6 | BD178222 | Fatty aci |
| 664 | 34 | 94.4 | 245595 | 2 | AC098435 | Rattus no | 737 | 33 | 91.7 | 1434 | 3 | AY493438 | Thalassio |
| 665 | 34 | 94.4 | 247239 | 2 | AC091376 | Rattus no | 738 | 33 | 91.7 | 1461 | 3 | AF114440 | Caenorhab |
| 666 | 34 | 94.4 | 250064 | 2 | AC103494 | Rattus no | 739 | 33 | 91.7 | 1461 | 6 | BD242778 | Desaturas |
| 667 | 34 | 94.4 | 250629 | 2 | AC114044 | Rattus no | 740 | 33 | 91.7 | 1463 | 3 | AF031477 | Caenorhab |
| 668 | 34 | 94.4 | 258819 | 2 | AC118292 | Rattus no | 741 | 33 | 91.7 | 1463 | 6 | BD138943 | Desaturas |
| 669 | 34 | 94.4 | 259210 | 2 | AC073368 | Homo sapi | 742 | 33 | 91.7 | 1463 | 6 | AX003603 | Sequence |
| 670 | 34 | 94.4 | 259553 | 2 | AC135140 | Rattus no | 743 | 33 | 91.7 | 1482 | 8 | AY320288 | Rhizopus |
| 671 | 34 | 94.4 | 261024 | 1 | AB017256 | Wobachia | 744 | 33 | 91.7 | 1521 | 8 | AB070555 | Mortierel |
| 672 | 34 | 94.4 | 262101 | 2 | AC113760 | Rattus no | 745 | 33 | 91.7 | 1537 | 8 | AY583316 | Rhizopus |
| 673 | 34 | 94.4 | 266631 | 2 | AC130916 | Rattus no | 746 | 33 | 91.7 | 1546 | 8 | AB052086 | Mucor cjr |
| 674 | 34 | 94.4 | 267172 | 9 | BS000177 | Pan trogl | c 747 | 33 | 91.7 | 1581 | 5 | Z19545 X.la | laevis mR |
| 675 | 34 | 94.4 | 272952 | 2 | AC109685 | Rattus no | 748 | 33 | 91.7 | 1590 | 8 | AB020032 | Mortierel |
| 676 | 34 | 94.4 | 296821 | 2 | AC127127 | Rattus no | 749 | 33 | 91.7 | 1617 | 6 | AR080598 | Sequence |
| 677 | 34 | 94.4 | 300821 | 1 | AB017250 | Treponema | 750 | 33 | 91.7 | 1617 | 6 | AR098439 | Sequence |
| 678 | 34 | 94.4 | 301050 | 1 | AP003130 | Staphyloc | 751 | 33 | 91.7 | 1617 | 6 | ARI36018 | Sequence |
| 679 | 34 | 94.4 | 302881 | 2 | BX323850 | Danio rer | 752 | 33 | 91.7 | 1617 | 6 | AR125236 | Sequence |
| 680 | 34 | 94.4 | 302873 | 2 | AC098042 | Rattus no | 753 | 33 | 91.7 | 1617 | 6 | AR235375 | Sequence |
| 681 | 34 | 94.4 | 325350 | 1 | AP004823 | Staphyloc | 754 | 33 | 91.7 | 1617 | 6 | BD082621 | Methods a |
| 682 | 34 | 94.4 | 325643 | 2 | AL512381 | Homo sapi | 755 | 33 | 91.7 | 1617 | 6 | BD092914 | Mortierel |
| 683 | 34 | 94.4 | 329709 | 1 | AP002997 | Mesorhizo | 756 | 33 | 91.7 | 1617 | 6 | AF110510 | Methods a |
| 684 | 34 | 94.4 | 334963 | 2 | AC114019 | Rattus no | 757 | 33 | 91.7 | 1644 | 8 | AF307942 | Mortierel |
| 685 | 34 | 94.4 | 340000 | 9 | AP001692 | Homo sapi | c 758 | 33 | 91.7 | 1650 | 8 | AY035052 | Arabidops |
| 686 | 34 | 94.4 | 340000 | 9 | AP001707 | Homo sapi | c 759 | 33 | 91.7 | 1667 | 8 | SCMET8 | X17271 Sacc |
| 687 | 34 | 94.4 | 340000 | 9 | HS21C018 | Homo sapi | 760 | 33 | 91.7 | 1743 | 8 | AB070556 | Mortierel |
| 688 | 34 | 94.4 | 343590 | 1 | AP003359 | Staphyloc | 761 | 33 | 91.7 | 1831 | 8 | AY392409 | Amylomyce |
| 689 | 34 | 94.4 | 347356 | 1 | BX640437 | Bordetell | 762 | 33 | 91.7 | 1856 | 8 | AF005096 | Ricinusc |
| 690 | 34 | 94.4 | 348093 | 2 | AC128471 | Rattus no | c 763 | 33 | 91.7 | 1900 | 1 | AXACEA | X93149 A.xy |
| 691 | 34 | 94.4 | 348251 | 1 | BX640423 | Bordetell | 764 | 33 | 91.7 | 1947 | 8 | AF465283 | Mortierel |
| 692 | 34 | 94.4 | 348517 | 1 | BX248354 | Corynebac | c 765 | 33 | 91.7 | 1980 | 6 | AR484379 | Sequence |
| 693 | 34 | 94.4 | 349726 | 1 | BX640421 | Bordetell | c 766 | 33 | 91.7 | 1980 | 6 | AX142873 | Sequence |
| 694 | 33 | 91.7 | 36 | 6 | AX577011 | Sequence | c 767 | 33 | 91.7 | 2000 | 6 | AX656198 | Sequence |
| 695 | 33 | 91.7 | 260 | 11 | AU025619 | Rattus no | c 768 | 33 | 91.7 | 2004 | 6 | AX813737 | Sequence |
| 696 | 33 | 91.7 | 306 | 6 | AR554370 | Sequence | c 769 | 33 | 91.7 | 2014 | 14 | TRA272198 | Tobacco r |
| 697 | 33 | 91.7 | 336 | 6 | AX072791 | Sequence | 770 | 33 | 91.7 | 2175 | 8 | AJ601391 | Mortierel |
| 698 | 33 | 91.7 | 386 | 6 | AX315800 | Sequence | c 771 | 33 | 91.7 | 2200 | 5 | XLEFLAA | X52975 X.la |
| 699 | 33 | 91.7 | 480 | 6 | C0049477 | Sequence | 772 | 33 | 91.7 | 2207 | 8 | AB070557 | Mortierel |
| 700 | 33 | 91.7 | 480 | 6 | C0064504 | Sequence | c 773 | 33 | 91.7 | 2799 | 9 | AK025159 | Homo sapi |
| 701 | 33 | 91.7 | 480 | 6 | CQ091451 | Sequence | 774 | 33 | 91.7 | 3004 | 1 | AF270259 | Staphyloc |
| 702 | 33 | 91.7 | 480 | 6 | CQ130277 | Sequence | 775 | 33 | 91.7 | 3004 | 6 | AR486213 | Sequence |
| 703 | 33 | 91.7 | 480 | 6 | CQ168902 | Sequence | 776 | 33 | 91.7 | 3004 | 6 | AX145577 | Sequence |
| 704 | 33 | 91.7 | 480 | 6 | CQ198020 | Sequence | c 777 | 33 | 91.7 | 3177 | 1 | AF269675 | Staphyloc |
| 705 | 33 | 91.7 | 480 | 6 | CQ213480 | Sequence | c 778 | 33 | 91.7 | 3177 | 6 | AR485631 | Sequence |
| 706 | 33 | 91.7 | 480 | 6 | CQ252060 | Sequence | c 779 | 33 | 91.7 | 3177 | 6 | AX144995 | Sequence |
| 707 | 33 | 91.7 | 480 | 6 | CQ289208 | Sequence | c 780 | 33 | 91.7 | 3216 | 14 | TRV9833 | Tobacco r |
| 708 | 33 | 91.7 | 480 | 6 | CQ326198 | Sequence | 781 | 33 | 91.7 | 3227 | 8 | SCNGR1 | Z14097 S.cer |
| 709 | 33 | 91.7 | 657 | 3 | AX142706 | Onchocerc | 782 | 33 | 91.7 | 3235 | 8 | SCYBR212W | S.cerevisia |
| 710 | 33 | 91.7 | 682 | 6 | AX840707 | Sequence | 783 | 33 | 91.7 | 3248 | 8 | AK106248 | Oryza sat |
| 711 | 33 | 91.7 | 684 | 4 | BOSZEV2 | Bos tauru | c 784 | 33 | 91.7 | 3320 | 1 | AF269607 | Staphyloc |
| 712 | 33 | 91.7 | 709 | 6 | BD146231 | Primer fo | c 785 | 33 | 91.7 | 3320 | 6 | AR485563 | Sequence |
| 713 | 33 | 91.7 | 709 | 6 | AX866169 | Sequence | c 786 | 33 | 91.7 | 3320 | 6 | AX144927 | Sequence |
| 714 | 33 | 91.7 | 862 | 8 | PSP16751 | Pyromyces s | c 787 | 33 | 91.7 | 3414 | 6 | BD159244 | Primer fo |
| 715 | 33 | 91.7 | 943 | 11 | G39469 | G39469 222313 Zebr | c 788 | 33 | 91.7 | 3414 | 6 | AX881738 | Sequence |
| 716 | 33 | 91.7 | 1044 | 6 | AX617312 | Sequence | c 789 | 33 | 91.7 | 3414 | 6 | BD012417 | A novel g |
| 717 | 33 | 91.7 | 1071 | 8 | AF621305 | Mortierel | c 790 | 33 | 91.7 | 3414 | 9 | AK027344 | Homo sapi |
| 718 | 33 | 91.7 | 1071 | 8 | AF307941 | Mortierel | c 791 | 33 | 91.7 | 3459 | 6 | AR270800 | Sequence |
| 719 | 33 | 91.7 | 1207 | 8 | AF244921 | Spinacia | 792 | 33 | 91.7 | 3459 | 6 | HSNGM07EG | Sequence |
| 720 | 33 | 91.7 | 1266 | 6 | CQ831420 | Sequence | c 793 | 33 | 91.7 | 3643 | 1 | AF269971 | Staphyloc |
| 721 | 33 | 91.7 | 1275 | 6 | BD242779 | Desaturas | c 794 | 33 | 91.7 | 3643 | 6 | AR485925 | Sequence |
| 722 | 33 | 91.7 | 1275 | 8 | AF139720 | Euglena g | c 795 | 33 | 91.7 | 3643 | 6 | AX145289 | Sequence |
| 723 | 33 | 91.7 | 1344 | 3 | AF078796 | Caenorhab | c 796 | 33 | 91.7 | 3751 | 6 | AX704751 | Sequence |
| 724 | 33 | 91.7 | 1344 | 6 | BD140482 | Desaturas | c 797 | 33 | 91.7 | 3780 | 3 | AF388524 | Dictyoste |
| 725 | 33 | 91.7 | 1344 | 6 | CQ831426 | Sequence | 798 | 33 | 91.7 | 3854 | 14 | AF368033 | Ndelle vi |
| 726 | 33 | 91.7 | 1344 | 6 | AX020906 | Sequence | c 799 | 33 | 91.7 | 3947 | 3 | AY280695 | Platyralp |
| 727 | 33 | 91.7 | 1344 | 6 | AX951583 | Sequence | c 800 | 33 | 91.7 | 4048 | 1 | AF444794 | Vibrio ch |
| 728 | 33 | 91.7 | 1374 | 6 | BD232180 | Compositi | c 801 | 33 | 91.7 | 4073 | 6 | AX269342 | Sequence |
| 729 | 33 | 91.7 | 1374 | 6 | AX413720 | Sequence | c 802 | 33 | 91.7 | 4473 | 8 | AF030976 | Ascobolus |
| 730 | 33 | 91.7 | 1374 | 6 | AX415732 | Sequence | 803 | 33 | 91.7 | 4828 | 3 | AK103435 | Oryza sat |
| 731 | 33 | 91.7 | 1374 | 6 | AX951591 | Sequence | 804 | 33 | 91.7 | 5000 | 3 | AF482397 | Dictyoste |
| 732 | 33 | 91.7 | 1374 | 8 | AF306634 | Mortierel | 805 | 33 | 91.7 | 5227 | 14 | AY008144 | Spodopter |
| 733 | 33 | 91.7 | 1374 | 8 | AF307940 | Mortierel | 806 | 33 | 91.7 | 5325 | 8 | AY583466 | Marchanti |
| 734 | 33 | 91.7 | 1374 | 8 | AF465281 | Mortierel | c 807 | 33 | 91.7 | 5941 | 8 | AIMASC2 | Ascobolus i |

| | | | | | | | | | | | | | | | |
|-------|----|------|-------|----|------------|--------------------|--------------|-------|------|--------|--------|----------|-------------|-------------|--------------------|
| C 808 | 33 | 91.7 | 7047 | 1 | LSEXOGC | X98238 | L.sake gene | C 881 | 33 | 91.7 | 83881 | 8 | AP004917 | AP004917 | Lotus cor |
| C 809 | 33 | 91.7 | 7099 | 3 | HR0AMD1 | D13507 | Holocynthia | 882 | 33 | 91.7 | 84554 | 8 | AC123571 | AC123571 | Medicago |
| C 810 | 33 | 91.7 | 7673 | 14 | HPV12 | X74466 | Human papill | 883 | 33 | 91.7 | 87428 | 3 | CEY64G10A | CEY64G10A | Caenorhab |
| C 811 | 33 | 91.7 | 7722 | 14 | HPU31785 | U31785 | Human papill | C 884 | 33 | 91.7 | 87967 | 8 | AC005223 | AC005223 | Arabidops |
| C 812 | 33 | 91.7 | 7726 | 14 | PH47CG | M32305 | Human papill | 885 | 33 | 91.7 | 89703 | 9 | AL356134 | AL356134 | Human DNA |
| C 813 | 33 | 91.7 | 7731 | 14 | HPU85660 | U85660 | Human papill | C 886 | 33 | 91.7 | 90291 | 9 | AP000173 | AP000173 | Homo sapi |
| C 814 | 33 | 91.7 | 7746 | 14 | PH55CG | M17463 | Human papill | C 887 | 33 | 91.7 | 91186 | 2 | AC118415_3 | AC118415_3 | Continuation (4 of |
| C 815 | 33 | 91.7 | 7746 | 14 | PH55CG | M22961 | Human papill | C 888 | 33 | 91.7 | 91186 | 2 | AC118415_3 | AC118415_3 | Continuation (4 of |
| C 816 | 33 | 91.7 | 8133 | 1 | AF060119 | AF060119 | Pasteurel | 889 | 33 | 91.7 | 92728 | 8 | CNS08C9D | CNS08C9D | Oriza sat |
| C 817 | 33 | 91.7 | 8546 | 6 | AX828406 | AX828406 | Sequence | 890 | 33 | 91.7 | 93196 | 2 | AC022085 | AC022085 | Homo sapi |
| C 818 | 33 | 91.7 | 8546 | 9 | HS306906 | HS306906 | Homo sapi | 891 | 33 | 91.7 | 93268 | 3 | AC024204 | AC024204 | Caenorhab |
| C 819 | 33 | 91.7 | 10066 | 1 | U67598 | U67598 | Methanocald | 892 | 33 | 91.7 | 93268 | 3 | AC024862 | AC024862 | Caenorhab |
| C 820 | 33 | 91.7 | 10383 | 1 | AE006705 | AE006705 | Sulfolobu | C 893 | 33 | 91.7 | 96337 | 9 | AC087349 | AC087349 | Homo sapi |
| C 821 | 33 | 91.7 | 11367 | 1 | AE006168 | AE006168 | Pasteurel | C 894 | 33 | 91.7 | 96597 | 6 | AX695914 | AX695914 | Sequence |
| C 822 | 33 | 91.7 | 11831 | 1 | AE006172 | AE006172 | Pasteurel | C 895 | 33 | 91.7 | 97862 | 2 | AC120823_4 | AC120823_4 | Continuation (5 of |
| C 823 | 33 | 91.7 | 13680 | 3 | AC024820 | AC024820 | Caenorhab | 896 | 33 | 91.7 | 99848 | 9 | HS34417 | HS34417 | Human DNA |
| C 824 | 33 | 91.7 | 13935 | 3 | PP156DSA | X96616 | P.primaurel | C 897 | 33 | 91.7 | 100400 | 9 | AC119744 | AC119744 | Homo sapi |
| C 825 | 33 | 91.7 | 15249 | 6 | AR353984 | AR353984 | Sequence | C 898 | 33 | 91.7 | 101333 | 8 | AP004030 | AP004030 | Oriza sat |
| C 826 | 33 | 91.7 | 15249 | 6 | AR353540 | AR353540 | Sequence | C 899 | 33 | 91.7 | 101365 | 2 | AP004748 | AP004748 | Oriza sat |
| C 827 | 33 | 91.7 | 15453 | 6 | BD093329 | BD093329 | Atopy gen | C 900 | 33 | 91.7 | 101589 | 5 | AL713963 | AL713963 | Zebrafish |
| C 828 | 33 | 91.7 | 17986 | 3 | U23451 | U23451 | Caenorhabdi | C 901 | 33 | 91.7 | 101589 | 9 | HSJ717M23 | HSJ717M23 | Human DNA |
| C 829 | 33 | 91.7 | 17986 | 3 | U23451 | U23451 | Caenorhabdi | 902 | 33 | 91.7 | 103550 | 2 | AP004003 | AP004003 | Oriza sat |
| C 830 | 33 | 91.7 | 18207 | 6 | AX828384 | AX828384 | Sequence | 903 | 33 | 91.7 | 105741 | 2 | AC140160 | AC140160 | Rattus no |
| C 831 | 33 | 91.7 | 18207 | 9 | AF156100 | AF156100 | Homo sapi | C 904 | 33 | 91.7 | 105741 | 2 | AC140160 | AC140160 | Rattus no |
| C 832 | 33 | 91.7 | 19230 | 3 | AC024821 | AC024821 | Caenorhab | C 905 | 33 | 91.7 | 106562 | 2 | AP004055 | AP004055 | Oriza sat |
| C 833 | 33 | 91.7 | 22348 | 9 | AP000332 | AP000332 | Homo sapi | C 906 | 33 | 91.7 | 108036 | 9 | AC084352 | AC084352 | Homo sapi |
| C 834 | 33 | 91.7 | 22683 | 3 | AC006656 | AC006656 | Caenorhab | C 907 | 33 | 91.7 | 109501 | 10 | AC084213 | AC084213 | Mus muscu |
| C 835 | 33 | 91.7 | 22683 | 3 | AC006656 | AC006656 | Caenorhab | 908 | 33 | 91.7 | 109964 | 2 | AP005677 | AP005677 | Oriza sat |
| C 836 | 33 | 91.7 | 24171 | 3 | CEC31A11 | Z83218 | Caenorhabdi | 909 | 33 | 91.7 | 110000 | 1 | AS017308_5 | AS017308_5 | Continuation (6 of |
| C 837 | 33 | 91.7 | 26076 | 3 | CEP14D7 | Z77658 | Caenorhabdi | 910 | 33 | 91.7 | 110000 | 1 | AS017332_1 | AS017332_1 | Continuation (2 of |
| C 838 | 33 | 91.7 | 26258 | 3 | U41018 | U41018 | Caenorhabdi | 911 | 33 | 91.7 | 110000 | 1 | AP006618_47 | AP006618_47 | Continuation (14 o |
| C 839 | 33 | 91.7 | 27884 | 8 | AP006537 | AP006537 | Lotus cor | 912 | 33 | 91.7 | 110000 | 1 | AP006840_13 | AP006840_13 | Continuation (22 o |
| C 840 | 33 | 91.7 | 29324 | 1 | BS16829KB | UJ22587 | Bacillus | 913 | 33 | 91.7 | 110000 | 1 | BX571856_21 | BX571856_21 | Continuation (22 o |
| C 841 | 33 | 91.7 | 29727 | 2 | CEH32801 | Z92800 | Caenorhabdi | 914 | 33 | 91.7 | 110000 | 1 | BX571856_22 | BX571856_22 | Continuation (23 o |
| C 842 | 33 | 91.7 | 31361 | 3 | AF016437 | AF016437 | Caenorhab | 915 | 33 | 91.7 | 110000 | 1 | BX571857_21 | BX571857_21 | Continuation (22 o |
| C 843 | 33 | 91.7 | 31361 | 3 | AF016437 | AF016437 | Caenorhab | C 916 | 33 | 91.7 | 110000 | 1 | CF000000_18 | CF000000_18 | Continuation (19 o |
| C 844 | 33 | 91.7 | 32723 | 3 | CEM88 | Z34802 | Caenorhabdi | 917 | 33 | 91.7 | 110000 | 2 | AC007194_3 | AC007194_3 | Continuation (4 of |
| C 845 | 33 | 91.7 | 32856 | 9 | AC139700 | AC139700 | Homo sapi | C 918 | 33 | 91.7 | 110000 | 2 | AC095237_1 | AC095237_1 | Continuation (2 of |
| C 846 | 33 | 91.7 | 33539 | 3 | U00067 | U00067 | Caenorhabdi | 919 | 33 | 91.7 | 110000 | 2 | AC095424_0 | AC095424_0 | Rattus no |
| C 847 | 33 | 91.7 | 35257 | 2 | AC149339 | AC149339 | Phakopsor | C 920 | 33 | 91.7 | 110000 | 2 | AC096204_2 | AC096204_2 | Continuation (3 of |
| C 848 | 33 | 91.7 | 35257 | 2 | CEZK1320 | Z46934 | Caenorhabdi | C 921 | 33 | 91.7 | 110000 | 2 | AC105872_0 | AC105872_0 | Rattus no |
| C 849 | 33 | 91.7 | 36116 | 2 | AC149332 | AC149332 | Phakopsor | C 922 | 33 | 91.7 | 110000 | 2 | AC109746_0 | AC109746_0 | Rattus no |
| C 850 | 33 | 91.7 | 37176 | 3 | CEP44G3 | Z83109 | Caenorhabdi | 923 | 33 | 91.7 | 110000 | 2 | AC109746_3 | AC109746_3 | Continuation (4 of |
| C 851 | 33 | 91.7 | 37176 | 3 | CEP44G3 | U53150 | Caenorhabdi | C 924 | 33 | 91.7 | 110000 | 2 | AC112426_2 | AC112426_2 | Continuation (3 of |
| C 852 | 33 | 91.7 | 38094 | 3 | AF040647 | AF040647 | Caenorhab | C 925 | 33 | 91.7 | 110000 | 2 | AC115558_1 | AC115558_1 | Continuation (2 of |
| C 853 | 33 | 91.7 | 38383 | 3 | CEP35H8 | Z36752 | Caenorhabdi | C 926 | 33 | 91.7 | 110000 | 2 | AC117408_2 | AC117408_2 | Continuation (3 of |
| C 854 | 33 | 91.7 | 39266 | 3 | CEP20E11 | Z81508 | Caenorhabdi | C 927 | 33 | 91.7 | 110000 | 2 | AC118415_2 | AC118415_2 | Continuation (3 of |
| C 855 | 33 | 91.7 | 40647 | 9 | HSU53583 | U53583 | Human chrom | 928 | 33 | 91.7 | 110000 | 2 | AC129442_4 | AC129442_4 | Continuation (5 of |
| C 856 | 33 | 91.7 | 41151 | 3 | CEC48B4 | Z29117 | Caenorhabdi | 929 | 33 | 91.7 | 110000 | 2 | AC130739_2 | AC130739_2 | Continuation (3 of |
| C 857 | 33 | 91.7 | 41258 | 3 | AF025453 | AF025453 | Caenorhab | C 930 | 33 | 91.7 | 110000 | 2 | AP006502_09 | AP006502_09 | Continuation (10 o |
| C 858 | 33 | 91.7 | 42300 | 3 | U80452 | U80452 | Caenorhab | C 931 | 33 | 91.7 | 110000 | 6 | AR271569_15 | AR271569_15 | Continuation (16 o |
| C 859 | 33 | 91.7 | 46022 | 5 | GGA289777 | AJ289777 | Gallus ga | 932 | 33 | 91.7 | 110000 | 6 | AR406002_6 | AR406002_6 | Continuation (7 of |
| C 860 | 33 | 91.7 | 46022 | 5 | GGA289778 | AJ289778 | Gallus ga | 933 | 33 | 91.7 | 110000 | 8 | CR380953_05 | CR380953_05 | Continuation (6 of |
| C 861 | 33 | 91.7 | 46022 | 5 | GGA289779 | AJ289779 | Gallus ga | C 934 | 33 | 91.7 | 110000 | 8 | CR382124_11 | CR382124_11 | Continuation (12 o |
| C 862 | 33 | 91.7 | 46148 | 3 | AC006624 | AC006624 | Caenorhab | 935 | 33 | 91.7 | 110000 | 8 | CR382127_12 | CR382127_12 | Continuation (13 o |
| C 863 | 33 | 91.7 | 48084 | 9 | HSBA259P1 | AL080273 | Human DNA | 936 | 33 | 91.7 | 110098 | 8 | AP004144 | AP004144 | Oriza sat |
| C 864 | 33 | 91.7 | 48888 | 2 | AC129939_4 | Continuation (5 of | C 937 | 33 | 91.7 | 110494 | 8 | AP004139 | AP004139 | Oriza sat | |
| C 865 | 33 | 91.7 | 48974 | 6 | AR161611 | AR161611 | Sequence | C 938 | 33 | 91.7 | 111128 | 9 | AC125421 | AC125421 | Homo sapi |
| C 866 | 33 | 91.7 | 48974 | 6 | BD080745 | BD080745 | Preseilli | C 939 | 33 | 91.7 | 111183 | 9 | AC008950 | AC008950 | Homo sapi |
| C 867 | 33 | 91.7 | 49274 | 10 | AF007560 | AF007560 | Mus muscu | C 940 | 33 | 91.7 | 112241 | 8 | AP003857 | AP003857 | Oriza sat |
| C 868 | 33 | 91.7 | 56675 | 2 | AC101826 | AC101826 | Mus muscu | C 941 | 33 | 91.7 | 112404 | 8 | OSJN00288 | OSJN00288 | Oriza sat |
| C 869 | 33 | 91.7 | 74999 | 2 | AC123371_4 | Continuation (5 of | 942 | 33 | 91.7 | 112518 | 2 | AC151142 | AC151142 | Bos tauru | |
| C 870 | 33 | 91.7 | 58464 | 2 | AC110049 | AC110049 | Homo sapi | C 943 | 33 | 91.7 | 112928 | 9 | AC105242 | AC105242 | Homo sapi |
| C 871 | 33 | 91.7 | 61635 | 9 | AC110812 | AC110812 | Homo sapi | 944 | 33 | 91.7 | 113326 | 8 | AP003999 | AP003999 | Oriza sat |
| C 872 | 33 | 91.7 | 65000 | 8 | AP006752 | AP006752 | Oriza sat | C 945 | 33 | 91.7 | 113415 | 2 | AP004860 | AP004860 | Oriza sat |
| C 873 | 33 | 91.7 | 68254 | 2 | AC117408_3 | Continuation (4 of | 946 | 33 | 91.7 | 114032 | 9 | AC104395 | AC104395 | Homo sapi | |
| C 874 | 33 | 91.7 | 74049 | 2 | AC135331 | AC135331 | Homo sapi | 947 | 33 | 91.7 | 114493 | 2 | AC142483 | AC142483 | Rattus no |
| C 875 | 33 | 91.7 | 74166 | 2 | AC151820 | AC151820 | Xenopus t | C 948 | 33 | 91.7 | 114493 | 2 | AC142483 | AC142483 | Rattus no |
| C 876 | 33 | 91.7 | 74319 | 5 | AL139162 | AL139162 | Human DNA | 949 | 33 | 91.7 | 115468 | 8 | AP005093 | AP005093 | Oriza sat |
| C 877 | 33 | 91.7 | 74910 | 5 | AL606722 | AL606722 | Zebrafish | 950 | 33 | 91.7 | 116796 | 9 | AL450468 | AL450468 | Human DNA |
| C 878 | 33 | 91.7 | 75556 | 2 | AC025993 | AC025993 | Homo sapi | 951 | 33 | 91.7 | 117048 | 2 | AC109629 | AC109629 | Mus muscu |
| C 879 | 33 | 91.7 | 77273 | 8 | AB022223 | AB022223 | Arabidops | C 952 | 33 | | | | | | |

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954 33 91.7 119535 8 OSJN00016
c 955 33 91.7 119691 8 AP003743
33 91.7 120228 8 AC112514
c 956 33 91.7 120492 9 AC092580
33 91.7 121470 8 AC133608
c 957 33 91.7 121755 9 AP001181
33 91.7 123897 2 AC144684
c 958 33 91.7 124026 8 AP004086
33 91.7 124028 8 AP005567
c 959 33 91.7 124166 8 AC137074
33 91.7 124489 9 HSDJ760C5
c 960 33 91.7 124920 8 BS000193
33 91.7 125380 9 AC145388
c 961 33 91.7 125829 9 AC127002
33 91.7 128420 8 AC087547
c 962 33 91.7 129420 8 AC087547
33 91.7 129539 2 CNS095BM
c 963 33 91.7 129540 8 CNS08CAW
33 91.7 129641 9 AC008560
c 964 33 91.7 129656 2 AC141351
33 91.7 129856 9 AC016620
c 965 33 91.7 130130 2 AC117804
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c 966 33 91.7 130907 8 AP003848
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c 967 33 91.7 131689 9 AC010588
33 91.7 133085 8 AC137668
c 968 33 91.7 133106 8 AP004759
33 91.7 133741 10 AL606930
c 969 33 91.7 133896 8 AC125496
33 91.7 134246 9 AC125617
c 970 33 91.7 135934 10 AL929095
33 91.7 135940 8 AC137699
c 971 33 91.7 136073 2 AP004773
33 91.7 137779 8 AP005843
c 972 33 91.7 138380 10 AC138111
33 91.7 138646 5 BX088562
c 973 33 91.7 138668 8 AC092749
33 91.7 138942 14 AF325155
c 974 33 91.7 139342 9 HSB4504H3
33 91.7 140055 2 AC023003
c 975 33 91.7 140063 8 AP005314
33 91.7 140142 2 AC143959
c 976 33 91.7 140261 8 AP005490
33 91.7 140720 8 AC135792
c 977 33 91.7 141041 8 AC087550
c1000 33 91.7 141041 8 AC087550

ALIGNMENTS

RESULT 1
AX253333/c
LOCUS AX253333 Sequence 39 from Patent WO0170993. 20 bp DNA linear PAT 10-OCT-2001
DEFINITION
ACCESSION AX253333
VERSION AX253333.1 GI:16073873
SOURCE
synthetic construct
ORGANISM
other sequences; artificial sequences.
REFERENCE
1 Winther,M.D., Smith,H.L., Allen,S.J., Ponton,A. and de Antueno,R.J.
AUTHORS Polynucleotides that control delta-6-desaturase genes and methods
TITLE for identifying compounds for modulating delta-6-desaturase
JOURNAL Patent: WO 0170993-A 39 27-SEP-2001;
FEATURES
source
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"

AL606446 Oryza sat
AP003743 Oryza sat
AC112514 Oryza sat
AC092580 Homo sapi
AC133608 Oryza sat
AP001181 Homo sapi
AC144684 Rattus no
AP004086 Oryza sat
AP005567 Oryza sat
AC137074 Genomic s
AL078587 Human DNA
BS000193 Pan trogl
AC145388 Oryza sat
AC127002 Homo sapi
AC087547 Oryza sat
BX569687 Oryza sat
AL844499 Oryza sat
AC008560 Homo sapi
AC141351 Rattus no
AC016620 Homo sapi
AC117804 Mus muscu
AC116524 Mus muscu
AL935067 Oryza sat
AL935067 Oryza sat
AL935067 Oryza sat
AC137668 Medicago
AP004759 Oryza sat
AL606930 Mouse DNA
AC125496 Oryza sat
AC125617 Homo sapi
AL929095 Mouse DNA
AC137699 Genomic s
AP004773 Oryza sat
AP005843 Oryza sat
AC138111 Mus muscu
BX088562 Zebrafish
AC092749 Genomic s
AC148658 Oryza sat
AF325155 Spodopter
AL121585 Human DNA
AC023003 Homo sapi
AP005314 Oryza sat
AC143959 Macaca mu
AP005490 Oryza sat
AC135792 Oryza sat
AC087550 Oryza sat

ORIGIN
Alignment Scores:
Pred. No.: 2.81 Length: 20
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 6
US-10-029-756-20 (1-6) x AX253333 (1-20)
Oy 1 PheGlnIleGluHisHis 6
|||||
Db 20 TTCCAGATCGAGCACCAC 3
RESULT 2
AR247897
LOCUS AR247897 266 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 3256 from patent US 6476212.
ACCESSION AR247897
VERSION AR247897.1 GI:27295771
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 266)
AUTHORS Lalgudi,R.V., Ito,L.Y. and Sherman,B.K.
TITLE Polynucleotides and polypeptides derived from corn ear
JOURNAL Patent: US 6476212-A 3256 05-NOV-2002;
FEATURES
Location/Qualifiers
1..266
source
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 52 Length: 266
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 6
US-10-029-756-20 (1-6) x AR247897 (1-266)
Oy 1 PheGlnIleGluHisHis 6
|||||
Db 78 TTCCAGATTGAGCACCAT 95
RESULT 3
AR246607
LOCUS AR246607 291 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 1966 from patent US 6476212.
ACCESSION AR246607
VERSION AR246607.1 GI:27294481
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 291)
AUTHORS Lalgudi,R.V., Ito,L.Y. and Sherman,B.K.
TITLE Polynucleotides and polypeptides derived from corn ear
JOURNAL Patent: US 6476212-A 1966 05-NOV-2002;
FEATURES
Location/Qualifiers
1..291
source
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 57.6 Length: 291
Score: 36.00 Matches: 6
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AR246607 (1-291)

QY 1 PheGlnIleGluHis 6
DB 228 TTCCAGATCGACCAT 245

RESULT 4

AR272626/c AR272626 347 bp DNA linear PAT 10-APR-2003

LOCUS DEFINITION Sequence 355 from patent US 6504010.

ACCESSION AR272626

VERSION AR272626.1 GI:29704511

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 347)

AUTHORS Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S.,

Carter, D., Retter, M.W., Mannion, J. and Fan, L.

TITLE Compositions and methods for the therapy and diagnosis of lung

cancer

JOURNAL Patent: US 6504010-A 355 07-JAN-2003;

FEATURES Location/Qualifiers

source 1..347

 /organism="unknown"

 /mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 70.2 Length: 347
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AR272626 (1-347)

QY 1 PheGlnIleGluHis 6
DB 284 TTCCAGATCGACCAT 267

RESULT 5

AR276207/c AR276207 347 bp DNA linear PAT 10-APR-2003

LOCUS DEFINITION Sequence 355 from patent US 6509448.

ACCESSION AR276207

VERSION AR276207.1 GI:29709852

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 347)

AUTHORS Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S.,

Carter, D., Retter, M.W., Mannion, J., Fan, L. and Wang, A.

TITLE Compositions and methods for the therapy and diagnosis of lung

cancer

JOURNAL Patent: US 6509448-A 355 21-JAN-2003;

FEATURES Location/Qualifiers

source 1..347

 /organism="unknown"

 /mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 70.2 Length: 347
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AR276207 (1-347)

QY 1 PheGlnIleGluHis 6
DB 284 TTCCAGATCGACCAT 267

RESULT 6

AR406482/c AR406482 347 bp DNA linear PAT 18-DEC-2003

LOCUS DEFINITION Sequence 355 from patent US 6630574.

ACCESSION AR406482

VERSION AR406482.1 GI:40156293

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 347)

AUTHORS Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S.,

Carter, D., Retter, M.W., Mannion, J. and Fan, L.

TITLE Compositions and methods for the therapy and diagnosis of lung

cancer

JOURNAL Patent: US 6630574-A 355 07-OCT-2003;

FEATURES Location/Qualifiers

source 1..347

 /organism="unknown"

 /mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 70.2 Length: 347
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AR406482 (1-347)

QY 1 PheGlnIleGluHis 6
DB 284 TTCCAGATCGACCAT 267

RESULT 7

AR440332/c AR440332 347 bp DNA linear PAT 20-FEB-2004

LOCUS DEFINITION Sequence 355 from patent US 6667154.

ACCESSION AR440332

VERSION AR440332.1 GI:42666492

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 347)

AUTHORS Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S.,

Carter, D., Retter, M.W., Mannion, J. and Fan, L.

TITLE Compositions and methods for the therapy and diagnosis of lung

cancer

JOURNAL Patent: US 6667154-A 355 23-DEC-2003;

FEATURES Location/Qualifiers

source 1..347

 /organism="unknown"

 /mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 70.2 Length: 347
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

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Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AR440332 (1-347)

Qy 1 PheGlnIleGluHis 6
Db 284 TTCCAGATCGAGCACCAC 267

RESULT 8
AR472490/c AR472490 347 bp DNA linear PAT 20-FEB-2004
LOCUS Sequence 355 from patent US 6686447.
DEFINITION AR472490
ACCESSION AR472490
VERSION AR472490.1 GI:42707819
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
AUTHORS Unclassified.
TITLE 1 (bases 1 to 347)
JOURNAL Wang, T., and Fan, L.
FEATURES Compositions and methods for the therapy and diagnosis of lung
SOURCE Patent: US 6686447-A 355 03-FEB-2004;
Location/Qualifiers
1..347
/mol_type="unknown"
/db_xref="genomic DNA"

ORIGIN
Alignment Scores: 70.2 Length: 347
Pred. No.: 36.00 Matches: 6
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

US-10-029-756-20 (1-6) x AR472490 (1-347)

Qy 1 PheGlnIleGluHis 6
Db 284 TTCCAGATCGAGCACCAC 267

RESULT 9
AR543143/c AR543143 347 bp DNA linear PAT 08-OCT-2004
LOCUS Sequence 355 from patent US 6746846.
DEFINITION AR543143
ACCESSION AR543143
VERSION AR543143.1 GI:53935819
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS 1 (bases 1 to 347)
TITLE Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S.,
Carter, D., Retter, M.W., Mannion, J., and Fan, L.
JOURNAL Methods for diagnosing lung cancer
FEATURES Patent: US 6746846-A 355 08-JUN-2004;
Location/Qualifiers
1..347
/mol_type="unknown"
/db_xref="genomic DNA"

ORIGIN
Alignment Scores: 70.2 Length: 347
Pred. No.: 36.00 Matches: 6
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

US-10-029-756-20 (1-6) x AR543143 (1-347)

Qy 1 PheGlnIleGluHis 6
Db 284 TTCCAGATCGAGCACCAC 267

RESULT 10
AX062728/c AX062728 347 bp DNA linear PAT 24-JAN-2001
LOCUS Sequence 355 from Patent WO0100828.
DEFINITION AX062728
ACCESSION AX062728
VERSION AX062728.1 GI:12540586
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Wang, T., Bangur, C.S., Lodes, M.J., Fanger, G.R., Vedvick, T.S.,
Carter, D., Retter, M.W., and Mannion, J.
TITLE Compositions and methods for the therapy and diagnosis of lung
JOURNAL cancer
FEATURES Patent: WO 0100828-A 355 04-JAN-2001;
CORIXA CORPORATION (US)
Location/Qualifiers
1..347
/mol_type="Homo sapiens"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores: 70.2 Length: 347
Pred. No.: 36.00 Matches: 6
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

US-10-029-756-20 (1-6) x AX062728 (1-347)

Qy 1 PheGlnIleGluHis 6
Db 284 TTCCAGATCGAGCACCAC 267

RESULT 11
AX367645/c AX367645 347 bp DNA linear PAT 16-FEB-2002
LOCUS Sequence 355 from Patent WO0204514.
DEFINITION AX367645
ACCESSION AX367645
VERSION AX367645.1 GI:18855732
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1
JOURNAL Wang, T., Watanabe, Y., Henderson, R.A., Johnson, J.C., Retter, M.W.,
Marnerakis, M., Carter, D., Fanger, G.R., Vedvick, T.S., Bangur, C.S.,
McNabb, A., Fanger, N., Switzer, A., McNeill, P.D., and Clapper, J.D.
FEATURES Compositions and methods for the therapy and diagnosis of lung
SOURCE Patent: WO 0204514-A 355 17-JAN-2002;
CORIXA CORPORATION (US)
Location/Qualifiers
1..347
/mol_type="Homo sapiens"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores: 70.2 Length: 347
Pred. No.: 36.00 Matches: 6
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

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Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AX367645 (1-347)

QY 1 PheGlnIleGluHis 6
|||||
Db 284 TTCCAGATCGAGCACCAT 267

RESULT 12
LOCUS AR484509/c 372 bp DNA linear PAT 14-MAY-2004
DEFINITION Sequence 1855 from patent US 6703492.
ACCESSION AR484509
VERSION AR484509.1 GI:47247612
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 372)
AUTHORS Kimmerly, W.J.
TITLE Staphylococcus epidermidis nucleic acids and proteins
JOURNAL Patent: US 6703492-A 1855 09-MAR-2004;
FEATURES Location/Qualifiers
source
1..372
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 75.9 Length: 372
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AR484509 (1-372)

QY 1 PheGlnIleGluHis 6
|||||
Db 154 TTCCAAATCGAGCACCAT 137

RESULT 13
LOCUS AX143133/c 372 bp DNA linear PAT 31-MAY-2001
DEFINITION Sequence 1855 from Patent WO0134809.
ACCESSION AX143133
VERSION AX143133.1 GI:14282438
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Kimmerly, W.J.
TITLE Staphylococcus epidermidis nucleic acids and proteins
JOURNAL Patent: WO 0134809-A 1855 17-MAY-2001;
FEATURES GLAXO GROUP LIMITED (GB)
Location/Qualifiers
source
1..372
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic nucleic acid sequence"

ORIGIN
Alignment Scores:
Pred. No.: 75.9 Length: 372
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AX143133 (1-372)

QY 1 PheGlnIleGluHis 6
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Db 154 TTCCAAATCGAGCACCAT 137

RESULT 14
LOCUS AR221976 449 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 38 from patent US 6428990.
ACCESSION AR221976
VERSION AR221976.1 GI:23329279
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 449)
AUTHORS Mukerji, P., Leonard, A.E.Y., Huang, Y.-S. and Parker-Barnes, J.M.
TITLE Human desaturase gene and uses thereof
JOURNAL Patent: US 6428990-A 38 06-AUG-2002;
FEATURES Location/Qualifiers
source
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/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 93.9 Length: 449
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AR221976 (1-449)

QY 1 PheGlnIleGluHis 6
|||||
Db 248 TTCCAGATTGAGCACCAT 265

RESULT 15
LOCUS AR221975 473 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 37 from patent US 6428990.
ACCESSION AR221975
VERSION AR221975.1 GI:23329278
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 473)
AUTHORS Mukerji, P., Leonard, A.E.Y., Huang, Y.-S. and Parker-Barnes, J.M.
TITLE Human desaturase gene and uses thereof
JOURNAL Patent: US 6428990-A 37 06-AUG-2002;
FEATURES Location/Qualifiers
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/mol_type="genomic DNA"

ORIGIN
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Pred. No.: 99.6 Length: 473
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AR221975 (1-473)

Qy 1 PheGlnIleGluHisHis 6
|||||
Db 279 TTCAGATTCGAGCACCAT 296

RESULT 16
AX840703
LOCUS AX840703 480 bp DNA linear PAT 17-DEC-2003
DEFINITION Sequence 5 from Patent WO03078639.
ACCESSION AX840703
VERSION AX840703.1 GI:39978890
KEYWORDS Pavlova lutheri
SOURCE Pavlova lutheri
ORGANISM Pavlova lutheri
Eukaryota; Haptophyceae; Pavlovaales; Pavlova.

REFERENCE 1
AUTHORS Graham, I.A. and Tonon, T.D.
TITLE Transgenic plants expressing enzymes involved in fatty acid biosynthesis
JOURNAL Patent: WO 03078639-A 5 25-SEP-2003;
THE UNIVERSITY OF YORK (GB)
FEATURES
source location/Qualifiers
1. 480
/organism="Pavlova lutheri"
/mol_type="unassigned DNA"
/db_xref="taxon:2832"

ORIGIN
Alignment Scores: 101 Length: 480
Pred. No.: 36.00 Matches: 6
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

US-10-029-756-20 (1-6) x AX840703 (1-480)

Qy 1 PheGlnIleGluHisHis 6
|||||
Db 55 TTCAGATTCGAGCACCAT 72

RESULT 17
BD082632
LOCUS BD082632 520 bp DNA linear PAT 27-AUG-2002
DEFINITION Methods and compositions for synthesis of long chain polyunsaturated fatty acids.
ACCESSION BD082632
VERSION BD082632.1 GI:22628242
KEYWORDS JP 2001523091-A/12.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 520)
AUTHORS Knutzon, D., Mukerji, P., Huang, Y.S., Thurmond, J., Chaudhary, S. and Leonard, A.E.Y.
TITLE Methods and compositions for synthesis of long chain polyunsaturated fatty acids
JOURNAL Patent: JP 2001523091-A 12 20-NOV-2001;
CALGENE LLC, ABBOTT LABORATORIES
COMMENT PD 20-NOV-2001
PF 10-APR-1998 JP 1998544053
PR 11-APR-1997 US 08/834655
PI DEBORAH KNUTZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI THURMOND,
PI SUNITA CHAUDHARY, AMANDA EUN YEONG LOENARD
PC C12N15/53, C12N15/81, C12N5/02, C12N5/10, C12N1/19, C12P7/64 PC
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CC A23L1/30
CC Topology: Linear;
FH Key Location/Qualifiers.

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source 1. 520
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/mol_type="genomic DNA"
/db_xref="taxon:32644"

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Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

US-10-029-756-20 (1-6) x BD082632 (1-520)

Qy 1 PheGlnIleGluHisHis 6
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Db 273 TTCAGATTCGAGCACCAC 290

RESULT 18
BD082647
LOCUS BD082647 520 bp DNA linear PAT 27-AUG-2002
DEFINITION Methods and compositions for synthesis of long chain polyunsaturated fatty acids.
ACCESSION BD082647
VERSION BD082647.1 GI:22628257
KEYWORDS JP 2001523092-A/7.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 520)
AUTHORS Knutzon, D., Mukerji, P., Huang, Y.S., Thurmond, J., Chaudhary, S. and Leonard, A.E.Y.
TITLE Methods and compositions for synthesis of long chain polyunsaturated fatty acids
JOURNAL Patent: JP 2001523092-A 7 20-NOV-2001;
CALGENE LLC, ABBOTT LABORATORIES
COMMENT PN JP 2001523092-A/7
PD 20-NOV-2001
PF 10-APR-1998 JP 1998544176
PR 11-APR-1997 US 08/833610
PI DEBORAH KNUTZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI THURMOND,
PI SUNITA CHAUDHARY, AMANDA EUN YEONG LEONARD
PC C12N15/53, C12N15/83, C12N5/10, C12P7/64, C11B1/00, A61K31/20, A23L1/ PC
A23K1/00
CC Topology: Linear;
FH Key Location/Qualifiers.

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Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

US-10-029-756-20 (1-6) x BD082647 (1-520)

Qy 1 PheGlnIleGluHisHis 6
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Db 273 TTCAGATTCGAGCACCAC 290

RESULT 19
BD092937

LOCUS BD092937 520 bp DNA linear PAT 27-AUG-2002
DEFINITION Methods and compositions for synthesis of long chain polyunsaturated fatty acids in plants.
ACCESSION BD092937
VERSION BD092937.1 GI:22638548
KEYWORDS JP 2001527395-A/24.
SOURCE synthetic construct
ORGANISM Homo sapiens (human)
REFERENCE 1 (bases 1 to 520)
AUTHORS Knutzon,D., Mukerji,P., Huang,Y.S., Thurmond,J., Chaudhary,S. and Leonard,A.E.Y.
TITLE Methods and compositions for synthesis of long chain polyunsaturated fatty acids in plants
JOURNAL Patent: JP 2001527395-A 24 25-DEC-2001;
CALGENE LLC,ABBOTT LABORATORIES
COMMENT PN JP 2001527395-A/24
PD 25-DEC-2001
PR 10-APR-1998 JP 1998544175
PF 11-APR-1997 US 08/833610,11-APR-1997 US 08/834033 PR 11-APR-1997 US 08/834655,24-OCT-1997 US 08/956985 PI
DEBORAH KNUTZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI THURMOND,
PI SUNITA CHAUDHARY, AMANDA EUN YEONG LEONARD
PC C12N15/53, C12N15/82, C12N5/10, C12P7/64, C11B1/00, A61K31/20, A23L1/30, A23K1/00
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FH Key Location/Qualifiers.
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/db_xref="taxon:32630"
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Query Match: 100.00% Indels: 0
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Qy 1 PheGlnIleGluHis 6
Db 273 TTTCAGATCGAGCACCAC 290
RESULT 20
BD147335
LOCUS BD147335 560 bp DNA linear PAT 17-JAN-2003
DEFINITION Primer for synthesizing full-length cDNA and use thereof.
ACCESSION BD147335
VERSION BD147335.1 GI:27853093
KEYWORDS JP 2002191363-A/2178.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 560)
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primer for synthesizing full-length cDNA and use thereof
JOURNAL Patent: JP 2002191363-A 2178 09-JUL-2002;
HELIIX RESEARCH INSTITUTE
COMMENT PN JP 2002191363-A/2178
PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU PI SAITO,

PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU, PI KEIICHI NAGAI, TETSUJI OTSUKI
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key
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FT Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Query Match: 100.00% Indels: 0
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Qy 1 PheGlnIleGluHis 6
Db 294 TTCCAGATTGAGCACCAC 311
RESULT 21
AX867273
LOCUS AX867273 560 bp DNA linear PAT 17-DEC-2003
DEFINITION Sequence 2178 from Patent EP1074617.
ACCESSION AX867273
VERSION AX867273.1 GI:40021651
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
TITLE Primers for synthesizing full-length cDNA and their use
JOURNAL Patent: EP 1074617-A 2178 07-FEB-2001;
Research Association for Biotechnology (JP)
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Alignment Scores:
Pred. No.: 120 Length: 560
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-029-756-20 (1-6) x AX867273 (1-560)
Qy 1 PheGlnIleGluHis 6
Db 294 TTCCAGATTGAGCACCAC 311
RESULT 22
AR221955
LOCUS AR221955 655 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 3 from patent US 6428990.

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ACCESSION AR221955
VERSION AR221955.1 GI:23329258
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 655)
AUTHORS Mukerji, P., Leonard, A.E.Y., Huang, Y.-S. and Parker-Barnes, J.M.
TITLE Human desaturase gene and uses thereof
JOURNAL Patent: US 642890-A 3 06-AUG-2002;
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Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-029-756-20 (1-6) x AR221955 (1-655)
Qy 1 PheGlnIleGluHis 6
Db 242 TTCCAGATTGACCAT 259
RESULT 23
BD082635
LOCUS
DEFINITION Methods and compositions for synthesis of long chain
polyunsaturated fatty acids.
ACCESSION BD082635
VERSION BD082635.1 GI:22628245
KEYWORDS JP 2001523091-A/15.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 655)
AUTHORS Knutzon, D., Mukerji, P., Huang, Y.S., Thurmond, J., Chaudhary, S. and
Leonard, A.E.Y.
TITLE Methods and compositions for synthesis of long chain
polyunsaturated fatty acids
JOURNAL CALGENE LLC ABBOTT LABORATORIES
COMMENT PN JP 2001523091-A/15
PD 20-NOV-2001
PF 10-APR-1998 JP 1998544053
PR 11-APR-1997 US 08/834655
PI DEBORAH KNUTZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI
THURMOND,
PI SUNITA CHAUDHARY, AMANDA EUN YEONG LOENARD
PC C11B1/00, A61K31/20,
C12N15/53, C12N15/81, C12N9/02, C12N5/10, C12N1/19, C12P7/64 PC
A23L1/30
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CC Topology: Linear;
FH Key Location/Qualifiers.
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Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-029-756-20 (1-6) x BD082635 (1-655)
Qy 1 PheGlnIleGluHis 6
Db 242 TTCCAGATTGACCAT 259
RESULT 23
BD082635
LOCUS
DEFINITION Methods and compositions for synthesis of long chain
polyunsaturated fatty acids.
ACCESSION BD082635
VERSION BD082635.1 GI:22628245
KEYWORDS JP 2001523091-A/15.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 655)
AUTHORS Knutzon, D., Mukerji, P., Huang, Y.S., Thurmond, J., Chaudhary, S. and
Leonard, A.E.Y.
TITLE Methods and compositions for synthesis of long chain
polyunsaturated fatty acids
JOURNAL CALGENE LLC ABBOTT LABORATORIES
COMMENT PN JP 2001523091-A/15
PD 20-NOV-2001
PF 10-APR-1998 JP 1998544053
PR 11-APR-1997 US 08/834655
PI DEBORAH KNUTZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI
THURMOND,
PI SUNITA CHAUDHARY, AMANDA EUN YEONG LOENARD
PC C11B1/00, A61K31/20,
C12N15/53, C12N15/81, C12N9/02, C12N5/10, C12N1/19, C12P7/64 PC
A23L1/30
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
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Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-029-756-20 (1-6) x BD082635 (1-655)
Qy 1 PheGlnIleGluHis 6
Db 242 TTCCAGATTGACCAT 259

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Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-029-756-20 (1-6) x BD082635 (1-655)
Qy 1 PheGlnIleGluHis 6
Db 242 TTCCAGATTGACCAT 259
RESULT 24
BD082650
LOCUS
DEFINITION Methods and compositions for synthesis of long chain
polyunsaturated fatty acids.
ACCESSION BD082650
VERSION BD082650.1 GI:22628260
KEYWORDS JP 2001523092-A/10.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 655)
AUTHORS Knutzon, D., Mukerji, P., Huang, Y.S., Thurmond, J., Chaudhary, S. and
Leonard, A.E.Y.
TITLE Methods and compositions for synthesis of long chain
polyunsaturated fatty acids
JOURNAL CALGENE LLC ABBOTT LABORATORIES
COMMENT PN JP 2001523092-A/10
PD 20-NOV-2001
PF 10-APR-1998 JP 1998544176
PR 11-APR-1997 US 08/833610
PI DEBORAH KNUTZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI
THURMOND,
PI SUNITA CHAUDHARY, AMANDA EUN YEONG LEONARD
PC C12N15/53, C12N15/83, C12N5/10, C12P7/64, C11B1/00, A61K31/20, A23L1/
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CC Topology: Linear;
FH Key Location/Qualifiers.
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Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-029-756-20 (1-6) x BD082650 (1-655)
Qy 1 PheGlnIleGluHis 6
Db 242 TTCCAGATTGACCAT 259
RESULT 25
BD092929
LOCUS
DEFINITION Methods and compositions for synthesis of long chain
polyunsaturated fatty acids in plants.
ACCESSION BD092929
VERSION BD092929.1 GI:22638540
KEYWORDS JP 2001527395-A/16.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 655)

```

AUTHORS Knutzon,D., Mukerji,P., Huang,Y.S., Thurmond,J., Chaudhary,S. and Leonard,A.E.Y.
 TITLE Methods and compositions for synthesis of long chain polyunsaturated fatty acids in plants
 JOURNAL Patent: JP 2001527395-A 16 25-DEC-2001;
 COMMENT CALGENE LLC,ABBOTT LABORATORIES
 PN JP 2001527395-A/16
 PD 25-DEC-2001
 PF 10-APR-1998 JP 1998544175
 PR 11-APR-1997 US 08/833610,11-APR-1997 US 08/834033 PR
 11-APR-1997 US 08/834655,24-OCT-1997 US 08/956985 PI
 DEBORAH KUTZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI
 THURMOND,
 PI SUNITA CHAUDHARY, AMANDA EUN YEONG LEONARD
 PC C12N15/53, C12N15/82, C12N5/10, C12P7/64, C11B1/00, A61K31/20, A23J11/ PC
 30, A23K1/00
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 CC topology: Linear;
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 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-10-029-756-20 (1-6) x BD092929 (1-655)
 QY 1 PheGlnIleGluHis 6
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 DB 242 TTCCAGATTGACCACT 259
 RESULT 26
 BD148047
 LOCUS 739 bp DNA linear PAT 17-JAN-2003
 DEFINITION Primer for synthesizing full-length cDNA and use thereof.
 ACCESSION BD148047
 VERSION BD148047.1 GI:27853805
 KEYWORDS JP 2002191363-A/2890.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 739)
 AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
 TITLE Primer for synthesizing full-length cDNA and use thereof
 JOURNAL Patent: JP 2002191363-A 2890 09-JUL-2002;
 COMMENT HELIX RESEARCH INSTITUTE
 OS Homo sapiens (human)
 PN JP 2002191363-A/2890
 PD 09-JUL-2002
 PF 28-JUL-2000 JP 2000280990
 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
 PI SAITO,
 PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
 PI KEIICHI NAGAI, TETSUJI OTSUKI
 PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
 10, C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
 Primer for synthesizing full-length cDNA and use thereof FH Key
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FT Location/Qualifiers
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 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
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 QY 1 PheGlnIleGluHis 6
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 DB 339 TTCCAGATTGACCACT 356
 RESULT 27
 AX867985
 LOCUS 739 bp DNA linear PAT 17-DEC-2003
 DEFINITION Sequence 2890 from Patent EP1074617.
 ACCESSION AX867985
 VERSION AX867985.1 GI:40022848
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
 TITLE Primers for synthesizing full-length cDNA and their use
 JOURNAL Patent: EP 1074617-A 2890 07-FEB-2001;
 COMMENT Research Association for Biotechnology (JJP)
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 Best Local Similarity: 100.00% Mismatches: 0
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 US-10-029-756-20 (1-6) x AX867985 (1-739)
 QY 1 PheGlnIleGluHis 6
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 DB 339 TTCCAGATTGACCACT 356
 RESULT 28
 CQ780299
 LOCUS 808 bp DNA linear PAT 17-MAR-2004
 DEFINITION Sequence 439 from Patent EP1396543.
 ACCESSION CQ780299
 VERSION CQ780299.1 GI:45536371
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,

Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and Koga,H. for synthesizing full length cDNA clones and their use
 Patents: EP 1396543-A 439 10-MAR-2004;
 Research Association for Biotechnology (JP)

FEATURES
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 /mol_type="unassigned DNA"
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 Pred. No.: 182 Length: 808
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 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x CQ780299 (1-808)

Qy 1 PheGlnlleGluHis 6
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Db 706 TTTCAGATTGAGCACCAC 723

RESULT 29
 CQ781966
 LOCUS CQ781966 808 bp DNA linear PAT 17-MAR-2004
 DEFINITION Sequence 2106 from Patent EP1396543.
 ACCESSION CQ781966
 VERSION CQ781966.1 GI:45538022
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
 Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
 Koga,H.
 Primers for synthesizing full length cDNA clones and their use
 Patent: EP 1396543-A 2106 10-MAR-2004;
 Research Association for Biotechnology (JP)

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ORIGIN
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 Percent Similarity: 100.00% Conservative: 0
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 Query Match: 100.00% Indels: 0
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US-10-029-756-20 (1-6) x CQ781966 (1-808)

Qy 1 PheGlnlleGluHis 6
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Db 706 TTTCAGATTGAGCACCAC 723

RESULT 30
 BD125008
 LOCUS BD125008 808 bp DNA linear PAT 18-SEP-2002
 DEFINITION Primer for synthesizing full-length cDNA and use thereof.
 ACCESSION BD125008
 VERSION BD125008.1 GI:23219953
 KEYWORDS JP 2002017375-A/439.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
 Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
 Koga,H.
 Primer for synthesizing full-length cDNA and use thereof
 Patent: JP 2002017375-A 439 22-JAN-2002;
 HELIX RESEARCH INSTITUTE

TITLE
 JOURNAL
 COMMENT
 OS Homo sapiens (human)
 PN JP 2002017375-A/439
 PD 22-JAN-2002
 PF 07-JUL-2000 JP 2000253172
 PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
 PI ISHII,
 PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
 SHINICHI KOJIMA,
 PI TETSUJI OTSUKI,HISASHI KOGA
 PC
 C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
 10,
 PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
 Primer for synthesizing full-length cDNA and use thereof FH Key

FT source 1..808
 Location/Qualifiers
 FT /organism="Homo sapiens (human)".
 source 1..808
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

ORIGIN
 Alignment Scores:
 Pred. No.: 182 Length: 808
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x BD125008 (1-808)

Qy 1 PheGlnlleGluHis 6
 |||||

Db 706 TTTCAGATTGAGCACCAC 723

RESULT 31
 BD126675
 LOCUS BD126675 808 bp DNA linear PAT 18-SEP-2002
 DEFINITION Primer for synthesizing full-length cDNA and use thereof.
 ACCESSION BD126675
 VERSION BD126675.1 GI:23221620
 KEYWORDS JP 2002017375-A/2106.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
 Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
 Koga,H.
 Primer for synthesizing full-length cDNA and use thereof
 Patent: JP 2002017375-A 2106 22-JAN-2002;
 HELIX RESEARCH INSTITUTE

TITLE
 JOURNAL
 COMMENT
 OS Homo sapiens (human)
 PN JP 2002017375-A/2106
 PD 22-JAN-2002
 PF 07-JUL-2000 JP 2000253172
 PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
 PI ISHII,
 PI YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI

SHINICHI KOJIMA,
PI TETSUJI OTSUKI, HISASHI KOGA
PC
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
10, C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
PC, C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00 CC
Primer for synthesizing full-length cDNA and use thereof FH Key

Location/Qualifiers
FT source 1..808
FT /organism='Homo sapiens (human)'.
Location/Qualifiers

FEATURES
source
1..808
/organism='Homo sapiens'
/mol_type='genomic DNA'
/db_xref='taxon:9606'

ORIGIN

Alignment Scores:
Pred. No.: 182 Length: 808
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x BD126675 (1-808)

Qy 1 PheGlnIleGluHis 6

Db 706 TTTCAGATTGACACCAT 723

RESULT 32

LOCUS AR221961 864 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 12 from patent US 6428990.
ACCESSION AR221961
VERSION AR221961.1 GI:23329264

KEYWORDS SOURCE

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 864)

AUTHORS Mukerji, P., Leonard, A.E.Y., Huang, Y.-S. and Parker-Barnes, J.M.

TITLE Human desaturase gene and uses thereof

JOURNAL Patent: US 6428990-A 12 06-AUG-2002;

FEATURES Location/Qualifiers

source 1..864

/organism='unknown'

/mol_type='genomic DNA'

ORIGIN

Alignment Scores:

Pred. No.: 196 Length: 864

Score: 36.00 Matches: 6

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AR221961 (1-864)

Qy 1 PheGlnIleGluHis 6

Db 670 TTTCAGATTGACACCAT 687

RESULT 33

LOCUS AR547128/c 876 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 2259 from patent US 6747137.
ACCESSION AR547128
VERSION AR547128.1 GI:53940303

KEYWORDS SOURCE

Unknown.

REFERENCE 1 (bases 1 to 876)

AUTHORS Weinstock, K.G. and Bush, D.

TITLE Nucleic acid sequences relating to Candida albicans for diagnostics

JOURNAL Patent: US 6747137-A 2259 08-JUN-2004;

FEATURES Location/Qualifiers

source 1..876

/organism='unknown'

/mol_type='genomic DNA'

ORIGIN

Alignment Scores:

Pred. No.: 266 Length: 1132

Score: 36.00 Matches: 6

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 1 Gaps: 0

ORGANISM

Unknown.

REFERENCE 1 (bases 1 to 876)

AUTHORS Weinstock, K.G. and Bush, D.

TITLE Nucleic acid sequences relating to Candida albicans for diagnostics

JOURNAL Patent: US 6747137-A 2259 08-JUN-2004;

FEATURES Location/Qualifiers

source 1..876

/organism='unknown'

/mol_type='genomic DNA'

ORIGIN

Alignment Scores:

Pred. No.: 200 Length: 876

Score: 36.00 Matches: 6

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AR547128 (1-876)

Qy 1 PheGlnIleGluHis 6

Db 478 TTCCAAATTGACACCAT 461

RESULT 34

LOCUS AF270385 1132 bp DNA linear BCT 01-AUG-2000
DEFINITION Staphylococcus epidermidis strain SRI clone step.4043f09a genomic
sequence.
ACCESSION AF270385
VERSION AF270385.1 GI:9624299

KEYWORDS Staphylococcus epidermidis

ORGANISM Staphylococcus epidermidis

REFERENCE 1 (bases 1 to 1132)

AUTHORS Kimmerly, W.J., Taylor, J. David., Nelsen, A.J., Godlevski, M.M.,

Rubino, M.A., Nelson, F.J., Rivers, P.R., Torruella-Miller, I.,

Listenbee, S., Ashanti, C., Altschuler, G., Mamo, L., Shepherd, N.S.,

Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D.H., Miller, G.S. and

Furdon, P.J.

TITLE Transposon-mediated sequencing of the Staphylococcus epidermidis

genome

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1132)

AUTHORS Taylor, J. David., Kimmerly, W.J., Nelsen, A.J., Godlevski, M.M.,

Rubino, M.A., Nelson, F.J., Rivers, P.R., Torruella-Miller, I.,

Listenbee, S., Ashanti, C., Altschuler, G., Mamo, L., Shepherd, N.S.,

Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D.H., Miller, G.S. and

Furdon, P.J.

TITLE Direct Submission

JOURNAL Submitted (22-MAY-2000) Departments of Genomic Sciences and

Bioinformatics, Genetics Directorate, Glaxo Wellcome, Inc., 5 Moore

Drive, Research Triangle Park, North Carolina 27709-3398, USA

FEATURES Location/Qualifiers

source 1..1132

/organism='Staphylococcus epidermidis'

/mol_type='genomic DNA'

/db_xref='taxon:1282'

/clone='step.4043f09a'

ORIGIN

Alignment Scores:

Pred. No.: 266 Length: 1132

Score: 36.00 Matches: 6

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AF270385 (1-1132)

Qy 1 PheGlnIleGluHisHis 6
 Db 359 TTTCAAATCGAGCACCAT 376

RESULT 35

AR486339 AR486339 1132 bp DNA linear PAT 14-MAY-2004

LOCUS Sequence 4425 from patent US 6703492.

DEFINITION AR486339

ACCESSION AR486339

VERSION AR486339.1 GI:47249442

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .1132

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
 Pred. No.: 266 Length: 1132
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AR486339 (1-1132)

Qy 1 PheGlnIleGluHisHis 6
 Db 359 TTTCAAATCGAGCACCAT 376

RESULT 36

AX145703 AX145703 1132 bp DNA linear PAT 31-MAY-2001

LOCUS Sequence 4425 from Patent WO0134809.

DEFINITION AX145703

ACCESSION AX145703

VERSION AX145703.1 GI:14284268

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .1132

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="synthetic nucleic acid sequence"

ORIGIN

Alignment Scores:
 Pred. No.: 266 Length: 1132
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AX145703 (1-1132)

Qy 1 PheGlnIleGluHisHis 6
 Db 359 TTTCAAATCGAGCACCAT 376

RESULT 37

AR410208 AR410208 1320 bp DNA linear PAT 18-DEC-2003

LOCUS Sequence 28 from patent US 6635451.

DEFINITION AR410208

ACCESSION AR410208

VERSION AR410208.1 GI:40161449

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .1320

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
 Pred. No.: 317 Length: 1320
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AR410208 (1-1320)

Qy 1 PheGlnIleGluHisHis 6
 Db 1123 TTTCAGATCGAGCACCAT 1140

RESULT 38

AX467713 AX467713 1320 bp DNA linear PAT 16-JUL-2002

LOCUS Sequence 3 from Patent WO0226946.

DEFINITION AX467713

ACCESSION AX467713

VERSION AX467713.1 GI:21900886

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .1320

/organism="Thraustochytrium sp."

/mol_type="unassigned DNA"

/db_xref="taxon:145168"

/note="unnamed protein product"

CDS

/protein_id="CAD42497.1"
 /db_xref="GI:21900887"
 /translation="MGKSGRGAAREMTAEANGDKRKTILIEGVLYDATNFKHPGGS
 IINPLTEAGVDATQAYREFHQRSGKADYKLSPLKLDASKVESRFSKAEQARRDAM
 TRDYAAPREELVAEGYFDPISPHMIVRVVEIVAFSLFVLMKASPTSLVLGVVMNG
 IAQRCGVMHEMGHGSFTGVILDDRMCEFFYGVCGMGSHYKWNKHSHAAAPNRL
 EHDVDLTLFLVAFNERVVRKYPGSLALNLRVQAYLFAPVSCLLGLGTLVLRPR
 YMLRCKHMEFVWIFAYIGVIFWLSMGALGYSFGTSVGMVLCSPGFGCIYIFLPFAVSH
 TFLPVTNPEDQLHWLEAYADHTVNISTKSWLVTWMSNLNFQIEHHULFPTAPQRFPE

ISPRVEALFKRHNLPPYDLPYTSVAVTTTFANLYSVGHSVGADTKKQD"

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ORIGIN
Alignment Scores:
Pred. No.: 317 Length: 1320
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AX467713 (1-1320)

Qy 1 PheGlnlleGluHisHis 6
Db 1123 TTTCAGATCGAGCACCAC 1140

RESULT 39
AX577003 AX577003 1320 bp DNA linear PAT 08-JAN-2003
DEFINITION Sequence 28 from Patent WO02081668.
ACCESSION AX577003
VERSION AX577003.1 GI:27646347
KEYWORDS
SOURCE
ORGANISM
Thraustochytrium aureum
Thraustochytrium aureum
Eukaryota; stramenopiles; Labyrinthulida; Thraustochytriidae;
Thraustochytrium.
REFERENCE
1
AUTHORS Mukerji, P., Huang, Y.S., Das, T., Thurmond, J. and Pereira, S.L.
TITLE Desaturase genes and uses thereof
JOURNAL Patent: WO 02081668-A 28 17-OCT-2002;
Abbott Laboratories (US)
FEATURES
source
1. 1320
/organism="Thraustochytrium aureum"
/mol_type="unassigned DNA"
/db_xref="taxon:42467"

ORIGIN
Alignment Scores:
Pred. No.: 317 Length: 1320
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AX577003 (1-1320)

Qy 1 PheGlnlleGluHisHis 6
Db 1123 TTTCAGATCGAGCACCAC 1140

RESULT 40
AX951587 AX951587 1320 bp DNA linear PAT 08-JAN-2004
DEFINITION Sequence 27 from Patent WO03093482.
ACCESSION AX951587
VERSION AX951587.1 GI:40781945
KEYWORDS
SOURCE
ORGANISM
Thraustochytrium
Thraustochytrium
Eukaryota; stramenopiles; Labyrinthulida; Thraustochytriidae.
REFERENCE
1
AUTHORS Cirpus, P., Renz, A., Lerchl, J. and Kuijpers, A.M.
TITLE Method for producing multiple unsaturated fatty acids in plants
JOURNAL Patent: WO 03093482-A 27 13-NOV-2003;
BASF Plant Science GmbH (DE)
FEATURES
source
1. 1320
/organism="Thraustochytrium"
/mol_type="unassigned DNA"
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CDS

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/db_xref="taxon:4774"
1. 1320
/notes="unnamed protein product; Delta-5-Desaturase"
/codon_start=1
/db_xref="GI:40781946"
/db_xref="GI:40781946"
/translation="MGKSGRSRAARENTAEANGDKRKTLLIEGLVLDATNFKHPGGS
IINFLTEGEAGVDATQAYREFHQSGKADKYLSPLKLDASKVSRFSAKQQRDAM
TRDYAAPREELVAEGYFDPISPHMIYRVEIVAFALFALMSKASPTSLVGVVMMG
IAQRCGWVHEMGHGSFTGIWLDLDRMCEFFYVGCGMSGHYWKQSHKHAAPNRL
EHDVDLNTPLVAENRVRKVPKGSLLALMLRQVAYLFAVPSCLLIGLWTLVLPFR
YMLTKRHRMEFVWIFARYIGWFSLMGALGYSPGTSVGMVLCSEGLGCIYIFLOPAVSH
THLPVTNPEDOLHMLEYAADHTYNISTKSHLVWMMNLNFQIEHHLFPPTAPQRFKE
ISPRVEALFKRHNLPPYDLPYTSVAVTTTFANLYSVGHSVGADTKKQD"
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ORIGIN

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Alignment Scores:
Pred. No.: 317 Length: 1320
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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US-10-029-756-20 (1-6) x AX951587 (1-1320)

Qy 1 PheGlnlleGluHisHis 6

Db 1123 TTTCAGATCGAGCACCAC 1140

RESULT 41

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AF489588 AF489588 1320 bp mRNA linear PLN 08-APR-2002
LOCUS Thraustochytrium sp. ATCC21685 delta-5 fatty acid desaturase mRNA,
complete cds.
DEFINITION
ACCESSION AF489588
VERSION AF489588.1 GI:20069122
KEYWORDS
SOURCE
ORGANISM
Thraustochytrium sp. ATCC21685
Thraustochytrium sp. ATCC21685
Eukaryota; stramenopiles; Labyrinthulida; Thraustochytriidae;
Thraustochytrium.
REFERENCE
1 (bases 1 to 1320)
AUTHORS Qiu, X., Hong, H. and MacKenzie, S.L.
TITLE Identification of a Delta 4 fatty acid desaturase from
Thraustochytrium sp. involved in the biosynthesis of docosahexaenoic
acid by heterologous expression in Saccharomyces cerevisiae and
Brassica juncea
JOURNAL J. Biol. Chem. 276 (34), 31561-31566 (2001)
MEDLINE 21402888
PUBMED 11397798
```

REFERENCE

2 (bases 1 to 1320)

Qiu, X., Hong, H. and MacKenzie, S.L.

Direct Submission

Submitted (28-FEB-2002) Research & Development, Bioriginal Food &

Science Corporation, 102 Melville Street, Saskatoon, SK S7J 0R1,

Canada

Location/Qualifiers

1. 1320

/organism="Thraustochytrium sp. ATCC21685"

/mol_type="mRNA"

/strain="ATCC 21685"

/db_xref="ATCC:21685"

/db_xref="taxon:191040"

1. 1320

/note="FAD5"

/product="delta-5 fatty acid desaturase"

/protein_id="AA009687.1"

/db_xref="GI:20069123"

/translation="MGKSGRSRAARENTAEANGDKRKTLLIEGLVLDATNFKHPGGS

IINFLTEGEAGVDATQAYREFHQSGKADKYLSPLKLDASKVSRFSAKQQRDAM

TRDYAAPREELVAEGYFDPISPHMIYRVEIVAFALFALMSKASPTSLVGVVMMG

IAQRCGWMHEMGHSFTGVIWLDRCMCEFFYGVCGMCSGHYKWNQHSKHAAAPNRL
EHDVLDLPLVAENRVRVKVPGSLLALWLRVOAYLPAVPSCLLGLGWTLVLRH
YMLTKRMEFWIIFAXIYGFSLMGALGYSFGTSGMYLCSFGLGIYIFLPQAVSH
THLPVTNPEDQLHLEAYADHTVNISTKSLVTVWNSNLNFQIEHHLFFPTAPQPRFKE
ISPRVEALFKRHNLFPYDLPTYSVSTTFANLYSVGHSVGADTKQD"

ORIGIN

Alignment Scores:
Pred. No.: 317 Length: 1320
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-029-756-20 (1-6) x AF489588 (1-1320)

Qy 1 PheGlnIleGluHisHis 6
|||||
Db 1123 TTTCAGATCGAGACCAC 1140

RESULT 42
AX577009
LOCUS AX577009 1329 bp DNA linear PAT 08-JAN-2003
DEFINITION Sequence 34 from Patent WO02081668.
ACCESSION AX577009
VERSION AX577009.1 GI:27646350
KEYWORDS Isochrysis galbana
SOURCE Isochrysis galbana
ORGANISM Isochrysis galbana
Eukaryota; Haptophyceae; Isochrysidales; Isochrysis.

REFERENCE 1
AUTHORS Mukerji, P., Huang, Y.S., Dae, T., Thurmond, J. and Pereira, S.L.
TITLE Desaturase genes and uses thereof
JOURNAL Patent: WO 02081668-A 34 17-OCT-2002;
Abbott Laboratories (US)

FEATURES
source
1..1329
/organism="Isochrysis galbana"
/mol_type="unassigned DNA"
/db_xref="taxon:37099"

ORIGIN

Alignment Scores:
Pred. No.: 319 Length: 1329
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AX577009 (1-1329)

Qy 1 PheGlnIleGluHisHis 6
|||||
Db 1132 TTTCAGATCGAGACCAC 1149

RESULT 43
CQ729637
LOCUS CQ729637 1335 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 15571 from Patent WO02068579.
ACCESSION CQ729637
VERSION CQ729637.1 GI:42301265
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
human exons or transcripts, for detecting expression and other uses
thereof

JOURNAL Patent: WO 02068579-A 15571 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
source
1..1335
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 321 Length: 1335
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x CQ729637 (1-1335)

Qy 1 PheGlnIleGluHisHis 6
|||||
Db 1141 TTCCAGATTGAGCACCAT 1158

RESULT 44
AR221953
LOCUS AR221953 1335 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 1 from patent US 6428990.
ACCESSION AR221953
VERSION AR221953.1 GI:23329256
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1335)
AUTHORS Mukerji, P., Leonard, A.E.Y., Huang, Y.-S. and Parker-Barnes, J.M.
TITLE Human desaturase gene and uses thereof
JOURNAL Patent: US 6428990-A 1 06-AUG-2002;

FEATURES
source
1..1335
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 321 Length: 1335
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AR221953 (1-1335)

Qy 1 PheGlnIleGluHisHis 6
|||||
Db 1141 TTCCAGATTGAGCACCAT 1158

RESULT 45
AX253297
LOCUS AX253297 1335 bp DNA linear PAT 10-OCT-2001
DEFINITION Sequence 3 from Patent WO0170993.
ACCESSION AX253297
VERSION AX253297.1 GI:16073841
KEYWORDS Rattus sp.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1
AUTHORS Winther, M.D., Smith, H.L., Allen, S.J., Ponton, A. and de Antueno, R.J.
TITLE Polynucleotides that control delta-6-desaturase genes and methods
for identifying compounds for modulating delta-6-desaturase


```
JOURNAL Patent: WO 0170993-A 3 27-SEP-2001;
AUTHORS Scotia Holdings plc (GB)
FEATURES Location/Qualifiers
source 1..1335
/organism="Rattus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:10118"
ORIGIN
Alignment Scores:
Pred. No.: 321 Length: 1335
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-029-756-20 (1-6) x AX253297 (1-1335)
Qy 1 PheGlnIleGluHis 6
Db 1141 TTCAGATTGAGCACCAC 1158
RESULT 46
AX253298
LOCUS AX253298 1335 bp DNA linear PAT 10-OCT-2001
DEFINITION Sequence 4 from Patent WO0170993.
ACCESSION AX253298
VERSION AX253298.1 GI:16073842
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Winther,M.D., Smith,H.L., Allen,S.J., Ponton,A. and de Antueno,R.J.
TITLE Polynucleotides that control delta-6-desaturase genes and methods
for identifying compounds for modulating delta-6-desaturase
JOURNAL Patent: WO 0170993-A 4 27-SEP-2001;
Scotia Holdings plc (GB)
FEATURES Location/Qualifiers
source 1..1335
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 321 Length: 1335
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-029-756-20 (1-6) x AX253298 (1-1335)
Qy 1 PheGlnIleGluHis 6
Db 1141 TTCAGATTGAGCACCAC 1158
RESULT 47
BD091695
LOCUS BD091695 1335 bp DNA linear PAT 27-AUG-2002
DEFINITION Process for producing lipid and microorganism secreting lipid.
ACCESSION BD091695
VERSION BD091695.1 GI:22637306
KEYWORDS WO 0175069-A/1.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
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REFERENCE 1 (bases 1 to 1335)
AUTHORS Suzuki,O., Ono,K., Aki,T., Shimauchi,T., Nakajima,T. and Kondo,A.
TITLE Process for producing lipid and microorganism secreting lipid
JOURNAL Patent: WO 0175069-A 1 11-OCT-2001;
IDEMITSU PETROCHEMICAL CO LTD.OSAMU SUZUKI,KAZUHISA ONO, TSUNEHIRO
AKI, TOSHITSUGU SHIMAUCHI,TOSHIAKI NAKAJIMA,AKIHIRO KONDO
COMMENT OS Rattus norvegicus (rat)
PN WO 0175069-A/1
PD 11-OCT-2001
PF 31-MAR-2000 WO 2000JP002129
PI OSAMU SUZUKI,KAZUHISA ONO, TSUNEHIRO AKI,TOSHITSUGU SHIMAUCHI,
PI TOSHIAKI NAKAJIMA,AKIHIRO KONDO
PC C12N1/19,C12N15/53,C12P7/64/(C12N1/19,C12R1.865), (C12P7/64,
PC C12R1.865)
CC
FH Key Location/Qualifiers
FT CDS (1)..(1332).
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source 1..1335
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
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Alignment Scores:
Pred. No.: 321 Length: 1335
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-029-756-20 (1-6) x BD091695 (1-1335)
Qy 1 PheGlnIleGluHis 6
Db 1141 TTCAGATTGAGCACCAC 1158
RESULT 48
AF199596
LOCUS AF199596 1335 bp mRNA linear PRI 21-JUN-2000
DEFINITION Homo sapiens delta-5 desaturase mRNA, complete cds.
ACCESSION AF199596
VERSION AF199596.1 GI:6842049
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1335)
AUTHORS Cho,H.P., Nakamura,M. and Clarke,S.D.
TITLE Cloning, expression, and fatty acid regulation of the human delta-5
desaturase
JOURNAL J. Biol. Chem. 274 (52), 37335-37339 (1999)
MEDLINE 20069725
PUBMED 10601301
REFERENCE 2 (bases 1 to 1335)
AUTHORS Cho,H.P. and Clarke,S.D.
TITLE Direct Submission
JOURNAL Submitted (28-OCT-1999) Nutritional Sciences, University of Texas
at Austin, PAI 5.30, Austin, TX 78751, USA
FEATURES
source 1..1335
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="11"
/map="11q12.2-q13"
1..1335
/codon_start=1
/product="delta-5 desaturase"
/protein_id="AAF29378.1"
/db_xref="GI:6842050"
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/translation="MADPPLAAETAAGLTPTRYFTWDEVAQRSCCEERWLVIDRKVN
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LLCAVLSAQAGLQHDGHLVSFSTSKWHLHFFVIGHLKGAPASWNNHMFQ
HAKPNCFRKDPDINMHFFPALGKILSVELGKQKKNYPYNNHOKKFFFLIGPALLP
LYQWYIFYFVIQIRKKWVDLAWMITFYVRFLLTVPLGLKAFGLGLFFIVRFLSNWF
VWVTONHPIHMDHNDWVSTQLATCNVHKSADFNSGHLNFQIEHLLPPTMP
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ORIGIN

Alignment Scores:
Pred. No.: 321 Length: 1335
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-029-756-20 (1-6) x AF199596 (1-1335)

Qy 1 PheGlnIleGluHisHis 6
Db 1141 TTCAGATTGACCAT 1158

RESULT 49

AF226273 1335 bp mRNA linear PRI 17-MAY-2000
LOCUS Homo sapiens delta-5 fatty acid desaturase (FADS5) mRNA, complete cds.
DEFINITION

ACCESSION AF226273

VERSION AF226273.1 GI:7861969

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1335)

AUTHORS Leonard,A.E., Kelder,B., Bobik,E.G., Chuang,L.T.,

Parker-Barnes,J.M., Thurmond,J.M., Kroeger,P.E., Kopchick,J.J.,

Huang,Y.-S. and Mukerji,P.

TITLE cDNA cloning and characterization of human Delta5-desaturase

JOURNAL Biochem. J. 347 Pt 3, 719-724 (2000)

PUBMED 10769175

REFERENCE 2 (bases 1 to 1335)

AUTHORS Leonard,A.E., Kelder,B., Bobik,E.G., Chuang,L.-T.,

Parker-Barnes,J.M., Thurmond,J.M., Kroeger,P.E., Kopchick,J.J.,

Huang,Y.-S. and Mukerji,P.

TITLE Direct Submission

JOURNAL Submitted (18-JAN-2000) Strategic Discovery Research, RPD of Abbott

Laboratories, 3300 Steiner Rd., Columbus, OH 43219, USA

FEATURES

Location/Qualifiers

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/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/map="between FEN1 and FTH1"

1..1335

/gene="FADS5"

1..1335

/gene="FADS5"

/note="involved in arachidonic acid biosynthesis"

/codon_start=1

/product="delta-5 fatty acid desaturase"

/protein_id="AAF70457.1"

/db_xref="GI:7861970"

/translation="MADPPLAAETAAGLTPTRYFTWDEVAQRSCCEERWLVIDRKVN

ISETRRHGGSRVISHYAGMDATDPFVAFHINKGLVKKNYNSLLIGELSPQSPFP

TKNELTDEPRELRATVHGMGMKANVFFLLYLLHLLDGAALWLTWVGTSFLPF

LLCAVLSAQAGLQHDGHLVSFSTSKWHLHFFVIGHLKGAPASWNNHMFQ

HAKPNCFRKDPDINMHFFPALGKILSVELGKQKKNYPYNNHOKKFFFLIGPALLP

LYQWYIFYFVIQIRKKWVDLAWMITFYVRFLLTVPLGLKAFGLGLFFIVRFLSNWF
VWVTONHPIHMDHNDWVSTQLATCNVHKSADFNSGHLNFQIEHLLPPTMP
RHNHYKVAPLVQSLCAKHGIEYQSKPLLSAFADIHLSKESGQLWLDAYLHQ"

ORIGIN

Alignment Scores:
Pred. No.: 321 Length: 1335
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-029-756-20 (1-6) x AF226273 (1-1335)

Qy 1 PheGlnIleGluHisHis 6
Db 1141 TTCAGATTGACCAT 1158

RESULT 50

AX577005 1338 bp DNA linear PAT 08-JAN-2003
LOCUS AX577005
DEFINITION Sequence 30 from Patent WO02081668.
ACCESSION AX577005
VERSION AX577005.1 GI:27646348

KEYWORDS Thraustochytrium aureum

SOURCE Thraustochytrium aureum

ORGANISM Thraustochytrium aureum

REFERENCE 1

AUTHORS Mukerji,P., Huang,Y.S., Das,T., Thurmond,J. and Pereira,S.L.

TITLE Desaturase genes and uses thereof

JOURNAL Patent: WO 02081668-A 30 17-OCT-2002;

FEATURES

Location/Qualifiers

1..1338

/organism="Thraustochytrium aureum"

/mol_type="unassigned DNA"

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ORIGIN

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Pred. No.: 322 Length: 1338
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AX577005 (1-1338)

Qy 1 PheGlnIleGluHisHis 6
Db 1135 TTCAGATCGACCAT 1152

RESULT 51

AF536525 1341 bp mRNA linear PLN 18-NOV-2003
LOCUS AF536525
DEFINITION Anemone leveillei delta-6-fatty acid desaturase mRNA, complete cds.
ACCESSION AF536525
VERSION AF536525.1 GI:33330960

KEYWORDS Anemone leveillei

SOURCE Anemone leveillei

ORGANISM Anemone leveillei

REFERENCE 1 (bases 1 to 1341)

AUTHORS Whitney,H.M., Michaelson,L.V., Sayanova,O., Pickett,J.A. and

Napier,J.A.

TITLE Functional characterisation of two cytochrome b5-fusion desaturases

from Anemone leveillei: the unexpected identification of a fatty

acid

acid

acid

acid

acid

acid

acid

acid

acid

acid

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JOURNAL acid delta6-desaturase
MEDLINE Planta 217 (6), 983-992 (2003)
PUBMED 22882798
REFERENCE 2 (bases 1 to 1341)
AUTHORS Whitney, H.M., Pickett, J.A., Sayanova, O. and Napier, J.A.
TITLE Direct Submission
JOURNAL Submitted (08-AUG-2002) Crop Performance & Improvement, Long Ashton
Research Station, Long Ashton, Bristol BS41 9AP, UK
FEATURES
    Location/Qualifiers
        1..1341
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        1..1341
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            /product="delta-6-fatty acid desaturase"
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        HYNIMTSELRNMQIFSNVYVSGVSGVSKRYNAHIAVNSLEYDPLQVPLVY
        STAPDSLSHFYRKMTFDVAREFLVSFQHWTFYPLMAIGRVSLAQISGVLSKVP
        LPDRHLEWGLVFWAMVYSLTISCLPNWVERVIFAVNFAVTGHOHVCFLNHSYQV
        YTGAPCANDEKQTKGISIDISCPWTDWFGGLQFQIEHHLFPMRPRCNLRKISPFV
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ORIGIN
Alignment Scores:
Pred. No.: 323 Length: 1341
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-029-756-20 (1-6) x AF536525 (1-1341)

Qy 1 PheGlnIleGluHis 6
Db 1108 TTTCAGATTGAGCATCAT 1125

RESULT 52
LOCUS AY131238 1347 bp mRNA linear PLN 17-AUG-2002
DEFINITION Argania spinosa delta-6-desaturase mRNA, complete cds.
ACCESSION AY131238
VERSION AY131238.1 GI:22296825
KEYWORDS Argania spinosa
SOURCE Argania spinosa
ORGANISM Argania spinosa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; Ericales; Sapotaceae; Argania.
REFERENCE 1 (bases 1 to 1347)
AUTHORS El Filali, A., Anderson, M. and Abbas, K.
TITLE Characterization and cloning of delta-6-desaturase in Argania
spinosa fruit
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1347)
AUTHORS El Filali, A., Anderson, M. and Abbas, K.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Biologie Moleculaire, Faculte des Sciences,
Ibn Batouta, Rabat, Rabat 1014, Morocco
FEATURES
    Location/Qualifiers
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CDS

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PGLYVYVSDSLNKFMGIFPAANCLSGISIGSKWNHNAHIAHIAVNSLEYDPLQVPLFL
VSSKFGSLTSHFYERKLTIDLSRFPVSKQHWTFYTIMCAARLNMYVQSILMLTK
RNVSYRAHELGLVFSIWIYPLVSLPNWGERIMFVIAVSVTGMQVQFSLNHFSS
SVYVKGPNGNWTFQTDGLDIDSCPPMMDWFGGLQFQIEHHLFPMRPRCNLRITSP
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ORIGIN
Alignment Scores:
Pred. No.: 324 Length: 1347
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-029-756-20 (1-6) x AY131238 (1-1347)

Qy 1 PheGlnIleGluHis 6
Db 1114 TTCCAAATTGAGCATCAT 1131

RESULT 53
LOCUS HSA325501/c HSA325501 1347 bp DNA linear PRI 18-JUL-2002
DEFINITION Homo sapiens genomic sequence surrounding NotI site, Clone
NB6-702R.
ACCESSION AJ325501
VERSION AJ325501.1 GI:15869895
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1347)
AUTHORS Kutsenko, A.S., Gizatullin, R.Z., Al-Amin, A.N., Wang, F., Kvasha, S.M.,
Podowski, R.M., Matushkin, Y.G., Gyanchandani, A., Muravenko, O.V.,
Levitsky, V.G., Kolchanov, N.A., Protopopov, A.I., Kashuba, V.I.,
Kisselev, L.L., Wasserman, W., Wahlestedt, C. and Zabarovsky, E.R.
TITLE NotI flanking sequences: a tool for gene discovery and verification
of the human genome
JOURNAL Nucleic Acids Res. 30 (14), 3163-3170 (2002)
MEDLINE 22131767
PUBMED 12136098
REFERENCE 2 (bases 1 to 1347)
AUTHORS Zabarovsky, E.R.
TITLE Direct Submission
JOURNAL Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
Sweden
FEATURES
    Location/Qualifiers
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            /clone="NB6-702R"

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-029-756-20 (1-6) x HSA325501 (1-1347)

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Qy 1 PheGlnIleGluHisHis 6
Db 1002 TTTCAATAGACCATCAT 985
RESULT 54
AF478472 1365 bp mRNA linear VRT 06-NOV-2003
LOCUS Salmo salar delta-5 fatty acyl desaturase (Fadsd5) mRNA, complete cds.
DEFINITION AF478472
SOURCE AF478472.1 GI:18958527
ORGANISM Salmo salar (Atlantic salmon)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
1 (bases 1 to 1365)
Hastings,N. Jr., Agaba,M.K., Tocher,D.R. and Teale,A.J.
The Evolution of Delta-5 Fatty Acyl Desaturase Genes in Marine and
Freshwater Teleosts
Unpublished
JOURNAL
REFERENCE 2 (bases 1 to 1365)
Hastings,N. Jr., Agaba,M.K., Tocher,D.R. and Teale,A.J.
Direct Submission
TITLE Submitted (28-JAN-2002) Institute of Aquaculture, Pathfoot
JOURNAL Building, Stirling FK9 4LA, Scotland
FEATURES
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1..1365
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/protein_id="AAU82631.1"
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QWLVIDRKYNTQWAKRHPGGIRVISHFAGEDATEAFSAFLDANFVRKFLKPLLIG
ELAPTESQDHQKNAALVQDFQALRDHVERGLRLARLLFSLVGLHLLLEALALGL
LWVGTSLTLLCSMLATSOAQAQWLDYCHLSVCKKSSWNHKLHKPVHGLKGA
SANWNHRHFGHAKPNVFRKDPDINSLPFLVLDQFVEYGIKKLKMYPHHQHQIF
FLIGPELVIPVFIQIPRTMFSQSDWDVLAWSMFSYLRFCCYFFGFGSVALLIS
FVRELESHVFMVVTQMNLPMEMDHERHQDLWTQLSATCNIEQSTFDFSGHLNFQ
IEHILFPTMPRHNYHLVAPLVRTLCEKHGVPYQVKTLQKGMTDVVRSLLKSGDLWLDA
YLHK"

ORIGIN
Alignment Scores:
Pred. No.: 329 Length: 1365
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0
US-10-029-756-20 (1-6) x AF478472 (1-1365)
Qy 1 PheGlnIleGluHisHis 6
Db 1171 TTTCAGATTGACCATCAT 1188
RESULT 55
AY234126 1385 bp mRNA linear PLN 04-MAY-2003
LOCUS Primula vialii sphingolipid delta-8 desaturase mRNA, complete cds.
DEFINITION AY234126
ACCESSION AY234126
VERSION AY234126.1 GI:30350278
KEYWORDS

Qy 1 PheGlnIleGluHisHis 6
Db 1152 TTTCAGATCGAGCACCAT 1169
RESULT 56
RNO494720 1442 bp mRNA linear ROD 12-JUL-2002
LOCUS Rattus norvegicus mRNA for putative fatty acid desaturase (fads3 gene).
DEFINITION RNO494720
ACCESSION AJ494720
VERSION AJ494720.1 GI:21742818
KEYWORDS fads3 gene; fatty acid desaturase.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1
AUTHORS D'Andrea,S., Guillou,H., Jan,S., Daval,S., Rioux,V. and Legrand,P.
TITLE Characterization of a novel putative fatty acid desaturase from rat
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1442)

Primula vialii
Primula vialii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; Ericales; Primulaceae; Primula.
1 (bases 1 to 1385)
Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and
Napier,J.A.
Identification of Primula fatty acid Delta(6)-desaturases with n-3
substrate preferences(1)
FEBS Lett. 542 (1-3), 100-104 (2003)
22615586
JOURNAL
MEDLINE
PUBMED
REFERENCE 2 (bases 1 to 1385)
Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and
Napier,J.A.
Direct Submission
TITLE Submitted (10-FEB-2003) Crop Performance & Improvement, Long Ashton
JOURNAL Research Station, Long Ashton, Bristol BS41 9AP, UK
FEATURES
source
1..1385
/organism="Primula vialii"
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LGHDSGHYQIMSSRKTNRPAQLVSGNCLAGISIAWKWNHNAHHLACNSLDYDPLDLOH
MPFFVSSKFFSLTSRFDYDKLRFDSVSRFLVSYQHWSPVPMCLARINLPAQSFML
LFSRAKVPDFRQIFGIGVFWVYPLLVSCLPNNGERIMFVVASFRVTGQHVQFCLN
HFSAEVYLGPPEGNDWFEKQTAGTLNISCPSWMDWFGGLQFQIEHHLFPLRPSQLR
KVSPFVRDLCKHNLAYNIASFMANVLTLTLRNAAIQARDLSNPPTPKNLVWEAVNT
HG"

ORIGIN
Alignment Scores:
Pred. No.: 335 Length: 1385
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0
US-10-029-756-20 (1-6) x AY234126 (1-1385)
Qy 1 PheGlnIleGluHisHis 6
Db 1152 TTTCAGATCGAGCACCAT 1169
RESULT 56
RNO494720 1442 bp mRNA linear ROD 12-JUL-2002
LOCUS Rattus norvegicus mRNA for putative fatty acid desaturase (fads3 gene).
DEFINITION RNO494720
ACCESSION AJ494720
VERSION AJ494720.1 GI:21742818
KEYWORDS fads3 gene; fatty acid desaturase.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1
AUTHORS D'Andrea,S., Guillou,H., Jan,S., Daval,S., Rioux,V. and Legrand,P.
TITLE Characterization of a novel putative fatty acid desaturase from rat
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1442)

AUTHORS Legrand,P.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-2002) Legrand P., Sciences Animales, Laboratoire
de Biochimie ENSAR-INRA, 65, Rue de Saint-Brieuc, 35000 Rennes,
France

FEATURES Location/Qualifiers
source
1. .1442
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague Dawley"
/db_xref="taxon:10116"
/tissue_type="liver"
/clone_lib="marathon-ready cdna"

gene
1. .1442
/gene="fada3"
89. .1438
/gene="fada3"
/codon_start=1
/evidence=experimental
/product="putative fatty acid desaturase"
/protein_id="CAD38527.1"
/db_xref="GI:21742819"
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/db_xref="UniProt/TREMBL:Q8K1P9"

/translation="MGVGEGGGPGPPGAPLGIPIFRWQIQRHDLPGDKWLV
IERVYDISWAQRHGGSLRIHHSADATDAFHQDLHFVRKFLKILLIGELAP
EERVDQNAQALIEDPRALQAAEDMKLFADTTFFALLGLHILAMELLAWLLVLL
PGWVSSVLAALILAIQAQWCLQHDILGHASIPKSRWNHVAQFVNGQLKGFSAHW
WNFRHQHAKPNILFHKDPDVTVAPELVLLGSSVEYKCKRYLPYLNHLYRFLIGP
PLLLIVNEVENLAYMLVCMQWTLDLAAASFYRFFLSYFYGATGTLFFLVAVRVL
ESHWFVITQNNHPIKEIGHKRDWASSQAATCNVPSLFDWFSGLHNFQIEHHL
PPTMPRHNYRVRVPLVKAFCAGHGLHYEVKPLTALVDIIGSLKKSGDIWLDAVLIHQ"

ORIGIN

Alignment Scores: 350 Length: 1442
Pred. No.: 36.00 Matches: 6
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 10

US-10-029-756-20 (1-6) x RN0494720 (1-1442)

Oy 1 PheGlnIleGluHisHis 6

Db 1244 TTCAGATTGACACCAC 1261

RESULT 57
BD195601 1478 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION 70 human secreted proteins.
ACCESSION BD195601
VERSION BD195601.1 GI:33005371
KEYWORDS JP 2002519990-A/62.
SOURCE unidentified
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 1478)
AUTHORS Ruben,S.M., Rosen,C.A., Fischer,C.L., Soppet,D.R., Carter,K.C.,
Bednarek,D., Endress,G.A., Yu,G.L., N.J., Feng,P., Young,P.E.,
Greene,J.M., Ferrie,A.M., Duan,R., Hu,J.S., Florence,K.A.,
Olsen,H.S., Ebner,R., Brewer,L.A., Moore,P.A., Shi,Y.,
Lafleur,D.W., Li,Y., Zeng,Z. and Kyaw,H.

70 human secreted proteins
PATENT: JP 2002519990-A 62 02-JUL-2002;
HUMAN GENOME SCIENCES INC
COMMENT OS Unidentified
PN JP 2002519990-A/62
PD 02-JUL-2002
PF 06-MAR-1998 JP 1998538875
PR 07-MAR-1997 US 60/040162,07-MAR-1997 US 60/040333 PR
07-MAR-1997 US 60/038621,07-MAR-1997 US 60/040161 PR

07-MAR-1997 US 60/040626,07-MAR-1997 US 60/040334 PR
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11-APR-1997 US 60/043580,11-APR-1997 US 60/043568 PR
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23-MAY-1997 US 60/047614,23-MAY-1997 US 60/047501 PR
06-JUN-1997 US 60/048974,06-JUN-1997 US 60/048964 PR
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22-AUG-1997 US 60/056631,22-AUG-1997 US 60/056632 PR
22-AUG-1997 US 60/056892,22-AUG-1997 US 60/056876 PR
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22-AUG-1997 US 60/056887,22-AUG-1997 US 60/057761 PR
05-SEP-1997 US 60/057650

PI STEVEN M RUBEN,CRAIG A ROSEN,CARRIE L FISCHER,DANIEL R SOPPET,
PI KENNETH C CARTER,DANIEL P BEDNARIK,GREGORY
A ENDRESS,GUO LIANG

PI YU,JIAN NI,
PI PING FENG,PAUL E YOUNG,JOHN M GREENE,ANN
M FERRIE,ROXANNE DUAN,
PI JING SHAN HU,KIMBERLY A FLORENCE,HENRIK
S OLSEN,REINHARDT EBNER,
PI LAURIE A BREWER,PAUL A MOORE,YANGGU SHI,DAVID W LAFLEUR PI
YI LI,ZHIZHEN ZENG.

PI HLA KYAW
PC C12N15/12,C12N5/10,C12N1/21,C07K14/47,C07K16/18,C12Q1/69, PC
GO1N33/50,
PC GO1N33/53,GO1N33/68,A61K38/17
CC Strandedness: Double;
CC Topology: Linear;
CC 70 human secreted proteins
FH Key Location/Qualifiers
FT source 1. .1478
FT /organism='Unidentified'.
Location/Qualifiers
1. .1478
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FEATURES
source

ORIGIN

Alignment Scores:

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Pred. No.: 360 Length: 1478
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-10-029-756-20 (1-6) x BD195601 (1-1478)

Qy 1 PheGlnIleGluHisHis 6
Db 947 TTCAGATCGAGCACCAC 964

RESULT 58
LOCUS CQ775646 1478 bp DNA linear PAT 11-MAR-2004
DEFINITION Sequence 63 from Patent EP1394252.
ACCESSION CQ775646
VERSION CQ775646.1 GI:45379034
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Olsen,H.S., Yu,G.L., Endress,G.A., Bednarik,D.P., Carter,K.C.,
Feng,P., Soppet,D.R., Young,P.E., Duan,D.R., Florence,K.A.,
Greene,J.M., Fischer,C.L., Hu,J.S., Ruben,S.M., Ebner,R.,
Brewer,L.A., Ferrie,A.M., Moore,P.A., Ni,J., Shi,Y., Lafleur,D.W.,
Li,Y., Zeng,Z., Kyaw,H. and Rosen,C.A.
70 human secreted proteins
TITLE Patent: EP 1394252-A 63 03-MAR-2004;
JOURNAL HUMAN GENOME SCIENCES, INC. (US)
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/db_xref="taxon:32644"

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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-10-029-756-20 (1-6) x CQ775646 (1-1478)

Qy 1 PheGlnIleGluHisHis 6
Db 947 TTCAGATCGAGCACCAC 964

RESULT 59
LOCUS AR352656 1478 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 63 from patent US 6590075.
ACCESSION AR352656
VERSION AR352656.1 GI:33757914
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1478)
AUTHORS Ruben,S.M., Rosen,C.A., Fischer,C.L., Soppet,D.R., Carter,K.C.,
Bednarik,D.P., Endress,G.A., Yu,G.-L., Ni,J., Feng,P., Young,P.E.,
Greene,J.M., Ferrie,A.M., Duan,R., Hu,J.-S., Florence,K.A.,
Olsen,H.S., Ebner,R., Brewer,L.A. and Shi,Y.
Secreted protein H0A250
TITLE Patent: US 6590075-A 63 08-JUL-2003;
JOURNAL Location/Qualifiers
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1. .1478
/organism="unknown"

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Score: 36.00 Matches: 6
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-10-029-756-20 (1-6) x AR352656 (1-1478)

Qy 1 PheGlnIleGluHisHis 6
Db 947 TTCAGATCGAGCACCAC 964

RESULT 60
LOCUS AB074149 1498 bp mRNA linear VRT 13-NOV-2001
DEFINITION Oncorhynchus masou mRNA for putative delata 6-desaturase, complete
cde.
ACCESSION AB074149
VERSION AB074149.1 GI:16904664
KEYWORDS Oncorhynchus masou (cherry salmon)
ORGANISM Oncorhynchus masou
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
REFERENCE 1
AUTHORS Sirisunay,S., Yoshizaki,G., Kiron,V., Takeuchi,T. and Gen,K.
TITLE delta6-desaturase-like cDNA in masou salmon form2
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1498)
AUTHORS Sirisunay,S., Yoshizaki,G., Kiron,V., Takeuchi,T. and Gen,K.
TITLE Direct Submission
JOURNAL Submitted (10-NOV-2001) Soranuth Sirisunay, Tokyo University of
Fisheries, Aquatic Bioscience; 4-5-7 Konan, Minato-ku, Tokyo
108-8477, Japan (E-mail:soranuth@yahoo.com, Tel:81-3-5463-0555,
Fax:81-3-5463-0553)
FEATURES
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NWNHHRFHAKPNVSKDPDINSLVFLVGDQKPYEYIKKLYKMPYHHQHYFFL
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ORIGIN
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Pred. No.: 365 Length: 1498
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 5

US-10-029-756-20 (1-6) x AB074149 (1-1498)

Qy 1 PheGlnIleGluHisHis 6

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Db 1243 TTTCCAGATTGACACCAT 1260
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RESULT 61
AF126798 1508 bp mRNA linear ROD 21-JUN-2000
LOCUS Mus musculus delta-6 fatty acid desaturase mRNA, complete cds.
DEFINITION AF126798
ACCESSION AF126798
VERSION AF126798.1 GI:4406525
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1508)
AUTHORS Cho,H.P., Nakamura,M.T. and Clarke,S.D.
TITLE Delta-6 desaturase
JOURNAL J. Biol. Chem. 274 (1), 471-477 (1999)
MEDLINE 99085046
PUBMED 9867867
REFERENCE 2 (bases 1 to 1508)
AUTHORS Cho,H.P., Nakamura,M.T. and Clarke,S.D.
TITLE Direct Submission
JOURNAL Submitted (08-FEB-1999) Nutritional Sciences, University of Texas
at Austin, Painter 5.30 (A2700), Austin, TX 78712, USA
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TLTAVLATSOAQGNLQHDYCHLSVYKYSIWNHVVKFVIGHLKGASANNWNRHP
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VWVQMHLVMEIDLDHYDRWDFSSQLAATCNVEQSFNDWFSGLNFQIEHLLFPPTMP
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Alignment Scores:
Pred. No.: 368 Length: 1508
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-10-029-756-20 (1-6) x AF126798 (1-1508)
Qy 1 PheGlnIleGluHis 6
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Db 1215 TTTCCAGATTGACACCAT 1232
|||||
RESULT 62
BC055950 1539 bp mRNA linear ROD 04-NOV-2003
LOCUS Mus musculus fatty acid desaturase 3, mRNA (cdna clone
DEFINITION BC055950
IMAGE:4208582), partial cds.
ACCESSION BC055950
VERSION BC055950.1 GI:33585850
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1539)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,P.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altechul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Haileh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.P., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Ustin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Huly,S.M.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettner,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whitting,M., Madan,A., Young,A.C., Shvachenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalley,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE 22388257
PUBMED 12477932
REFERENCE 2 (bases 1 to 1539)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK
COMMENT NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAC Plate: 120 Row: k Column: 2
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis.
FEATURES
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/clone="IMAGE:4208582"
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/clone_lib="NCI CGAP_C024"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
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/db_xref="GI:33585851"
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CDS
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FVMQQLGFSFQHQHAKPNIFHKDPDVTVPVFLLGESSVEYGGKKRRYLP
YHQLHFFFLGPPLLLVNFEVENLAYMLVCMQWTDLLWAASFYRFFLSYSPFYGA
TGTLFVAVRVLSESHWFVMTQNNHHPKEIGHEKRDWASSQLAATCNVEPSLFDW
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1. .168
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/gene="Fads3"
/note="Heme 1; Region: Heme/Steroid binding domain. This
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of proteins. This family also includes proteins that bind
to steroids. The family includes progesterone receptors.
Many members of this subfamily are membrane anchored by an
N-terminal transmembrane alpha helix. This family also
includes a domain in some chitin synthases. There is no
known ligand for this domain in the chitin synthases"
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/strains="Sprague Dawley"
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Pred. NO.: 377 Length: 1539
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
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US-10-029-756-20 (1-6) x BC055950 (1-1539)

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Qy 1 PheGlnIleGluHis 6
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Db 1021 TTCAGATTGACACAC 1038
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RESULT 63

AB021980

LOCUS

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DEFINITION Rattus norvegicus mRNA for delta-6 fatty acid desaturase, complete cds.
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ACCESSION

AB021980

VERSION

AB021980.1 GI:4514721

KEYWORDS

delta-6 fatty acid desaturase.

SOURCE

Rattus norvegicus

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

REFERENCE

1 (sites)

Aki, T., Shimada, Y., Inagaki, K., Higashimoto, H., Kawamoto, S.,

Shigeta, S., Ono, K. and Suzuki, O.

Molecular cloning and functional characterization of rat delta-6

fatty acid desaturase

JOURNAL

Biochem. Biophys. Res. Commun. 255 (3), 575-579 (1999)

MEDLINE

99160394

PUBMED

10049752

REFERENCE

2 (bases 1 to 1546)

Aki, T.

Direct Submission

Submitted (31-DEC-1998) Tsunehiro Aki, Hiroshima University,

Department of Molecular Biotechnology; 1-4-1 Kagamiyama,

Higashi-Hiroshima, Hiroshima 739-8527, Japan

(E-mail: aki@ipc.hiroshima-u.ac.jp, Tel:81-824-24-7755,

Fax:81-824-22-7191).

Sequence updated (25-Feb-1999).

COMMENT

FEATURES

source

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Location/Qualifiers

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TVTAFVLAATSAQAGWLDQHLGVYKKSINWNIHVKFVIGHLKGASANNWNRHP
QHKAPNIFHKDPDKSLHVLGEMQPLEYKGLKYLIPYHQLHFFFLGPPLLIP
MYFQYQIIMTIRRDWDLAWAISVYARFYTYPFYGLGALVFLNFIKFLSHWF
VWTQNNHVMIEDLDHYRDFSSQLAATCNVEQSPFNDMFSGHLNFQIEHHLFPTMP
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Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
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US-10-029-756-20 (1-6) x AB021980 (1-1546)

Qy 1 PheGlnIleGluHis 6

|||||

Db 1237 TTCAGATTGACACAC 1254

RESULT 64

AB069727

LOCUS

DEFINITION

Oreochromis niloticus Fadad6 mRNA for putative delta-6 fatty acyl

desaturase, complete cds.

ACCESSION

AB069727

VERSION

AB069727.1 GI:15147882

KEYWORDS

Oreochromis niloticus (Nile tilapia)

ORGANISM

Oreochromis niloticus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;

Labroidae; Cichlidae; Oreochromis.

REFERENCE

1

Sirisunay, S., Yoshizaki, G., Kiron, V., Takeuchi, T., Satoh, S. and

Watanabe, T.

Molecular cloning, Expression, and Activity of the Nile Tilapia

(Oreochromis niloticus) Delta-6 Fatty Acyl Desaturase

JOURNAL

Unpublished

REFERENCE

2 (bases 1 to 1576)

Sirisunay, S., Yoshizaki, G., Kiron, V., Takeuchi, T., Satoh, S. and

Watanabe, T.

Direct Submission

Submitted (09-AUG-2001) Soranuth Sirisunay, Tokyo University of

Fisheries, Aquatic Biosciences, Konan 4-5-7, Minato, Tokyo

108-8477, Japan (E-mail: soranuth@yahoo.com, Tel:81-3-5463-0555,

Fax:81-3-5463-0553)

FEATURES

source

1. .1576

Location/Qualifiers

/organism="Oreochromis niloticus"

/mol_type="mRNA"

/db_xref="taxon:8128"

1. .1576

/gene="Fadad6"

110. .1447

/gene="Fadad6"

/codon_start=1

Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgou,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>
Series: IRAP Plate: 123 Row: i Column: 2
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 9790070.

FEATURES
source
Location/Qualifiers
1..1608
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clones="MGC:68002 IMAGE:5137343"
/tissue type="Liver, normal. 5 month old male mouse."
/clone_lib="NCI CGAP_Li9"
/lab_host="DH10B"
/note="Vector: PCMV-SPORT6"
gene
1..1608
/gene="Fads2"
/db_xref="LocusID:56473"
/db_xref="MGI:1930079"
63..1397
/gene="Fads2"
/codon_start=1
/product="fatty acid desaturase 2"
/protein_id="AAH57189.1"
/db_xref="GI:34785344"
/db_xref="LocusID:56473"
/db_xref="MGI:1930079"
/translation="MGKGNQGESGTERQAPMPTFRWEEIQKHLRTRDMLVIDRKVY
NKTWSRHPGCHRVIGYSGEDATDAFRAFLDLDFVGFKLPLLIGELAPEPSLD
RGKSSQITEDFRALKTAEADNMFLPFTLLSHIIVNESLAWFILSYFGTGMIP
TLTAVFLATSOAQALOHQDHYGLSVYKSIWNHVVHKFVIGHLKASANWNNRHF
OHAAPNIHFHDPDIKSLHVLGEMQPLEYKGLKXLPVYNHOFYEFLLGPPLLIP
MYFQOIMTMSRDWDLNAISYMRFFTYIPFYGILGALVFLNFRFLSHWF
VWVTOMHLVNEIDLHDYRWFSQLAATCNVEQSFNDWFSGLNLFQIEHLLPFTMP
RHNLHKIAPLKYSLCAKHGIEYQEKPLLRALIDIVSSLKXSGELWLDAYLHK"

ORIGIN

Alignment Scores:
Pred. No.: 396 Length: 1608
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-10-029-756-20 (1-6) x BC057189 (1-1608)

Qy 1 PheGlnIleGluHisHis 6
|||||
Db 1203 TTCCAGATTGACACCAC 1220
RESULT 67
AY332747 1619 bp mRNA linear PLN 07-NOV-2003
LOCUS
DEFINITION Pavlova lutheri delta-4 fatty acid desaturase (des1) mRNA, complete
cds
AY332747
VERSION AY332747.1 GI:37683438
KEYWORDS
SOURCE Pavlova lutheri
ORGANISM Pavlova lutheri
Eukaryota; Haptophyceae; Pavlova; Pavlova.
REFERENCE
1 (bases 1 to 1619)
Tonon,T., Harvey,D., Larson,T.R. and Graham,I.A.
AUTHORS
TITLE Identification of a very long chain polyunsaturated fatty acid
delta4-desaturase from the microalga Pavlova lutheri

JOURNAL
MEDLINE
PUBMED
REFERENCE
2 (bases 1 to 1619)
Tonon,T., Harvey,D., Larson,T.R. and Graham,I.A.
AUTHORS
TITLE
JOURNAL
FEATURES
source
Location/Qualifiers
1..1619
/organism="Pavlova lutheri"
/mol_type="mRNA"
/strain="CCAP 931/1"
/db_xref="taxon:2832"
1..1619
/gene="des1"
/note="Pldes1"
60..1397
/gene="des1"
/note="pldes1"
/codon_start=1
/product="delta-4 fatty acid desaturase"
/protein_id="AAQ98793.1"
/db_xref="GI:37683439"
/translation="MPPSAASEGVAAELRAAEVASYTRKAVDERPDLTIVGDVYDAK
AFRDEHPGGAHFVSLFGGRDATEAFMEYTHRRAMPKARMSKFFVUGSLDASEKPTQADSA
YLRICAEVNALLPKSGGFAPPSYMLKAAALVVAASVIEGYMLLRGKTLILLSTVFLGLV
FAMTGINIQHDANHGALSRHSVINYCIQYAADNIGGNMVLQSHVVMHLLHTNDVDA
DPQKAGVLRLEKPTDGMFWHALQQLYIILPGEAMYAFKLLFLDALBELLAWRWEGEKI
SPLARALFAVACKLGFWARFVALPLWLQPTVHTALCICATVCTGSGFYLAFFFIISH
NFDGVSGVGPGLSPRSATFVQRQVETSSNVGGYMLGLVGLNGLNFQIEHLLFPRLLHS
YYAQIADPVVRTHIEKLGFKYRHPFTVGSNLSMLQHMGMKMGTRFGEAKGGKAE"

ORIGIN

Alignment Scores:
Pred. No.: 399 Length: 1619
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0
US-10-029-756-20 (1-6) x AY332747 (1-1619)
Qy 1 PheGlnIleGluHisHis 6
|||||
Db 1194 TTCCAGATCGACCAT 1211
RESULT 68
AY234124
LOCUS
DEFINITION Primula farinosa sphingolipid delta-8 desaturase mRNA, complete
cds.
AY234124
VERSION AY234124.1 GI:30350274
KEYWORDS
SOURCE Primula farinosa
ORGANISM Primula farinosa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; Ericales; Primulaceae; Primula.
REFERENCE
1 (bases 1 to 1681)
Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and
Napier,J.A.
AUTHORS
TITLE Identification of Primula fatty acid Delta(6)-desaturases with n-3
substrate preferences(1)
JOURNAL
MEDLINE
PUBMED
REFERENCE
2 (bases 1 to 1681)
Sayanova,O.V., Beaudoin,F., Michaelson,L.V., Shewry,P.R. and
Napier,J.A.
AUTHORS
TITLE Direct Submission

JOURNAL Submitted (10-FEB-2003) Crop Performance & Improvement, Long Ashton
 Research Station, Long Ashton, Bristol BS41 9AP, UK
 FEATURES
 source 1..1681
 /organism="Primula farinosa"
 /mol_type="rRNA"
 /db_xref="taxon:133892"
 53..1411
 /note="cytochrome b5 fusion desaturase"
 /codon_start=1
 /product="aphingolipid delta-8 desaturase"
 /protein_id="AAP23033.1"
 /db_xref="GI:30350275"
 /translation="WADPPNPPTGYITSSDLKAHKAAGDLWISHHGQYDVSSWAAL
 HPGTAPMALAGHDVDAFLAYHPPSTARLLPPLSANLLLEHYSVSTSDYRKLH
 NFHKLDTFTKSHVTCFTFVAMVLPFLSLGFCSDSTWVHLASGGVGMVAMIOSGW
 LGHDSGHVQIMSSRTNRPFAVLSCNLAGISIAWKNHNAHLACNSLDYDPLDLOH
 MPFFVSSKFNLSLTSRYDRKLNFDGVSRLVSVQHSFPYVCLARINLPAQSPML
 LFSRKVPDRVQEIFGIGVFWWYPLLVSLCPNMGEMFVVASFSVTGIQRVQCLN
 HPSAEVYLGPPGNDWFQKTAGTLNLSCHSMMDFHGGLOFQIEHHLFPLRLPSQLR
 KVSPPVRDLCKHNLPNVTSFTWANVLTLKLRNAATQARDLSNPTPKNLVWEAVNT
 HG"

ORIGIN

Alignment Scores:
 Pred. No.: 416 Length: 1681
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-10-029-756-20 (1-6) x AY234124 (1-1681)

Qy 1 PheGlnIleGluHis 6
 Db 1178 TTTCAGATCGAGCACCAT 1195

RESULT 69
 AR076814
 LOCUS 1684 bp DNA linear PAT 30-AUG-2000
 DEFINITION Sequence 1 from patent US 5959175.
 ACCESSION AR076814
 VERSION AR076814.1 GI:10003560
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1684)
 AUTHORS Thomas, T.L., Nunberg, A.N. and Beremand, P.D.
 TITLE Sunflower albumin 5', regulatory region for the modification of
 plant seed lipid composition
 JOURNAL Patent: US 5959175-A 1 28-SEP-1999;
 FEATURES Location/Qualifiers
 source 1..1684
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
 Pred. No.: 417 Length: 1684
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AR076814 (1-1684)

Qy 1 PheGlnIleGluHis 6
 Db 1156 TTCCAAATTGAGCATCAT 1173

RESULT 70
 AR084177
 LOCUS 1684 bp DNA linear PAT 01-SEP-2000
 DEFINITION Sequence 1 from patent US 5977436.
 ACCESSION AR084177
 VERSION AR084177.1 GI:10010948
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1684)
 AUTHORS Thomas, T.L. and Li, Z.
 TITLE Oleosin 5' regulatory region for the modification of plant seed
 lipid composition
 JOURNAL Patent: US 5977436-A 1 02-NOV-1999;
 FEATURES Location/Qualifiers
 source 1..1684
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
 Pred. No.: 417 Length: 1684
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AR084177 (1-1684)

Qy 1 PheGlnIleGluHis 6
 Db 1156 TTCCAAATTGAGCATCAT 1173

RESULT 71
 BD062571
 LOCUS 1684 bp DNA linear PAT 27-AUG-2002
 DEFINITION A sunflower albumin 5' regulatory region for the modification of
 plant seed lipid composition.
 ACCESSION BD062571
 VERSION BD062571.1 GI:22608174
 KEYWORDS JP 2001518795-A/1.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1684)
 AUTHORS Thomas, T.L., Beremand, P.D. and Nunberg, A.N.
 TITLE A sunflower albumin 5' regulatory region for the modification of
 plant seed lipid composition
 JOURNAL Patent: JP 2001518795-A 1 16-OCT-2001;
 COMMENT RHONE POULENC AGRO
 PN JP 2001518795-A/1
 PD 16-OCT-2001
 PF 09-APR-1998 JP 1998543140
 PR 09-APR-1997 US 08/831570
 PI TERRY L THOMAS, PHILLIP D BEREMAND, ANDREW N NUNBERG PC
 C12N15/82, C12N15/29, C12N15/53, A01H5/00, A01H5/10 CC Strandedness:
 Double;

CC Topology: Linear;
 FH Key Location/Qualifiers
 FT CDS 43..1387.

FEATURES
 source 1..1684
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

ORIGIN

Alignment Scores:
 Pred. No.: 417 Length: 1684
 Score: 36.00 Matches: 6

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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x BD062571 (1-1684)

Qy 1 PheGlnIleGluHisHis 6
|||||
Db 1156 TTCCAAATTGAGCATCAT 1173

RESULT 72
LOCUS BD070919 1684 bp DNA linear PAT 27-AUG-2002
DEFINITION An oleosin 5'regulatory region for the modification of plant seed
lipid composition.
ACCESSION BD070919
VERSION BD070919.1 GI:22616522
KEYWORDS JP 2001519668-A/1.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 1684)
AUTHORS Thomas,T.L. and Li,Z.
TITLE An oleosin 5'regulatory region for the modification of plant seed
lipid composition
JOURNAL Patent: JP 2001519668-A 1 23-OCT-2001;
COMMENT RHONE POULENC AGRO
OS Unidentified
PN JP 2001519668-A/1
PD 23-OCT-2001
PF 09-APR-1998 JP 1998543141
PR 09-APR-1997 US 08/831575
PI TERRY L THOMAS, ZHONGSEN LI
PC C12N15/82,C12N15/29,C12N15/53,A01H5/00,A01H5/10 CC
Strandedness: Double;
CC Topology: Linear;
CC An oleosin 5'regulatory region for the modification of plant
seed lipid
CC composition
FH Key 43..1387.
FT CDS Location/Qualifiers
source 1..1684
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Alignment Scores: 417 Length: 1684
Pred. No.: 36.00 Matches: 6
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

US-10-029-756-20 (1-6) x BD070919 (1-1684)

Qy 1 PheGlnIleGluHisHis 6
|||||
Db 1156 TTCCAAATTGAGCATCAT 1173

RESULT 73
LOCUS AR020904 1685 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 4 from patent US 5789220.
ACCESSION AR020904
VERSION AR020904.1 GI:3975519
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
unclassified.
REFERENCE 1 (bases 1 to 1685)
AUTHORS Thomas,T.L.
TITLE Production of gamma linolenic acid by a .DELTA.6-desaturase
```

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REFERENCE 1 (bases 1 to 1685)
AUTHORS Thomas,T.L., Reddy,A.S., Nuccio,M., Nunberg,A.N. and
Freyssinet,G.L.
TITLE Production of .gamma.-linolenic acid by a .DELTA.6-desaturase
JOURNAL Patent: US 5789220-A 4 04-AUG-1998;
FEATURES Location/Qualifiers
source 1..1685
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores: 417 Length: 1685
Pred. No.: 36.00 Matches: 6
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

US-10-029-756-20 (1-6) x I38430 (1-1685)

Qy 1 PheGlnIleGluHisHis 6
|||||
Db 1157 TTCCAAATTGAGCATCAT 1174

RESULT 74
LOCUS I38430 1685 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 4 from patent US 5614393.
ACCESSION I38430
VERSION I38430.1 GI:2084484
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
unclassified.
REFERENCE 1 (bases 1 to 1685)
AUTHORS Thomas,T.L., Reddy,A.S., Nuccio,M., Nunberg,A.N. and
Freyssinet,G.L.
TITLE Production of .gamma.-linolenic acid by a .DELTA.6-desaturase
JOURNAL Patent: US 5614393-A 4 25-MAR-1997;
FEATURES Location/Qualifiers
source 1..1685
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores: 417 Length: 1685
Pred. No.: 36.00 Matches: 6
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

US-10-029-756-20 (1-6) x I38430 (1-1685)

Qy 1 PheGlnIleGluHisHis 6
|||||
Db 1157 TTCCAAATTGAGCATCAT 1174

RESULT 75
LOCUS AR200408 1685 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 4 from patent US 6355861.
ACCESSION AR200408
VERSION AR200408.1 GI:20250482
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
unclassified.
REFERENCE 1 (bases 1 to 1685)
AUTHORS Thomas,T.L.
TITLE Production of gamma linolenic acid by a .DELTA.6-desaturase
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JOURNAL Patent: US 635861-A 4 12-MAR-2002;
 FEATURES Location/Qualifiers
 source 1..1685
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN

Alignment Scores:
 Pred. No.: 417 Length: 1685
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AR200408 (1-1685)

Qy 1 PheGlnIleGluHis 6
 Db 1157 TTCCAAATTGAGCATCAT 1174

RESULT 76

LOCUS AR455421 1685 bp DNA linear PAT 20-FEB-2004
 DEFINITION Sequence 4 from patent US 6683232.
 ACCESSION AR455421
 VERSION AR455421.1 GI:42689973
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE

1 (bases 1 to 1685)
 AUTHORS Thomas,T.L.
 TITLE Production of .gamma. linolenic acid by a .DELTA.6-desaturase
 JOURNAL Patent: US 6683232-A 4 27-JAN-2004;
 FEATURES Location/Qualifiers
 source 1..1685
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Alignment Scores:
 Pred. No.: 417 Length: 1685
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AR455421 (1-1685)

Qy 1 PheGlnIleGluHis 6
 Db 1157 TTCCAAATTGAGCATCAT 1174

RESULT 77

LOCUS AF007561 1685 bp mRNA linear PLN 05-JAN-1999
 DEFINITION Borago officinalis delta 6-desaturase mRNA, complete cds.
 ACCESSION AF007561
 VERSION AF007561.1 GI:4102020
 KEYWORDS
 SOURCE Borago officinalis
 ORGANISM Borago officinalis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Boraginaceae; Borago.

REFERENCE

1 (bases 1 to 1685)
 AUTHORS Nunberg,A.N., Beremand,P.D. and Thomas,T.L.
 TITLE Engineering of Plant Seed Oils to Produce Gamma Linolenic Acid
 JOURNAL (GLA)
 REFERENCE Unpublished
 2 (bases 1 to 1685)

AUTHORS Nunberg,A.N., Beremand,P.D. and Thomas,T.L.
 TITLE Direct Submission
 JOURNAL Submitted (09-JUN-1997) Biology, Texas A&M University, College
 Station, TX 77843, USA

FEATURES Location/Qualifiers
 source 1..1685
 /organism="Borago officinalis"
 /mol_type="mRNA"
 /db_xref="taxon:13363"
 /tissue_type="seed"
 /dev_stage="12 day post pollination"
 /note="membrane bound polysomal RNA"

CDS

44..1390
 /function="fatty acid desaturase"
 /function="produces gamma,linolenic acid from linoleic acid"
 /functions="produces octadecatetraenoic acid from alpha linolenic acid"
 /codon_start=1
 /product="delta 6-desaturase"
 /protein_id="AAD01410.1"
 /db_xref="GI:4102021"

/translation="MAAQIKKITYSDLNKHKDGLWISIQGKAYDVSDVVKDHPGG
 SPPLKSLAGQEVTDFAVAFHPASTKNLKDPEFTGYLKDYSVSVSKDYRKLVEFSK
 MGLYDKKHIMFATLCFIAMLPAMSVYGVLFCEGVLVHLSGCLMGFLMIQSGIHGD
 AGHYMVVSDSLNKFMGIFAANCLSGISIGWKNHNAHHIACNSLEYDPLQIIPFL
 VVSKFSGSLTSHFYEKRLTDSLSRFVSYQHWTFYIMCAARLNMYVQSLIMLLTK
 RNYSYRAQELIGCLVFIWYPLLVSLCPNMGERIMFVIASLVTGMOQVQFSLNHFSS
 SVYVGKPGNNWPEKQTDGLDIDSCPPMDWFGHGLQFOIEHILFPKQPCRLKISP
 YVIELCKKHNLPYNASFSKANENTLTLRLTALQARDITKPLPKNLWEALHTHG"

ORIGIN

Alignment Scores:
 Pred. No.: 417 Length: 1685
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-10-029-756-20 (1-6) x AF007561 (1-1685)

Qy 1 PheGlnIleGluHis 6
 Db 1157 TTCCAAATTGAGCATCAT 1174

RESULT 78

LOCUS AR221958 1686 bp DNA linear PAT 26-SEP-2002
 DEFINITION Sequence 6 from patent US 6428990.
 ACCESSION AR221958
 VERSION AR221958.1 GI:23329261
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE

1 (bases 1 to 1686)
 AUTHORS Mukerji,P., Leonard,A.E.Y., Huang,Y.-S. and Parker-Barnes,J.M.
 TITLE Human desaturase gene and uses thereof
 JOURNAL Patent: US 6428990-A 6 06-AUG-2002;
 FEATURES Location/Qualifiers
 source 1..1686
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN

Alignment Scores:
 Pred. No.: 418 Length: 1686
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

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US-10-029-756-20 (1-6) x AR221958 (1-1686)

Qy 1 PheGlnIleGluHisHis 6
Db 534 TTCAGATTGAGCACCAC 551

RESULT 79
BD082638 1686 bp DNA linear PAT 27-AUG-2002
LOCUS Methods and compositions for synthesis of long chain
DEFINITION poly-unsaturated fatty acids.
ACCESSION BD082638
VERSION BD082638.1 GI:22628248
KEYWORDS JP 2001523091-A/18.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1686)
AUTHORS Knutzon,D., Mukerji,P., Huang,Y.S., Thurmond,J., Chaudhary,S. and Leonard,A.E.Y.
TITLE Methods and compositions for synthesis of long chain
JOURNAL poly-unsaturated fatty acids
COMMENT Patent: JP 2001523091-A 18 20-NOV-2001;
CALGENE LLC,ABBOTT LABORATORIES
PN JP 2001523091-A/18
PD 20-NOV-2001
PF 10-APR-1998 JP 1998544053
PR 11-APR-1997 US 08/834655
PI DEBORAH KNUTZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI
THURMOND.
PI SUNITA CHAUDHARY, AMANDA EUN YEONG LOENARD
PC C12N15/53, C12N15/81, C12N9/02, C12N5/10, C12N1/19, C12P7/64 PC
,C11B1/00, A61K31/20,
PC A23K1/30
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
FEATURES
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/db_xref="taxon:32644"
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Alignment Scores: 418 Length: 1686
Pred. No.: 36.00 Matches: 6
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6
US-10-029-756-20 (1-6) x BD082638 (1-1686)

Qy 1 PheGlnIleGluHisHis 6
Db 534 TTCAGATTGAGCACCAC 551

RESULT 80
BD082653 1686 bp DNA linear PAT 27-AUG-2002
LOCUS Methods and compositions for synthesis of long chain
DEFINITION polyunsaturated fatty acids.
ACCESSION BD082653
VERSION BD082653.1 GI:22628263
KEYWORDS JP 2001523092-A/13.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1686)
AUTHORS Knutzon,D., Mukerji,P., Huang,Y.S., Thurmond,J., Chaudhary,S. and Leonard,A.E.Y.

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TITLE Methods and compositions for synthesis of long chain
JOURNAL polyunsaturated fatty acids
Patent: JP 2001523092-A 13 20-NOV-2001;
CALGENE LLC,ABBOTT LABORATORIES
PN JP 2001523092-A/13
PD 20-NOV-2001
PF 10-APR-1998 JP 1998544176
PR 11-APR-1997 US 08/833610
PI DEBORAH KNUTZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI
THURMOND.
PI SUNITA CHAUDHARY, AMANDA EUN YEONG LEONARD
PC C12N15/53, C12N15/83, C12N5/10, C12P7/64, C11B1/00, A61K31/20, A23L1/ PC
30, A23K1/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
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source
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Alignment Scores: 418 Length: 1686
Pred. No.: 36.00 Matches: 6
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6
US-10-029-756-20 (1-6) x BD082653 (1-1686)

Qy 1 PheGlnIleGluHisHis 6
Db 534 TTCAGATTGAGCACCAC 551

RESULT 81
BD092932 1686 bp DNA linear PAT 27-AUG-2002
LOCUS Methods and compositions for synthesis of long chain
DEFINITION polyunsaturated fatty acids in plants.
ACCESSION BD092932
VERSION BD092932.1 GI:22638543
KEYWORDS JP 2001527395-A/19.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 1686)
AUTHORS Knutzon,D., Mukerji,P., Huang,Y.S., Thurmond,J., Chaudhary,S. and Leonard,A.E.Y.
TITLE Methods and compositions for synthesis of long chain
JOURNAL polyunsaturated fatty acids in plants
Patent: JP 2001527395-A 19 25-DEC-2001;
CALGENE LLC,ABBOTT LABORATORIES
PN JP 2001527395-A/19
PD 25-DEC-2001
PF 10-APR-1998 JP 1998544175
PR 11-APR-1997 US 08/833610, 11-APR-1997 US 08/834033 PR
11-APR-1997 US 08/834655, 24-OCT-1997 US 08/956985 PI
DEBORAH KNUTZON, PRADIP MUKERJI, YUNG SHENG HUANG, JENNIFER PI
THURMOND.
PI SUNITA CHAUDHARY, AMANDA EUN YEONG LEONARD
PC C12N15/53, C12N15/82, C12N5/10, C12P7/64, C11B1/00, A61K31/20, A23L1/ PC
30, A23K1/00
CC Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
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1..1686
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/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN

Alignment Scores:
Pred. No.: 418 Length: 1686
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x BD092932 (1-1686)

Qy 1 PheGlnIleGluHis 6
|||||
Db 534 TTCCAGATTGACACCAC 551

RESULT 82

AX951561
LOCUS AX951561 1687 bp DNA linear PAT 08-JAN-2004
DEFINITION Sequence 1 from Patent WO03093482.

ACCESSION AX951561

VERSION AX951561.1 GI:40781919

KEYWORDS

SOURCE

ORGANISM

Borago officinalis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Boraginaceae; Borago.

REFERENCE

1 Cirpus, P., Renz, A., Lerchl, J. and Kuijpers, A.M.

AUTHORS Method for producing multiple unsaturated fatty acids in plants

TITLE Patent: WO 03093482-A 1 13-NOV-2003;

JOURNAL BASF Plant Science GmbH (DE)

FEATURES

source

1..1687

/organism="Borago officinalis"

/mol_type="unassigned DNA"

/db_xref="taxon:13363"

42..1388

/note="unnamed protein product; Delta-6-Desaturase"

/codon_start=1

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/db_xref="GI:40781920"

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SPPLKSLAGQVTDFAVFAHPASTWKNLDKFTGYLYKDYSEVSKDYKLVPEFSK

MGLDYKKGHIMPATLCFTAMLPAMSVYGLFCEGVLVHFGCLMGFLWIOSGWIGHD

AGHYNVVSDSLNKFMPGIFAANCLSGISIGMKNHNAHIAACNSLEYDPLQYIPFL

VSSKFFGSLTSHFYEKRLTFDSLRSFFVSYOHWTFYFIMCAARLNMYVQSLIMLLTK

RNVSYRAHELGLCVFSITWYPLLVSLCPNMGIRIMFVIAISLVTCMQQVQFSLNHFSS

SVYVCKPKGNWFEKQTDGTLDISCPNMDWPHGGLQFQIEHHLFPKMPRCNLKRISSP

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ORIGIN

Alignment Scores:
Pred. No.: 418 Length: 1687
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AX951561 (1-1687)

Qy 1 PheGlnIleGluHis 6
|||||
Db 1155 TTCCAAATTGACCATCAT 1172

RESULT 83

BOU79010

LOCUS BOU79010 1687 bp mRNA linear 'PLN 02-MAY-1997

DEFINITION Borago officinalis delta 6 desaturase mRNA, complete cds.

ACCESSION U79010
VERSION U79010.1 GI:2062402

SOURCE

ORGANISM

Borago officinalis

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Boraginaceae; Borago.

1 (bases 1 to 1687)

AUTHORS Sayanova, O., Smith, M.A., Lapinskas, P., Stobart, A.K., Dobson, G.,
Christie, W.W., Shewry, P.R. and Napier, J.A.

TITLE Expression of a borago desaturase cDNA containing an N-terminal
cytochrome b5 domain results in the accumulation of high levels of
delta6-desaturated fatty acids in transgenic tobacco

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 94 (8), 4211-4216 (1997)

MEDLINE 97268723

PUBMED 9108131

REFERENCE 2 (bases 1 to 1687)

AUTHORS Sayanova, O., Smith, M.A., Shewry, P.R. and Napier, J.A.

TITLE Direct Submission

JOURNAL Submitted (20-NOV-1996) Cell Biology, IACR-Long Ashton Research

Station, Long Ashton, Bristol BS18 9AF, UK

FEATURES

source

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/organism="Borago officinalis"

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/db_xref="taxon:13363"

42..1388

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AGHYNVVSDSLNKFMPGIFAANCLSGISIGMKNHNAHIAACNSLEYDPLQYIPFL

VSSKFFGSLTSHFYEKRLTFDSLRSFFVSYOHWTFYFIMCAARLNMYVQSLIMLLTK

RNVSYRAHELGLCVFSITWYPLLVSLCPNMGIRIMFVIAISLVTCMQQVQFSLNHFSS

SVYVCKPKGNWFEKQTDGTLDISCPNMDWPHGGLQFQIEHHLFPKMPRCNLKRISSP

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ORIGIN

Alignment Scores:
Pred. No.: 418 Length: 1687
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-029-756-20 (1-6) x BOU79010 (1-1687)

Qy 1 PheGlnIleGluHis 6
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Db 1155 TTCCAAATTGACCATCAT 1172

RESULT 84

AB070444

LOCUS AB070444

DEFINITION

Oncorhynchus masou FD6D mRNA for putative delata 6-desaturase,

complete cds.

ACCESSION AB070444

VERSION AB070444.1 GI:15281353

KEYWORDS

SOURCE

ORGANISM

Oncorhynchus masou (cherry salmon)

Eukaryota; Metazoa;

Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei;

Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

REFERENCE 1

AUTHORS Yoshizaki, G., Ishikawa, A., Takeuchi, T. and Gen, K.

TITLE delta6-desaturase-like cDNA in masou salmon

Unpublished
2 (bases 1 to 1692)
Yoshizaki, G., Ishikawa, A., Takeuchi, T. and Gen, K.
Direct Submission
Submitted (21-AUG-2001) Goro Yoshizaki, Tokyo University of
Fisheries; 4-5-7 Kounan, Minato-ku 108-8477, Japan
(E-mail: goro@okyo-u-fish.ac.jp, Tel: 81-3-5463-0558,
Fax: 81-3-5463-0558)

FEATURES
source
Location/Qualifiers
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174..1538
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ELAPESQDQKNAVLQVDFQAQALDRVSEGLRARPFLFSLYLGHLLLEALALGL
LWVGTSLTLICSLALTSQAQAGLQHDYGLSLVCKKSGWNHKLKHFVIGLKA
SANWNRHFQHHAKPNVSKDPDINSIHVFLGDKOPVEYGIKKLYMPVYHCHOYE
FLVGGPLIVPFFNIQIPRTMFSQDWDVLAWMTFYLRFCCTYPFFGFGSVALLS
FVRLESHFWFVNTOMSHLPMEMDHERHQDLTWLSATCNIEQSTDNWFSGLHNFQ
IEHLFTPMRPHNTHLVAPLVRALCEKHGVEYQVKTQKGMTDVVRSKSGDLWDA
YLHK"

ORIGIN
Alignment Scores:
Pred. No.: 419 Length: 1692
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-029-756-20 (1-6) x AB070444 (1-1692)
Qy 1 PheGlnIleGluHis 6
Db 1344 TTTCAGATTGAACCAT 1361

RESULT 85
BD228694 1700 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION
Delta 6 fatty acid desaturase.
ACCESSION
BD228694.1 GI:33038464
VERSION
JP 2002527051-A/2.
KEYWORDS
Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Petrukhin, K. and Caskey, T.C.
Delta 6 fatty acid desaturase
Patent: JP 2002527051-A 2 27-AUG-2002;
MERCK AND CO INC
OS Homo sapiens (human)
PN JP 2002527051-A/2
PD 27-AUG-2002
PF 05-OCT-1999 JP 2000575530
PR 09-OCT-1998 US 60/103760
PI KONSTANTIN PETRUKHIN, THOMAS C CASKEY
PC C12N15/09, A61P3/10, A61P9/10, A61P17/00, A61P27/02, A61P29/00, PC
A61P31/12,
PC C07K16/40, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/88, C12Q1/
PC 02, C12Q1/68,
PC G01N33/15, G01N33/50//A61K38/55, A61K39/395, A61K39/395, A61K39/

Unpublished
2 (bases 1 to 1692)
Yoshizaki, G., Ishikawa, A., Takeuchi, T. and Gen, K.
Direct Submission
Submitted (21-AUG-2001) Goro Yoshizaki, Tokyo University of
Fisheries; 4-5-7 Kounan, Minato-ku 108-8477, Japan
(E-mail: goro@okyo-u-fish.ac.jp, Tel: 81-3-5463-0558,
Fax: 81-3-5463-0558)

FEATURES
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Location/Qualifiers
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174..1538
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/protein_id="BAB63440.1"
/db_xref="GI:15281354"
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QMLVIDRKYNTITAKVPGGIRVISHFAGEDATEAFVAFHLEPNFVRKPLKLLIG
ELAPESQDQKNAVLQVDFQAQALDRVSEGLRARPFLFSLYLGHLLLEALALGL
LWVGTSLTLICSLALTSQAQAGLQHDYGLSLVCKKSGWNHKLKHFVIGLKA
SANWNRHFQHHAKPNVSKDPDINSIHVFLGDKOPVEYGIKKLYMPVYHCHOYE
FLVGGPLIVPFFNIQIPRTMFSQDWDVLAWMTFYLRFCCTYPFFGFGSVALLS
FVRLESHFWFVNTOMSHLPMEMDHERHQDLTWLSATCNIEQSTDNWFSGLHNFQ
IEHLFTPMRPHNTHLVAPLVRALCEKHGVEYQVKTQKGMTDVVRSKSGDLWDA
YLHK"

ORIGIN
Alignment Scores:
Pred. No.: 419 Length: 1692
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-029-756-20 (1-6) x AB070444 (1-1692)
Qy 1 PheGlnIleGluHis 6
Db 1344 TTTCAGATTGAACCAT 1361

RESULT 85
BD228694 1700 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION
Delta 6 fatty acid desaturase.
ACCESSION
BD228694.1 GI:33038464
VERSION
JP 2002527051-A/2.
KEYWORDS
Homo sapiens (human)
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Petrukhin, K. and Caskey, T.C.
Delta 6 fatty acid desaturase
Patent: JP 2002527051-A 2 27-AUG-2002;
MERCK AND CO INC
OS Homo sapiens (human)
PN JP 2002527051-A/2
PD 27-AUG-2002
PF 05-OCT-1999 JP 2000575530
PR 09-OCT-1998 US 60/103760
PI KONSTANTIN PETRUKHIN, THOMAS C CASKEY
PC C12N15/09, A61P3/10, A61P9/10, A61P17/00, A61P27/02, A61P29/00, PC
A61P31/12,
PC C07K16/40, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/88, C12Q1/
PC 02, C12Q1/68,
PC G01N33/15, G01N33/50//A61K38/55, A61K39/395, A61K39/395, A61K39/

PC 395, A61K45/00,
PC A61K48/00 G01N33/68, C12N15/00, C12N5/00, A61K37/64 CC Delta 6
fatty acid desaturase
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FT Location/Qualifiers
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ORIGIN
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Pred. No.: 422 Length: 1700
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x BD228694 (1-1700)
Qy 1 PheGlnIleGluHis 6
Db 1214 TTCCAGATCGAGCACCAC 1231

RESULT 86
AF134404 1705 bp mRNA linear PRI 19-MAY-1999
LOCUS
DEFINITION
Homo sapiens delta-6 fatty acid desaturase (CYB5RP) mRNA, complete
cde.
ACCESSION
AF134404 GI:4868365
VERSION
AF134404.1
KEYWORDS
Homo sapiens (human)
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li, W., Metzker, M.L., Caskey, C.T. and Petruchin, K.
Human retineta-specific delta 6 fatty acid desaturase
1 (bases 1 to 1705)
REFERENCE
AUTHORS
Li, W., Metzker, M.L., Caskey, C.T. and Petruchin, K.
JOURNAL
Unpublished
2 (bases 1 to 1705)
REFERENCE
AUTHORS
Li, W., Metzker, M.L., Caskey, C.T. and Petruchin, K.
JOURNAL
Direct Submission
Submitted (11-MAR-1999) Human Genetics, Merck Research
Laboratories, P.O. Box 4, West Point, PA 19486, USA
Location/Qualifiers
1..1705
/organism="Homo sapiens"
/mol_type="mRNA"
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ORIGIN

Alignment Scores:
 Pred. No.: 423 Length: 1705
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 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-10-029-756-20 (1-6) x AF134404 (1-1705)

Qy 1 PheGlnIleGluHis 6
 |||||
 Db 1214 TTCAGATCGAGCACCAC 1231

RESULT 87
 BC081776 1706 bp mRNA linear ROD 15-SEP-2004
 LOCUS
 DEFINITION Rattus norvegicus fatty acid desaturase 2, mRNA (CDNA clone)

ACCESSION MGC:93365 IMAGE:7128630, complete cds.
 VERSION BC081776.1 GI:51858587
 KEYWORDS MGC.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 1706)
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worrley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Sanchez, A., Whitting, M., Madan, A., Young, A.C., Rodriguez, S.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallos, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932

TITLE 2 (bases 1 to 1706)
 JOURNAL Director MGC Project.
 PUBMED Direct Submission
 REFERENCE Submitted (01-SEP-2004) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

TITLE NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 JOURNAL Contact: MGC help desk
 PUBMED Email: cgabs-remail.nih.gov
 REFERENCE Tissue Procurement: Howard Jacobs
 AUTHORS cDNA Library Preparation: Express Genomics
 TITLE cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 JOURNAL DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-sngc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

REMARK
 COMMENT Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAC Plate: 184 Row: d Column: 18
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 13786181.

FEATURES
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 Location/Qualifiers
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 /mol_type="mRNA"
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 /clone_lib="NIH MGC_236"
 /lab_host="DH10B"
 /note="vector: pExpress1"
 1..1706
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 /db_xref="RGD:68339"
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 /protein_id="AAH81776.1"
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 TVTAFVLATSOAQAQGLQHDYHLSYKKSINWHIVHKFVIGHLKGSANWNRHF
 QHAKNIFRHPDPIKSLHVLGEGWQPLEYKGGKKLYLPYNNHQHXYFLIGPPLLIIP
 MYFQYQITMTRRRDWDLAWAISYARFYTPFYFYLGLALVFLNFIPLFLESHWF
 VWTQNMHIVEIDLHRYDFWSSQLAATCNVEQSFNDFSGHLNFQIEHFLFPTMP
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ORIGIN
 Alignment Scores:
 Pred. No.: 423 Length: 1706
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-10-029-756-20 (1-6) x BC081776 (1-1706)

Qy 1 PheGlnIleGluHis 6
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 Db 1307 TTCAGATCGAGCACCAC 1324

RESULT 88
 BC049438 1708 bp mRNA linear VRT 30-JUN-2004
 LOCUS
 DEFINITION Danio rerio fatty acid desaturase 2, mRNA (CDNA clone MGC:56438
 IMAGE:5612204), complete cds.
 ACCESSION BC049438
 VERSION BC049438.1 GI:29436932
 KEYWORDS MGC.
 SOURCE Danio rerio (zebrafish)
 ORGANISM Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 1708)

REFERENCE
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, R.D., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worrley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Sanchez, A., Whitting, M., Madan, A., Young, A.C., Rodriguez, S.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallos, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932

TITLE 2 (bases 1 to 1706)
 JOURNAL Director MGC Project.
 PUBMED Direct Submission
 REFERENCE Submitted (01-SEP-2004) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

TITLE NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 JOURNAL Contact: MGC help desk
 PUBMED Email: cgabs-remail.nih.gov
 REFERENCE Tissue Procurement: Howard Jacobs
 AUTHORS cDNA Library Preparation: Express Genomics
 TITLE cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 JOURNAL DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-sngc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

REMARK
 COMMENT Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettner, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16999-16903 (2002)

12477932

2 (bases 1 to 1708)

Strausberg, R.

Direct Submission

Submitted (31-MAR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapsb-re@mail.nih.gov

Tissue Procurement: Dr. Sumio Sugano

cDNA Library Preparation: Dr. Sumio Sugano

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca

Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prabhu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAC Plate: 104 Row: e Column: 4

This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, similarity but not identity to protein.

Location/Qualifiers

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/db_xref="taxon:7955"

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/tissue_type="Whole body, adult male"

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/note="Vector: pME18S-FL3"

1..1708

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/note="synonyms: DRD5/D6, fb64c04, wu:fb64c04, Fadsd6, fb69e08, wu:fb69e08"

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95..1429

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ORIGIN

RHNYWRAAPRVRSLSCEKYGKYGKTYGAPADIIRSLSEKSGELMWLDAYLNK"

Alignment Scores:

Pred. No.: 424 Length: 1708

Score: 36.00 Matches: 6

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 5 Gaps: 0

US-10-029-756-20 (1-6) x BC049438 (1-1708)

Qy 1 PheGlnIleGluHisHis 6

Db 1235 TTCCAGATCGAGCATCAT 1252

RESULT 89

LOCUS AR264713 1717 bp DNA linear PAT 10-APR-2003

DEFINITION Sequence 2 from patent US 6492108.

ACCESSION AR264713

VERSION AR264713.1 GI:29693075

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1717)

AUTHORS Hallman, J.L., Guegler, K.J., Corley, N.C. and Shah, P.

TITLE Delta-6 desaturase homologs

JOURNAL Patent: US 6492108-A 2 10-DEC-2002;

FEATURES

Location/Qualifiers

1..1717

source /organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Alignment Scores:

Pred. No.: 426 Length: 1717

Score: 36.00 Matches: 6

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x AR264713 (1-1717)

Qy 1 PheGlnIleGluHisHis 6

Db 1218 TTCCAGATCGAGCACAC 1235

RESULT 90

LOCUS AY055749 1745 bp mRNA linear VRT 31-JUL-2003

DEFINITION Sparus aurata putative delta 6-desaturase (FD6D) mRNA, complete cds.

ACCESSION AY055749

VERSION AY055749.1 GI:23428437

KEYWORDS

SOURCE Sparus aurata (gilthead seabream)

ORGANISM Sparus aurata

REFERENCE 1 (bases 1 to 1745)

AUTHORS Seiliez, I., Panserat, S., Corraze, G., Kaushik, S. and Bergot, P.

TITLE Cloning and nutritional regulation of a Delta6-desaturase-like enzyme in the marine teleost gilthead seabream (Sparus aurata) (2003)

JOURNAL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 135 (3), 449-460

MEDLINE 22715572

PUBMED 12831765

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REFERENCE 2 (bases 1 to 1745)
AUTHORS Sellier,I., Panserat,S., Kaushik,S. and Bergot,P.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-2001) Fish Nutrition Laboratory, INRA,
St-Pee-sur-Nivelle 64310, France
FEATURES
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ORIGIN
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Pred. No.: 434 Length: 1745
Score: 36.00 Matches: 6
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0
US-10-029-756-20 (1-6) x AY055749 (1-1745)
Qy 1 PheGlnIleGluHis 6
Db 1299 TTTCAGATCGAGCACCAC 1316
RESULT 91
AX035942
LOCUS AX035942 1757 bp linear PAT 15-NOV-2000
DEFINITION Sequence 3 from Patent EP1035207.
ACCESSION AX035942
VERSION AX035942.1 GI:11191484
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1
AUTHORS Marquardt,A. and Weber,B.H.
TITLE Cdna molecules of the members of gene family encoding human fatty
acid desaturases and their use in diagnosis and therapy
JOURNAL Patent: EP 1035207-A 3 13-SEP-2000;
MULTIGENE BIOTECH GMBH (DE)
FEATURES
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US-10-029-756-20 (1-6) x AX035942 (1-1757)
Qy 1 PheGlnIleGluHis 6
Db 1277 TTCCAGATCGAGCACCAC 1294
RESULT 92
AF084560
LOCUS AF084560 1757 bp mRNA linear PRI 12-OCT-2000
DEFINITION Homo sapiens fatty acid desaturase 3 (FADS3) mRNA, complete cds.
ACCESSION AF084560
VERSION AF084560.1 GI:10798852
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1757)
AUTHORS Marquardt,A., Soehr,H., White,K. and Weber,B.H.
TITLE cdna cloning, genomic structure, and chromosomal localization of
three members of the human fatty acid desaturase family
JOURNAL Genomics 66 (2), 175-183 (2000)
MEDLINE 20318619
PubMed 10860662
REFERENCE 2 (bases 1 to 1757)
AUTHORS Marquardt,A., Soehr,H., Passmore,L.A., Kraemer,F., Rivera,A. and
Weber,B.H.F.
TITLE Direct Submission
JOURNAL Submitted (05-AUG-1998) Institute of Human Genetics, University of
Wuerzburg, Biozentrum, Am Hubland, Wuerzburg D-97074, Germany
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Pred. No.: 438 Length: 1757
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DB: 9 Gaps: 0
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US-10-029-756-20 (1-6) x AF084560 (1-1757)

Qy 1 PheGlnIleGluHisHis 6
 Db 1277 TTCCAGATCGAGCACCAC 1294

RESULT 93

BC063726

LOCUS

DEFINITION

Xenopus laevis hypothetical protein MGC68735, mRNA (cDNA clone

MGC:68735 IMAGE:4058230), complete cds.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Xenopus laevis

(African clawed frog)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;

Xenopodinae; Xenopus; Xenopus.

1 (bases 1 to 1781)

Klein,S.L., Strausberg,R.L., Wagner,L., Pontius,J., Clifton,S.W.

and Richardson,P.

Genetic and genomic tools for Xenopus research: The NIH Xenopus

initiative

Dev. Dyn. 225 (4), 384-391 (2002)

12454917

2 (bases 1 to 1781)

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,

Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,

Leachman,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Heieh,F.,

Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,

Shapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,

Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,

Carninci,P., Prange,C., Raha,S., Bosak,S.A., McEwan,P.J.,

Abramson,R.D., Mullahy,S.J., Bosak,S.A., Loquellano,N.A., Peters,G.J.,

McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,

Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,

Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,

Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S.,

Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,

Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,

Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,

Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smallos,D.E.,

Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

3 (bases 1 to 1781)

Klein,S. and Strausberg,R.

Direct Submission

Submitted (08-DEC-2003) National Institutes of Health, Xenopus Gene

Collection (XGC), National Institute of Child Health and Human

Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD

20892-7510, USA

NIH-MGC Project

Contact: XGC help desk

Email: cgapbs@mail.nih.gov

Tissue Procurement: Dr. Igor Dawid

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC),

Gaithersburg, Maryland;

Web site: http://www.nisc.nih.gov/

Contact: nisc_mgc@nih.gov

Ahter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,

Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,

Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,

Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,

Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,

McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
 Taurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
 Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 128 Row: m Column: 2.

FEATURES

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IPTITLLTISQAQWLQHFGLHSVFKSKWNRVFKFIICHLKGSANWNHRR

HFQHAKNIFSDPDVNMVNVFLGDTQVFEFGKGIKYLPPYHQLYPLIGPPLL

IPFYTIQIMKTMISRKDWDLANSISYTFEFTTFVFFGVLSGLVILNAVRIESH

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147..371

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/note="Cyt-b5; Region: Cytochrome b5-like Heme/Steroid

binding domain. This family includes heme binding domains

from a diverse range of proteins. This family also

includes proteins that bind to steroids. The family

includes progesterone receptors. Many members of this

subfamily are membrane anchored by an N-terminal

transmembrane alpha helix. This family also includes a

domain in some chitin synthases. There is no known ligand

for this domain in the chitin synthases"

/db_xref="CDD:pfam00173"

618..1307

/gene="MGC68735"

/note="FA desaturase; Region: Fatty acid desaturase"

/db_xref="CDD:pfam00487"

misc_feature

444

Length:

1781

Matches:

6

Conservative:

0

Mismatch:

0

Indels:

0

Gaps:

5

US-10-029-756-20 (1-6) x BC063726 (1-1781)

Qy 1 PheGlnIleGluHisHis 6

Db 1227 TTTCAGATTGACATCAT 1244

RESULT 94

AF309557

LOCUS

DEFINITION

Cyprinus carpio putative delta-6 fatty acyl desaturase (Fads6)

mRNA, complete cds.

ACCESSION

AF309557

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VERSION AF309557.1 GI:10954036
SOURCE Cyprinus carpio (common carp)
ORGANISM Cyprinus carpio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprinus.

REFERENCE
AUTHORS Hastings,N., Agaba,M., Tocher,D.R., Leaver,M.J., Dick,J.R.,
Sargent,J.R. and Teale,A.J.
TITLE A vertebrate fatty acid desaturase with Delta 5 and Delta 6
activities
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (25), 14304-14309 (2001)
PUBMED 11724940
REFERENCE
AUTHORS Hastings,N., Agaba,M.K., Tocher,D.R., Teale,A.J. and Sargent,J.R.
TITLE Direct Submission
JOURNAL Submitted (28-SEP-2000) Genetics, Institute of Aquaculture,
Stirling FK9 4LA, Scotland
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US-10-029-756-20 (1-6) x AF309557 (1-1790)

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DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:001-017-B11, full
insert sequence.
ACCESSION AK058543
VERSION AK058543.1 GI:32968561
KEYWORDS FLJ_CDNA; oligo-capping.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
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Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
AUTHORS The Rice Full-Length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-Length cDNA Project Team;

```

```

Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,
Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,
Kodama,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C.,
Ohtsuka,K., Shishiki,T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group: Ootomo,Y., Murakami,K.,
Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y.,
Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,
Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J.,
Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J.,
Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN;
Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,
Hara,A., Hashizume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,
Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y.,
Saito,R., Sasaki,D., Sato,K., Shibata,K., Shingawa,A., Shiraki,T.,
Yoshino,M. and Hayashizaki,Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
Science 301 (5631), 376-379 (2003)
2752273
PUBMED 12869764
2 (bases 1 to 1798)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K.,
Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayaishizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T.,
Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K.,
Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I.,
Kanagawa,S., Kato,H., Kawagashira,N., Kawai,J., Kawamata,M.,
Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M.,
Kodama,T., Kojima,K., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M.,
Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A.,
Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M.,
Namiki,T., Narikawa,R., Niikura,J., Nishi,K., Nomura,K.,
Numasaki,T., Ohneda,E., Ohno,M., Ohtsuka,K., Oka,M., Ooka,H.,
Osato,N., Ota,Y., Ootomo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K.,
Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K.,
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Tagawa,A., Takahashi,F., Takaku-Akashira,S., Tanaka,T., Tomaru,A.,
Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W.,
Yanada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and
Yoshimura,A.
Direct Submission
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602 Japan (E-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica
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URL : http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuka,K., Shishiki,T. and
Yamamoto,M.
FAIS Genome Sequencing & Analysis Group: Ootomo,Y., Iida,Y.,
Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M.,
Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J.,
Mizuno,K., Narikawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S.,
Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S.,
Yoshimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K.,
Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K.,
Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Kanagawa,S., Kato,H., Kawai,J.,
Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N.,
Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shingawa,A., Shiraki,T.,

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Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F.,
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Yasunishi, A. and Hayashizaki, Y.

FEATURES

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US-10-029-756-20 (1-6) x AK58543 (1-1798)

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RESULT 96

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LOCUS Homo sapiens fatty acid desaturase 3, mRNA (cdna clone MGC:4158
DEFINITION IMAGE:3532219), complete cds.
ACCESSION BC004901
VERSION BC004901.2 GI:33870184
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenman, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Uedin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Iu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzyzinski, M.I., Skalska, U., Smal, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1807)
Strausberg, R.
Direct Submission
Submitted (21-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
On Aug 19, 2003 this sequence version replaced gi:13436175.
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

TITLE

JOURNAL
PUBMED
REFERENCE
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (21-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT

On Aug 19, 2003 this sequence version replaced gi:13436175.
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: amadansystemsbio.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 11 Row: b Column: 11
This clone was selected for full length sequencing because it
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CDS

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US-10-029-756-20 (1-6) x BC004901 (1-1807)

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ACCESSION CQ776468
VERSION CQ776468.1 GI:45379858
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SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Ohtani, N., Sugita, Y., Yamaya, M., Kubo, H., Nagai, H. and Izuwara, K.

CQ776468
LOCUS Homo sapiens
DEFINITION Sequence 154 from Patent EP1394274.
ACCESSION CQ776468
VERSION CQ776468.1 GI:45379858
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ohtani, N., Sugita, Y., Yamaya, M., Kubo, H., Nagai, H. and Izuwara, K.

LOCUS AY458652 1838 bp mRNA linear VRT 26-NOV-2003
DEFINITION Salmo salar delta-6 fatty acyl desaturase (Fadsd6) mRNA, complete cds.

ACCESSION AY458652
VERSION AY458652.1 GI:38490060
KEYWORDS

SOURCE Salmo salar (Atlantic salmon)
ORGANISM Salmo salar
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.

REFERENCE 1 (bases 1 to 1838)
AUTHORS Zheng, X., Tocher, D.R., Dickson, C.A., Leaver, M.J. and Teale, A.J.
TITLE Cloning and characterization of delta 6 fatty acyl desaturase gene in Atlantic salmon (Salmo salar)

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1838)
AUTHORS Zheng, X., Tocher, D.R., Dickson, C.A., Leaver, M.J. and Teale, A.J.
TITLE Direct Submission
JOURNAL Submitted (05-NOV-2003) Institute of Aquaculture, University of Stirling, Stirling, Scotland FK9 4LA, United Kingdom

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US-10-029-756-20 (1-6) x AY458652 (1-1838)

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Search completed: June 8, 2005, 13:18:06
Job time : 1342.65 secs

GenCore version 5.1.6
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Run on: June 8, 2005, 10:31:05 ; Search time 2403.16 Seconds
(without alignments)
95.036 Million cell updates/sec

Title: US-10-029-756-20

Perfect score: 36

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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| c | 33 | 36 | 100.0 | 387 | 1 | AA428359 | AA428359 |
| c | 34 | 36 | 100.0 | 387 | 8 | BH635847 | BH635847 |
| c | 35 | 36 | 100.0 | 393 | 2 | BE097869 | BE097869 |
| c | 36 | 36 | 100.0 | 398 | 6 | CB774012 | AMGNNUC-M |
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| c | 40 | 36 | 100.0 | 408 | 6 | CB338121 | kb62909.y |
| c | 41 | 36 | 100.0 | 410 | 5 | BP664452 | BP664452 |
| c | 42 | 36 | 100.0 | 410 | 6 | CB803565 | AMGNNUC-M |
| c | 43 | 36 | 100.0 | 411 | 2 | BS019170 | bb49408.y |
| c | 44 | 36 | 100.0 | 413 | 5 | BQ491147 | BQ491147 |
| c | 45 | 36 | 100.0 | 414 | 2 | BB783485 | BB783485 |
| c | 46 | 36 | 100.0 | 416 | 1 | AU283982 | AU283982 |
| c | 47 | 36 | 100.0 | 418 | 1 | AA430733 | z20g08.r |
| c | 48 | 36 | 100.0 | 418 | 1 | AA488546 | ab37509.r |
| c | 49 | 36 | 100.0 | 419 | 6 | CB764557 | CB764557 |
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| c | 51 | 36 | 100.0 | 421 | 7 | CF140245 | CF140245 |
| c | 52 | 36 | 100.0 | 421 | 7 | CO707465 | DG32-8212 |
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| c | 54 | 36 | 100.0 | 429 | 1 | AV615350 | AV615350 |
| c | 55 | 36 | 100.0 | 429 | 7 | W53753 | md12f10.r1 |
| c | 56 | 36 | 100.0 | 430 | 2 | BE763399 | RC0-NT003 |
| c | 57 | 36 | 100.0 | 430 | 4 | BG302890 | FL40g03.x |
| c | 58 | 36 | 100.0 | 431 | 1 | AA003204 | mg46d09.r |
| c | 59 | 36 | 100.0 | 435 | 2 | BE763432 | RC0-NT003 |
| c | 60 | 36 | 100.0 | 436 | 1 | AA049958 | mj38g09.r |
| c | 61 | 36 | 100.0 | 440 | 1 | AL047548 | DKP2p586D |
| c | 62 | 36 | 100.0 | 441 | 6 | CD618243 | CD618243 |
| c | 63 | 36 | 100.0 | 442 | 7 | CN959568 | CN959568 |
| c | 64 | 36 | 100.0 | 442 | 7 | CN962628 | 10125_100 |
| c | 65 | 36 | 100.0 | 442 | 7 | CN966615 | 14112_100 |
| c | 66 | 36 | 100.0 | 443 | 1 | AA310580 | EST181401 |
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| c | 68 | 36 | 100.0 | 444 | 2 | BF890295 | 291915 MA |
| c | 69 | 36 | 100.0 | 444 | 5 | BQ101252 | lJ25h11.y |
| c | 70 | 36 | 100.0 | 445 | 4 | BG412193 | OV2_39_A0 |
| c | 71 | 36 | 100.0 | 446 | 1 | AA488410 | ab37g09.8 |
| c | 72 | 36 | 100.0 | 446 | 6 | CB841818 | M158-2428 |
| c | 73 | 36 | 100.0 | 447 | 7 | CK345055 | L0034F07- |
| c | 74 | 36 | 100.0 | 449 | 2 | BF890281 | 291897 MA |
| c | 75 | 36 | 100.0 | 449 | 2 | BF002756 | 7960f03.x |
| c | 76 | 36 | 100.0 | 452 | 1 | AA531459 | nj63c11.8 |
| c | 77 | 36 | 100.0 | 455 | 5 | BY260760 | BY260760 |
| c | 78 | 36 | 100.0 | 458 | 2 | BF917591 | IL3-UT011 |
| c | 79 | 36 | 100.0 | 458 | 2 | BF917881 | IL3-UT011 |
| c | 80 | 36 | 100.0 | 458 | 4 | B1059742 | IL3-UT011 |
| c | 81 | 36 | 100.0 | 458 | 7 | CN006019 | ip37f09.g |
| c | 82 | 36 | 100.0 | 461 | 4 | BM721986 | UI-E-E00- |

| | | | | | | | | | | | | | | |
|---|-----|----|-------|-----|---|-----------|-----------|-----|-----|-------|-------|-----|----------|----------|
| c | 83 | 36 | 100.0 | 463 | 6 | CA902069 | PCSC20399 | 156 | 36 | 100.0 | 551 | 6 | CA887095 | CA887095 |
| c | 84 | 36 | 100.0 | 465 | 6 | CD430143 | ETH1_17_D | c | 157 | 36 | 100.0 | 552 | 1 | AI178762 |
| c | 85 | 36 | 100.0 | 465 | 6 | CV520815 | 0089F0050 | c | 158 | 36 | 100.0 | 553 | 7 | CN299580 |
| c | 86 | 36 | 100.0 | 469 | 1 | AA478552 | zw59h12.s | c | 159 | 36 | 100.0 | 553 | 8 | CV067153 |
| c | 87 | 36 | 100.0 | 470 | 2 | AW490669 | UI-M-BH3- | c | 160 | 36 | 100.0 | 553 | 8 | CC119775 |
| c | 88 | 36 | 100.0 | 473 | 2 | BF706865 | BF706865 | c | 161 | 36 | 100.0 | 554 | 4 | BI714305 |
| c | 89 | 36 | 100.0 | 474 | 2 | BF756742 | BF756742 | c | 162 | 36 | 100.0 | 555 | 7 | CO687861 |
| c | 90 | 36 | 100.0 | 477 | 2 | BF890300 | 219121.MA | c | 163 | 36 | 100.0 | 557 | 2 | BE217386 |
| c | 91 | 36 | 100.0 | 477 | 4 | BGL58520 | RH122_41- | c | 164 | 36 | 100.0 | 557 | 4 | BM710500 |
| c | 92 | 36 | 100.0 | 477 | 4 | BM689101 | UI-E-COI- | c | 165 | 36 | 100.0 | 560 | 7 | CN283578 |
| c | 93 | 36 | 100.0 | 480 | 6 | CD343234 | EtEstee66 | c | 166 | 36 | 100.0 | 561 | 1 | AI133555 |
| c | 94 | 36 | 100.0 | 487 | 2 | BF654535 | 278752.MA | c | 167 | 36 | 100.0 | 562 | 6 | CD230348 |
| c | 95 | 36 | 100.0 | 489 | 2 | AW231075 | uo70eo4.Y | c | 168 | 36 | 100.0 | 563 | 7 | CO700792 |
| c | 96 | 36 | 100.0 | 489 | 5 | B0499479 | B0499479 | c | 169 | 36 | 100.0 | 566 | 6 | CA970401 |
| c | 97 | 36 | 100.0 | 490 | 2 | BF774199 | BF774199 | c | 170 | 36 | 100.0 | 566 | 6 | CB460442 |
| c | 98 | 36 | 100.0 | 492 | 2 | BE097454 | UI-R-BOI- | c | 171 | 36 | 100.0 | 570 | 7 | CO696124 |
| c | 99 | 36 | 100.0 | 496 | 9 | CR305637 | Medicago | c | 172 | 36 | 100.0 | 571 | 5 | BP240921 |
| c | 100 | 36 | 100.0 | 501 | 7 | CO696980 | DG32-106d | c | 173 | 36 | 100.0 | 571 | 7 | CO691565 |
| c | 101 | 36 | 100.0 | 502 | 2 | BF605837 | BF605837 | c | 174 | 36 | 100.0 | 572 | 5 | BP256407 |
| c | 102 | 36 | 100.0 | 505 | 6 | CD430275 | CD430275 | c | 175 | 36 | 100.0 | 573 | 4 | BI975702 |
| c | 103 | 36 | 100.0 | 506 | 1 | AI421947 | AI421947 | c | 176 | 36 | 100.0 | 574 | 4 | BI775998 |
| c | 104 | 36 | 100.0 | 506 | 6 | CA242493 | UI-H-FEI- | c | 177 | 36 | 100.0 | 577 | 2 | AW533321 |
| c | 105 | 36 | 100.0 | 506 | 6 | CB783557 | AMGNNUC:N | c | 178 | 36 | 100.0 | 577 | 7 | CO681421 |
| c | 106 | 36 | 100.0 | 507 | 2 | BE866647 | BE866647 | c | 179 | 36 | 100.0 | 578 | 5 | BU012940 |
| c | 107 | 36 | 100.0 | 507 | 7 | CO689654 | DG11-262f | c | 180 | 36 | 100.0 | 578 | 5 | CF891989 |
| c | 108 | 36 | 100.0 | 508 | 4 | BT539132 | 451316.MA | c | 181 | 36 | 100.0 | 581 | 5 | BP252288 |
| c | 109 | 36 | 100.0 | 509 | 1 | AA035970 | AA035970 | c | 182 | 36 | 100.0 | 581 | 5 | BP255845 |
| c | 110 | 36 | 100.0 | 509 | 2 | BE248798 | NF020803D | c | 183 | 36 | 100.0 | 582 | 5 | BP254298 |
| c | 111 | 36 | 100.0 | 509 | 2 | BF111253 | BF111253 | c | 184 | 36 | 100.0 | 582 | 5 | BP255848 |
| c | 112 | 36 | 100.0 | 509 | 4 | BG608740 | 307418.MA | c | 185 | 36 | 100.0 | 582 | 5 | BM709050 |
| c | 113 | 36 | 100.0 | 509 | 4 | BI229298 | BI229298 | c | 186 | 36 | 100.0 | 583 | 5 | BP219406 |
| c | 114 | 36 | 100.0 | 511 | 1 | AA789940 | AA789940 | c | 187 | 36 | 100.0 | 583 | 5 | BP352319 |
| c | 115 | 36 | 100.0 | 512 | 4 | BI103269 | BI103269 | c | 188 | 36 | 100.0 | 583 | 5 | BP352319 |
| c | 116 | 36 | 100.0 | 513 | 7 | CO684040 | CO684040 | c | 189 | 36 | 100.0 | 584 | 5 | BU018830 |
| c | 117 | 36 | 100.0 | 514 | 1 | AI1886741 | AI1886741 | c | 190 | 36 | 100.0 | 584 | 5 | CO682308 |
| c | 118 | 36 | 100.0 | 514 | 6 | CB441345 | DG11-241m | c | 191 | 36 | 100.0 | 585 | 5 | BP242668 |
| c | 119 | 36 | 100.0 | 517 | 7 | CO689183 | CO689183 | c | 192 | 36 | 100.0 | 585 | 6 | CB381262 |
| c | 120 | 36 | 100.0 | 518 | 5 | BU537967 | BU537967 | c | 193 | 36 | 100.0 | 585 | 6 | CA886644 |
| c | 121 | 36 | 100.0 | 518 | 5 | EX511690 | EX511690 | c | 194 | 36 | 100.0 | 588 | 6 | CA886644 |
| c | 122 | 36 | 100.0 | 520 | 6 | CA891796 | CA891796 | c | 195 | 36 | 100.0 | 589 | 6 | CD131172 |
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| c | 124 | 36 | 100.0 | 522 | 1 | AA642405 | AA642405 | c | 197 | 36 | 100.0 | 589 | 7 | CB842824 |
| c | 125 | 36 | 100.0 | 522 | 7 | CF115390 | CF115390 | c | 198 | 36 | 100.0 | 595 | 7 | CF892640 |
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| c | 127 | 36 | 100.0 | 525 | 4 | BT539140 | 451326.MA | c | 200 | 36 | 100.0 | 596 | 7 | CN299568 |
| c | 128 | 36 | 100.0 | 527 | 5 | BQ100940 | BQ100940 | c | 201 | 36 | 100.0 | 597 | 7 | CN283566 |
| c | 129 | 36 | 100.0 | 528 | 1 | AA642379 | AA642379 | c | 202 | 36 | 100.0 | 599 | 1 | AF084879 |
| c | 130 | 36 | 100.0 | 528 | 4 | BI075599 | BI075599 | c | 203 | 36 | 100.0 | 600 | 4 | BG803060 |
| c | 131 | 36 | 100.0 | 528 | 6 | CA510154 | UI-R-F50- | c | 204 | 36 | 100.0 | 600 | 7 | CK998942 |
| c | 132 | 36 | 100.0 | 528 | 7 | CO683782 | DG11-174m | c | 205 | 36 | 100.0 | 600 | 7 | CO680131 |
| c | 133 | 36 | 100.0 | 530 | 2 | AW246354 | AW246354 | c | 206 | 36 | 100.0 | 600 | 7 | CO696232 |
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| c | 135 | 36 | 100.0 | 533 | 8 | AQ331826 | AQ331826 | c | 208 | 36 | 100.0 | 602 | 7 | CO687520 |
| c | 136 | 36 | 100.0 | 535 | 2 | BF207014 | BF207014 | c | 209 | 36 | 100.0 | 603 | 6 | CA343707 |
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| c | 138 | 36 | 100.0 | 536 | 7 | CO590199 | CO590199 | c | 211 | 36 | 100.0 | 604 | 7 | CF750159 |
| c | 139 | 36 | 100.0 | 537 | 7 | CO684940 | CO684940 | c | 212 | 36 | 100.0 | 605 | 1 | AV682123 |
| c | 140 | 36 | 100.0 | 538 | 4 | BG231597 | BG231597 | c | 213 | 36 | 100.0 | 605 | 6 | CB494661 |
| c | 141 | 36 | 100.0 | 541 | 5 | BQ481262 | BQ481262 | c | 214 | 36 | 100.0 | 606 | 7 | CO687643 |
| c | 142 | 36 | 100.0 | 543 | 2 | BF073739 | BF073739 | c | 215 | 36 | 100.0 | 607 | 7 | CO685306 |
| c | 143 | 36 | 100.0 | 545 | 1 | AA814375 | AA814375 | c | 216 | 36 | 100.0 | 607 | 7 | CO685848 |
| c | 144 | 36 | 100.0 | 545 | 7 | CK823209 | CK823209 | c | 217 | 36 | 100.0 | 609 | 4 | BM322472 |
| c | 145 | 36 | 100.0 | 546 | 4 | BI340258 | BI340258 | c | 218 | 36 | 100.0 | 609 | 7 | CF725851 |
| c | 146 | 36 | 100.0 | 546 | 7 | CK823208 | CK823208 | c | 219 | 36 | 100.0 | 610 | 7 | CO687019 |
| c | 147 | 36 | 100.0 | 547 | 1 | AA262103 | AA262103 | c | 220 | 36 | 100.0 | 612 | 1 | AJ723990 |
| c | 148 | 36 | 100.0 | 547 | 5 | BM978181 | BM978181 | c | 221 | 36 | 100.0 | 612 | 7 | CO697676 |
| c | 149 | 36 | 100.0 | 548 | 1 | A1419315 | A1419315 | c | 222 | 36 | 100.0 | 614 | 5 | BP161817 |
| c | 150 | 36 | 100.0 | 548 | 5 | BU778445 | BU778445 | c | 223 | 36 | 100.0 | 614 | 7 | CO680725 |
| c | 151 | 36 | 100.0 | 548 | 6 | CA763181 | CA763181 | c | 224 | 36 | 100.0 | 615 | 9 | CO693874 |
| c | 152 | 36 | 100.0 | 549 | 9 | CR503302 | CR503302 | c | 225 | 36 | 100.0 | 615 | 9 | CR308748 |
| c | 153 | 36 | 100.0 | 550 | 6 | CA310472 | CA310472 | c | 226 | 36 | 100.0 | 617 | 2 | AW518845 |
| c | 154 | 36 | 100.0 | 550 | 7 | CF430228 | CF430228 | c | 227 | 36 | 100.0 | 617 | 7 | CO690386 |
| c | 155 | 36 | 100.0 | 550 | 7 | CF906442 | CF906442 | c | 228 | 36 | 100.0 | 618 | 5 | BP457290 |

| | | | | | | | | | | | | | |
|-------|----|-------|-----|---|----------|------------|-------|----|-------|-----|---|----------|-----------|
| C 229 | 36 | 100.0 | 618 | 6 | CA223458 | SCJFPL1C0 | 302 | 36 | 100.0 | 694 | 7 | CN975137 | 24841_125 |
| 230 | 36 | 100.0 | 619 | 5 | BQ515108 | EST622523 | C 303 | 36 | 100.0 | 698 | 2 | BE613347 | 601452439 |
| 231 | 36 | 100.0 | 620 | 5 | BP336712 | BP336712 | 304 | 36 | 100.0 | 699 | 6 | CB549753 | MMP00010 |
| C 232 | 36 | 100.0 | 621 | 5 | BO412264 | GA_Ed005 | 305 | 36 | 100.0 | 699 | 7 | CN971323 | 18820_123 |
| C 233 | 36 | 100.0 | 624 | 6 | CB433595 | omYKrb1b0 | 306 | 36 | 100.0 | 700 | 7 | CN977877 | 28550_125 |
| C 234 | 36 | 100.0 | 624 | 7 | CN987006 | 62688_125 | 307 | 36 | 100.0 | 700 | 7 | CV150079 | Mdfct3074 |
| C 235 | 36 | 100.0 | 624 | 7 | C0685119 | DG11-1376 | 308 | 36 | 100.0 | 702 | 5 | BU432572 | 603257617 |
| 236 | 36 | 100.0 | 625 | 4 | BG163730 | 602338937 | 309 | 36 | 100.0 | 703 | 2 | BE265009 | BE265009 |
| C 237 | 36 | 100.0 | 625 | 7 | CF904342 | A0421C04- | 310 | 36 | 100.0 | 704 | 4 | BI520098 | 603071227 |
| C 238 | 36 | 100.0 | 625 | 7 | C0683285 | DG11-167F | C 311 | 36 | 100.0 | 704 | 4 | CF924968 | MI_MQ1_01 |
| 239 | 36 | 100.0 | 626 | 4 | BG764766 | 602736370 | C 312 | 36 | 100.0 | 705 | 9 | AG171809 | Pan trogl |
| 240 | 36 | 100.0 | 629 | 4 | BG390559 | 602416330 | 313 | 36 | 100.0 | 707 | 4 | BG743815 | 602631480 |
| C 241 | 36 | 100.0 | 629 | 7 | C0679910 | DG11-1081 | 314 | 36 | 100.0 | 708 | 4 | BG743224 | 602634390 |
| 242 | 36 | 100.0 | 631 | 5 | BQ266834 | NISC fl15 | 315 | 36 | 100.0 | 709 | 7 | CN979203 | 30404_125 |
| C 243 | 36 | 100.0 | 632 | 4 | BJ580080 | BJ580080 | 316 | 36 | 100.0 | 709 | 7 | CN980205 | 1538_125 |
| 244 | 36 | 100.0 | 632 | 7 | CN983167 | 51780_126 | 317 | 36 | 100.0 | 710 | 7 | CN991754 | 68839_125 |
| 245 | 36 | 100.0 | 633 | 2 | BE313171 | 601149928 | 318 | 36 | 100.0 | 712 | 4 | BI220733 | 602938846 |
| 246 | 36 | 100.0 | 633 | 9 | CW513287 | 115_3_105 | 319 | 36 | 100.0 | 712 | 7 | CN283564 | 170005315 |
| 247 | 36 | 100.0 | 634 | 7 | CN984291 | 53246_126 | C 321 | 36 | 100.0 | 715 | 7 | CK448975 | PL1G11.SP |
| 248 | 36 | 100.0 | 635 | 6 | CA889164 | B0151B06- | 322 | 36 | 100.0 | 717 | 4 | BM386441 | UI-R-CN1 |
| C 249 | 36 | 100.0 | 636 | 4 | BG348983 | daa35e12. | 323 | 36 | 100.0 | 719 | 6 | CA316163 | CA316163 |
| C 250 | 36 | 100.0 | 638 | 7 | C0686285 | DG11-213K | 324 | 36 | 100.0 | 723 | 2 | BF341872 | 602016549 |
| 251 | 36 | 100.0 | 639 | 2 | BE394750 | 601311958 | 325 | 36 | 100.0 | 723 | 8 | BZ393699 | EINBJ96TF |
| 252 | 36 | 100.0 | 640 | 9 | CR342157 | Medicaco | 326 | 36 | 100.0 | 724 | 7 | CN283579 | 170004554 |
| C 253 | 36 | 100.0 | 641 | 2 | BE382648 | 601297091 | 327 | 36 | 100.0 | 726 | 4 | BG596229 | 602659360 |
| C 254 | 36 | 100.0 | 642 | 2 | AW005365 | wz85H09.x | C 328 | 36 | 100.0 | 727 | 7 | CF662243 | CCL010A01 |
| 255 | 36 | 100.0 | 642 | 2 | BE372542 | 601223991 | C 329 | 36 | 100.0 | 727 | 7 | CO681208 | DG11-1260 |
| 256 | 36 | 100.0 | 642 | 6 | CB441017 | 691336_MA | 330 | 36 | 100.0 | 730 | 5 | BU284808 | 603602290 |
| 257 | 36 | 100.0 | 642 | 7 | CN283560 | 170006002 | C 331 | 36 | 100.0 | 730 | 5 | BU626230 | UI-H-FG1- |
| 258 | 36 | 100.0 | 643 | 7 | CF894273 | CF894273 | C 332 | 36 | 100.0 | 730 | 7 | CO556817 | AGENCOURT |
| 259 | 36 | 100.0 | 647 | 7 | CN984455 | 53515_126 | C 333 | 36 | 100.0 | 732 | 6 | CB984229 | AGENCOURT |
| C 260 | 36 | 100.0 | 648 | 7 | CO701254 | DG32-199C | C 334 | 36 | 100.0 | 733 | 5 | BQ515109 | EST622524 |
| C 261 | 36 | 100.0 | 649 | 5 | BQ830430 | LL6in2233 | 335 | 36 | 100.0 | 733 | 6 | CD811236 | AGENCOURT |
| C 262 | 36 | 100.0 | 649 | 7 | C0684927 | DG11-193K | 336 | 36 | 100.0 | 735 | 7 | CO681550 | DG11-1301 |
| 263 | 36 | 100.0 | 650 | 4 | BI220930 | 602937493 | 337 | 36 | 100.0 | 737 | 4 | BG596721 | 602659743 |
| 264 | 36 | 100.0 | 650 | 7 | CF749409 | UI-N-H30- | C 338 | 36 | 100.0 | 738 | 4 | BG747608 | 602705067 |
| 265 | 36 | 100.0 | 651 | 4 | BG085082 | H3108D09- | C 339 | 36 | 100.0 | 741 | 5 | BX858026 | BX858026 |
| 266 | 36 | 100.0 | 651 | 7 | CV085518 | Mdfct3078 | C 340 | 36 | 100.0 | 742 | 9 | CL953412 | OBIRUA000 |
| 267 | 36 | 100.0 | 653 | 6 | CA247637 | SCCCFL506 | C 341 | 36 | 100.0 | 744 | 5 | BU617835 | UI-H-FE1- |
| 268 | 36 | 100.0 | 653 | 6 | CA247656 | CA247656 | 342 | 36 | 100.0 | 745 | 5 | BU772092 | SJEEHC06 |
| 269 | 36 | 100.0 | 654 | 4 | BG913139 | 602811753 | 343 | 36 | 100.0 | 745 | 4 | BG739802 | 602630537 |
| 270 | 36 | 100.0 | 655 | 4 | BI330126 | 602983730 | 344 | 36 | 100.0 | 745 | 9 | CNS02231 | Tetraodon |
| C 271 | 36 | 100.0 | 657 | 4 | BI850133 | Imagqc_1 | 345 | 36 | 100.0 | 747 | 7 | CV080482 | AGENCOURT |
| C 272 | 36 | 100.0 | 659 | 7 | CO708052 | DG32-9665 | 346 | 36 | 100.0 | 748 | 7 | CN989200 | 65204_125 |
| 273 | 36 | 100.0 | 660 | 2 | BE394608 | 601311841 | 347 | 36 | 100.0 | 748 | 9 | CD762498 | NDL_36F21 |
| 274 | 36 | 100.0 | 660 | 6 | CA390771 | cell14c09. | C 348 | 36 | 100.0 | 749 | 7 | CK129282 | AGENCOURT |
| C 275 | 36 | 100.0 | 663 | 2 | AW476589 | uq78c01.y | C 349 | 36 | 100.0 | 751 | 5 | BQ174168 | UI-N-DJ2- |
| C 276 | 36 | 100.0 | 664 | 4 | BN264661 | fw60d11.x | 350 | 36 | 100.0 | 753 | 4 | BG422898 | 602450074 |
| 277 | 36 | 100.0 | 666 | 6 | CA090832 | SCUTAM200 | 351 | 36 | 100.0 | 754 | 4 | BG696675 | 602658982 |
| 278 | 36 | 100.0 | 667 | 6 | CD618242 | 50661114H | C 352 | 36 | 100.0 | 755 | 5 | BU366986 | 603785574 |
| 279 | 36 | 100.0 | 667 | 4 | BI253447 | 602973776 | C 353 | 36 | 100.0 | 755 | 9 | AG413792 | Mus muscu |
| 280 | 36 | 100.0 | 670 | 6 | CB502892 | ssalplnb5 | 354 | 36 | 100.0 | 759 | 7 | CN978621 | 29464_125 |
| 281 | 36 | 100.0 | 671 | 9 | CB335063 | Medicaco | 355 | 36 | 100.0 | 761 | 7 | CK366282 | AGENCOURT |
| 282 | 36 | 100.0 | 672 | 7 | CN299579 | 170005399 | 356 | 36 | 100.0 | 764 | 4 | BG741398 | 602631955 |
| C 283 | 36 | 100.0 | 672 | 7 | CO700981 | DG32-190h | 357 | 36 | 100.0 | 767 | 7 | CN987671 | 63396_125 |
| 284 | 36 | 100.0 | 673 | 6 | CD762194 | GGEZSM102 | C 358 | 36 | 100.0 | 768 | 6 | CA371783 | 652372_NC |
| C 285 | 36 | 100.0 | 675 | 4 | BM103984 | fv41d12.x | 359 | 36 | 100.0 | 769 | 5 | BU724689 | SJMBJG09 |
| 286 | 36 | 100.0 | 675 | 6 | CA390905 | cell15h10. | C 360 | 36 | 100.0 | 770 | 7 | CN283577 | 170005318 |
| 287 | 36 | 100.0 | 677 | 4 | BI079348 | 602873712 | C 361 | 36 | 100.0 | 771 | 7 | CN169784 | AGENCOURT |
| C 288 | 36 | 100.0 | 679 | 7 | CN988761 | 64620_125 | C 362 | 36 | 100.0 | 771 | 9 | CG264591 | OGWGP72TH |
| 289 | 36 | 100.0 | 680 | 2 | BB630084 | BB630084 | 363 | 36 | 100.0 | 772 | 7 | CN324546 | AGENCOURT |
| C 290 | 36 | 100.0 | 683 | 6 | CD353781 | UI-M-GM0- | 364 | 36 | 100.0 | 773 | 5 | BU612805 | UI-N-EWO- |
| C 291 | 36 | 100.0 | 683 | 7 | CO819352 | CSECS153B | 365 | 36 | 100.0 | 774 | 4 | BG696258 | 602659396 |
| C 292 | 36 | 100.0 | 685 | 4 | BM156732 | fv55b07.x | 366 | 36 | 100.0 | 778 | 5 | BX860293 | BX860293 |
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| C 295 | 36 | 100.0 | 688 | 6 | CB171369 | JID602700 | 369 | 36 | 100.0 | 779 | 7 | CO123633 | GR_Eb050 |
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| | | | | | | | | | | | | | |
|-----|----|-------|------|---|----------|--------------------|-------|----|------|------|---|-----------|-----------|
| 521 | 36 | 100.0 | 1690 | 3 | CR608795 | CR608795 full-leng | 584 | 35 | 97.2 | 639 | 8 | AZ809669 | AZ809669 |
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| 536 | 35 | 97.2 | 300 | 1 | AJ484147 | AJ484147 AJ484147 | C 609 | 35 | 97.2 | 699 | 4 | BJ321063 | BJ321063 |
| 537 | 35 | 97.2 | 310 | 7 | R04815 | R04815 pk32e05.r1 | 610 | 35 | 97.2 | 702 | 5 | BQ540149 | BQ540149 |
| 538 | 35 | 97.2 | 325 | 4 | BG605209 | BG605209 WHE2330.A | 611 | 35 | 97.2 | 710 | 7 | CF473294 | CF473294 |
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| 548 | 35 | 97.2 | 442 | 7 | CN968710 | CN968710 16207.100 | C 621 | 35 | 97.2 | 758 | 9 | AG563870 | AG563870 |
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| 550 | 35 | 97.2 | 448 | 5 | BQ040319 | BQ040319 gdl4c05.Y | C 623 | 35 | 97.2 | 775 | 8 | BZ564928 | BZ564928 |
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| 555 | 35 | 97.2 | 504 | 4 | BM133143 | BM133143 TgBSTzvb1 | C 628 | 35 | 97.2 | 793 | 4 | BJ574080 | BJ574080 |
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| 557 | 35 | 97.2 | 516 | 5 | BQ236097 | BQ236097 Ta05038D | C 630 | 35 | 97.2 | 796 | 7 | CO978640 | CO978640 |
| 558 | 35 | 97.2 | 518 | 5 | BH265574 | BH265574 UK122TC04 | C 631 | 35 | 97.2 | 805 | 6 | CD826502 | CD826502 |
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| 560 | 35 | 97.2 | 521 | 4 | BJ464683 | BJ464683 BJ464683 | C 633 | 35 | 97.2 | 828 | 6 | CD815117 | CD815117 |
| 561 | 35 | 97.2 | 521 | 9 | CG816778 | CG816778 SOYDX94TH | C 634 | 35 | 97.2 | 847 | 7 | CO094655 | CO094655 |
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| 566 | 35 | 97.2 | 543 | 7 | CF114672 | CF114672 Shultzom1 | C 639 | 35 | 97.2 | 882 | 7 | CO072459 | CO072459 |
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| 572 | 35 | 97.2 | 554 | 1 | AI233903 | AI233903 EST230591 | C 645 | 35 | 97.2 | 921 | 7 | CN510503 | CN510503 |
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| 575 | 35 | 97.2 | 564 | 2 | BE423694 | BE423694 WHE0073.G | C 648 | 35 | 97.2 | 973 | 9 | CNS02M91 | CNS02M91 |
| 576 | 35 | 97.2 | 573 | 1 | AL810658 | AL810658 AL810658 | C 649 | 35 | 97.2 | 988 | 8 | CC299589 | CC299589 |
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| 579 | 35 | 97.2 | 590 | 8 | CL136127 | CL136127 ND.L1668 | C 652 | 35 | 97.2 | 1215 | 6 | CD505027 | CD505027 |
| 580 | 35 | 97.2 | 592 | 6 | CD527844 | CD527844 3529.L12 | C 653 | 35 | 97.2 | 1242 | 6 | CD505027 | CD505027 |
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| 587 | 35 | 97.2 | 616 | 8 | AZ395503 | AZ395503 IM0159D12 | C 660 | 34 | 94.4 | 319 | 9 | CC574270 | CC574270 |
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|-----|----|------|-----|---|----------|---------------------|-------|----|------|-----|---|----------|---------------------|
| 667 | 34 | 94.4 | 347 | 9 | CC599867 | CC599867 ZMMBBC040 | 740 | 34 | 94.4 | 472 | 7 | CV301192 | CV301192 EST888535 |
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| 670 | 34 | 94.4 | 360 | 1 | AV196325 | AV196325 AV196325 | 743 | 34 | 94.4 | 474 | 6 | CG239303 | CG239303 sab67h10. |
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| 672 | 34 | 94.4 | 360 | 6 | C10120 | C10120 C10120 Yuji | 745 | 34 | 94.4 | 474 | 8 | B76579 | B76579 RfC111-15N1 |
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| 674 | 34 | 94.4 | 360 | 7 | D76395 | D76395 CBLK117G2F | 747 | 34 | 94.4 | 480 | 7 | T42806 | T42806 6069 Lambda |
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| 676 | 34 | 94.4 | 364 | 5 | BF659307 | BF659307 BF659307 | c 749 | 34 | 94.4 | 484 | 1 | AV537777 | AV537777 AV537777 |
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| 680 | 34 | 94.4 | 376 | 8 | B2897113 | B2897113 CH240.111 | c 753 | 34 | 94.4 | 489 | 5 | BP614716 | BP614716 BP614716 |
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ALIGNMENTS

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RESULT 1
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DEFINITION HUMGS0003903 Human adult (K.Okubo) Homo sapiens cDNA, mRNA
ACCESSION C01909
VERSION C01909.1 GI:1434139
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL 1 (bases 1 to 122)
COMMENT BodyMap: human gene expression database
Contact: Okubo,K.
Institute for Molecular and Cellular Biol
Osaka University
1-3,Yamada-oka, Suita, Osaka Pref. 565, Japan
Tel: 06-877-5111(ex.3315)
Email: kousaku@imcb.osaka-u.ac.jp
We are not submitting the same cDNA sequence redundantly to DDBJ
sequence in this library and as well as in other 3'-directed
libraries, see 'http://www.imcb.osaka-u.ac.jp/bodymap'. The
sequences of the clones represented by this GS sequences is also

```

```

found there.
FEATURES             source
    source
    1..122
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /dev_stage="adult"
    /clone_lib="Human adult (K.Okubo)"
    /notes="One or more human adult tissue"

ORIGIN
Alignment Scores:
Pred. No.:      581      Length:      122
Score:          36.00    Matches:      6
Percent Similarity: 100.00%  Conservaive:  0
Best Local Similarity: 100.00%  Mismatches:  0
Query Match:     100.00%  Indels:       0
DB:              6       Gaps:         0

US-10-029-756-20 (1-6) x C01909 (1-122)

Qy  1 PheGlnIlecluhishis 6
Db  100 TTCAGATTGAGCACCAT 117

RESULT 2
LOCUS BF083018/c
DEFINITION QV1-CS0007-180900-376-e08 CS0007 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF083018
VERSION BF083018.1 GI:10876848
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 144)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P.,
Goldman,G.H., Carvalho,A.P., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LiCR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=kt2-QV1-CS0007-180
900-376-e08&t3=2000-09-18&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 7
High quality sequence stop: 143.
Location/Qualifiers
    1..144
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /dev_stage="Adult"
    /clone_lib="CS0007"
    /notes="Organ: colon_est; Vector: puc18; Site 1: SmaI;
    Site 2: SmaI; A mini-library was made by cloning products
    derived from ORESTES PCR (U.S. Letters Patent application

```


No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Alignment Scores:
 Pred. No.: 709 Length: 144
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x BF083018 (1-144)

Qy 1 PheGlnIleGluHisHis 6
 |||||

Db 131 TTCACATTGACCAAT 114

RESULT 3

CO420590 158 bp mRNA linear EST 02-JUL-2004
 LOCUS GGEZHC1014H04.g Hc1 Gallus gallus cDNA clone GGEZHC1014H04, mRNA
 DEFINITION

ACCESSION CO420590
 VERSION CO420590.1 GI:49636838
 KEYWORDS EST.

SOURCE

ORGANISM

Gallus gallus (chicken)
 Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.

REFERENCE

1 (bases 1 to 158)
 Silva,C.S., Jorge,E.C., Patricio,M., Ledur,M.C. and Coutinho,L.L.
 Authors
 Title
 Discovery of new genes expressed in the chicken pituitary and hypothalamus

JOURNAL

COMMENT

Unpublished (2004)
 Contact: Clarissa S. Silva
 Laboratory of Animal Biotechnology, Dep. of Animal Production
 ESALQ - University of Sao Paulo
 Av. Padua Dias, 11, Piracicaba, SP, 13418-900, Brazil
 Tel: 55 19 3429 4434
 Fax: 55 19 3429 4285
 Email: cssilva@esalq.usp.br and llcouth@esalq.usp.br
 PCR Primers

FEATURES

source

Location/Qualifiers

1..158
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /db_xref="taxon:9031"
 /clone="GGEZHC1014H04"
 /tissue_type="pituitary and hypothalamus"
 /dev_stage="21 days old"
 /lab_host="DH10B"
 /clone_lib="HC1"

/note="Vector: pSPOR1; Site 1: NotI; Site 2: SalI; This cDNA library was constructed with the SuperScript Plasmid System with Gateway technology kit (Invitrogen), following manufacture's protocols. Plasmid DNA was purified using a modified alkaline lysis method. Sequencing reactions were conducted using the Kit Big Dye Terminator Cycle Sequencing Ready Reaction (Applied Biosystems) according to the manufacturer's recommendations. Clones were sequenced by the 5' end with T7 primer. Sequencing reactions were analyzed on ABI Prism 3100 Genetic Analyzer (Applied Biosystems). The quality and clustering of the ESTs were analyzed using the softwares Phred/Gap3. Only EST sequences with Phred quality greater than 20 and at least 150 bp were considered for clustering."

ORIGIN

Alignment Scores:

Alignment Scores:
 Pred. No.: 793 Length: 158
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-10-029-756-20 (1-6) x CO420590 (1-158)

Qy 1 PheGlnIleGluHisHis 6
 |||||

Db 103 TTCACATTGACCAAT 120

RESULT 4

AA841755/c

LOCUS

DEFINITION

AA841755

VERSION

KEYWORDS

SOURCE

ORGANISM

Brugia malayi

Brugia malayi

Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 Onchocercidae; Brugia.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1997)

Contact: Blaxter ML

Institute of Cell, Animal and Population Biology

University of Edinburgh

Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9

3JT, UK.

Tel: +44 131 650 6760

Fax: +44 131 670 5450

Email: mark.blaxter@ed.ac.uk

The ABI trace of this sequence can be viewed at

http://www.sanger.ac.uk/bugia/3b6/WB3D6V6H01T3.html

Seq primer: T3.

FEATURES

source

Location/Qualifiers

1..169

/organism="Brugia malayi"

/mol_type="mRNA"

/strain="T3S Labs"

/db_xref="taxon:6279"

/clone="3D6V6H01"

/sex="mixed"

/dev_stage="third stage larvae, six days after infection"

/lab_host="E. coli XLI-Blue"

/clone_lib="Brugia malayi day 6 post-infection third stage

larvae SAW96MLW-Bml3d6"

/note="Vector: lambdaZapII (Unizap XR); Site 1: Eco R I

(5' end); Site 2: Xho I (3' end); Brugia malayi is a

lymphatic filarial nematode parasite of humans. mRNA was

prepared from third stage larvae of Brugia malayi isolated

from the peritoneal cavity of jirds six days after

infection. The mRNA was converted to double stranded cDNA

using reverse transcriptase and oligo(dT) followed by

RNAse H and DNAPol I. The library had 2 x 10E5 independent

recombinants and average insert size was 900 base pairs.

The library was constructed by Michelle Lizotte-Waniewski.

The library is available from The Filarial Genome Project

Resource Center: contact Dr. S.A. Williams, Clark Science

Center, Smith College, Northampton, MA 01063 USA phone +1

413 585 3826 fax +1 413 585 3786 email genome@smith.edu."

ORIGIN

Alignment Scores:

Pred. No.: 859 Length: 169
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AA841755 (1-169)

Qy 1 PheGlnIleGluHisHis 6
 |||||
 Db 52 TTTCAAATCGACACCAT 35

RESULT 5

AI747918 184 bp mRNA linear EST 22-JUN-1999
 LOCUS u104a01.y1 Sugano mouse kidney mkia Mus musculus cDNA clone
 DEFINITION IMAGE:2065032 5' similar to TR:060427 BC269730 2. ; mRNA
 sequence.

ACCESSION AI747918

VERSION AI747918.1 GI:5126182

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS

1 (bases 1 to 184)
 Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
 Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
 Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
 Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
 Waterston, R., and Wilson, R.

Waterston, R. and Wilson, R.

The WashU-NCI Mouse EST Project 1999

Unpublished (1999)

CONTACT: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MG1:994220

Possible reversed clone: similarity on wrong strand

Seq primer: custom primer used

High quality sequence stop: 69.

Location/Qualifiers

FEATURES

source
 1..184
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CS7BL"
 /db_xref="taxon:10090"
 /clone="IMAGE:2065032"
 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"

/clone_lib="Sugano mouse kidney mkia"
 /note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII
 (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
 was primed with an oligo(dT) primer
 [ATCGGCGCTTTTCTTTTCTTTT]; double-stranded cDNA was
 ligated to a DraIII adaptor [TGTGGCTACTGG], digested
 and cloned into distinct DraIII sites of the pME18S-FL3
 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
 be used to isolate the cDNA insert. Size selection was
 performed to exclude fragments <1.5kb. Library
 constructed by Dr. Sumio Sugano (University of Tokyo
 Institute of Medical Science). Custom primers for
 sequencing: 5' end primer CTCTGCTCTAAAGCTCGC and 3' end
 primer CGACCTGCGCTCGACCA."

ORIGIN

Alignment Scores:

Pred. No.: 952 Length: 184
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AI747918 (1-184)

Qy 1 PheGlnIleGluHisHis 6
 |||||
 Db 65 TTCCAGATTGAGCACCAC 82

RESULT 6

AA369496 196 bp mRNA linear EST 21-APR-1997
 LOCUS EST80921 Placenta II Homo sapiens cDNA 5' end, mRNA sequence.
 DEFINITION AA369496
 ACCESSION AA369496
 VERSION AA369496.1 GI:2021816

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS

1 (bases 1 to 196)
 Adams, M.D., Soares, M.B., Kerlavage, A.R., Fields, C. and Venter, J.C.
 Rapid cDNA sequencing (expressed sequence tags) from a
 directionally cloned human infant brain cDNA library

Nat. Genet. 4, 373-380 (1993)

JOURNAL 94004965

PUBMED 8401585

Other ESTs: THCL52140

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlavage@tigr.org

For clone availability, additional sequence and expression

information related to this EST, please check the TIGR Human Gene

Index (<http://www.tigr.org/tdb/hgi/hgi.html>)

Seq primer: M13 Reverse.

Location/Qualifiers

1..196

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="ATCC (inhost):174097"

/db_xref="taxon:9606"

/tissue_type="placenta"

/dev_stage="fetus"

/clone_lib="Placenta II"

/note="Organ: placenta; Vector: pBluescript SK-; Site_1:
 EcoRI; Site_2: XhoI"

ORIGIN

Alignment Scores:
 Pred. No.: 1.03e+03 Length: 196
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AA369496 (1-196)

Qy 1 PheGlnIleGluHisHis 6
 |||||
 Db 169 TTCCAGATTGAGCACCAC 186

RESULT 7

AZ404851/c

LOCUS

AZ404851

207 bp DNA linear

GSS 03-OCT-2000

```

DEFINITION      1M0173D08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION       AZ404851
VERSION         AZ404851.1  GI:10528864
KEYWORDS        GSS.
SOURCE          Mus musculus (house mouse)
ORGANISM        Mus musculus
REFERENCE       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS         Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
                Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
                Niederhausern,A. and Wright,D., Weiss,R.
TITLE           Mouse whole genome scaffolding with paired end reads from 10kb
                plasmid inserts
JOURNAL         Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
                University of Utah
                University of Utah
                Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                84112, USA
                Tel: 801 585 5606
                Fax: 801 585 7177
                Email: ddunne@genetics.utah.edu
                Insert Length: 10000 Std Error: 0.00
                Plate: 0173 row: D column: 08
                Seq primer: CGTTGTAAACGACGCCAGT
                Class: plasmid ends
                High quality sequence stop: 207.
FEATURES        Location/Qualifiers
                1..207
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0173D08"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /note="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
ORIGIN
Alignment Scores:
Pred. No.:      1.1e+03      Length:      207
Score:          36.00      Matches:      6
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             8      Gaps:          0

US-10-029-756-20 (1-6) x AZ404851 (1-207)

Qy              1 PheGlnIleGluHisHis 6
                ||||||||||||||||

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Db              99 TTCCAGATCGAGCACCAT 82
RESULT 8
AW579368/1
LOCUS          240 bp      mRNA      linear      EST 16-MAR-2000
DEFINITION    PM2-DT0062-080100-002-g04 DT0062 Homo sapiens cDNA, mRNA sequence.
ACCESSION     AW579368
VERSION       AW579368.1  GI:7254430
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE         HCGP http://www.ludwig.org.br/ORESTES.
                The FAPESP/LICR Human Cancer Genome Project
JOURNAL       Unpublished (1999)
COMMENT       Contact: Simpson A.J.G.
                Laboratory of Cancer Genetics
                Ludwig Institute for Cancer Research
                Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                Brazil
                Tel: +55-11-2704922
                Fax: +55-11-2707001
                Email: asimpson@ludwig.org.br
                This sequence was derived from the FAPESP/LICR Human Cancer Genome
                Project. This entry can be seen in the following URL
                http://www.ludwig.org.br/scripts/gethtml2.pl?t1=PM2&t2=PM2-DT0062-
                080100-002-g04&t3=2000-01-08&t4=1)
                Seq primer: puc 18 forward
                High quality sequence stop: 40
                High quality sequence stop: 240.
FEATURES       Location/Qualifiers
                1..240
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /dev_stage="Adult"
                /clone_lib="DT0062"
                /note="Organ: denis draugh; Vector: puc18; Site 1: SmaI;
                Site 2: SmaI; A mini-library was made by cloning products
                derived from ORESTES PCR (U.S. Letters Patent application
                No. 196,716 - Ludwig Institute for Cancer Research)
                profiles into the puc 18 vector. Reverse transcription of
                tissue mRNA and cDNA amplification were performed under
                low stringency conditions."
ORIGIN
Alignment Scores:
Pred. No.:      1.31e+03      Length:      240
Score:          36.00      Matches:      6
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             2      Gaps:          0

US-10-029-756-20 (1-6) x AW579368 (1-240)

Qy              1 PheGlnIleGluHisHis 6
                ||||||||||||||||
Db              31 TTCCAGATCGAGCACCAT 14
RESULT 9
BF871924/c
LOCUS          246 bp      mRNA      linear      EST 17-JAN-2001
DEFINITION    CM4-ET0095-011100-405-h01 ET0095 Homo sapiens cDNA, mRNA sequence.
ACCESSION     BF871924
VERSION       BF871924.1  GI:12262054
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS       Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE
AUTHORS 1 (bases 1 to 246)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel.: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM4&t2=CM4-ET0095-
01100-405-h01&t3=2000-11-01&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 14
High quality sequence stop: 246.
FEATURES
source
Location/Qualifiers
1..246
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="ET0095"
/notes="Organ: lung tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORSTES PCR (U.S. Letters Patent application
No. 196, 716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
ORIGIN
Alignment Scores:
Pred. No.: 1.35e+03 Length: 246
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-10-029-756-20 (1-6) x BF871924 (1-246)
Qy 1 PheGlnIleGluHisHis 6
|||||
Db 131 TTCACGATTGACACCAC 114
RESULT 10
BQ587416/c
LOCUS BQ587416 248 bp mRNA linear EST 06-DEC-2002
DEFINITION S013303-024-010-001-T7 MPZ-ADIS-024-leaf Beta vulgaris cDNA clone
ACCESSION BQ587416
VERSION BQ587416.1 GI:26116998
EST.
KEYWORDS Beta vulgaris
SOURCE Beta vulgaris
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
AUTHORS 1 (bases 1 to 248)
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.

```

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and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
JOURNAL 22362189
MEDLINE 12472698
PUBMED
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 248 Std Error: 0.00
Plate: 10 row: 0 column: 01
Seq primer: T7; GTAATACGACTCATTATAGGC.
FEATURES
source
Location/Qualifiers
1..248
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:185442"
/db_xref="taxon:161934"
/clone="024-010-001"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MPZ-ADIS-024-leaf"
/notes="vector: pCMVSPORT6; Site_1: Sali; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"
ORIGIN
Alignment Scores:
Pred. No.: 1.36e+03 Length: 248
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0
US-10-029-756-20 (1-6) x BQ587416 (1-248)
Qy 1 PheGlnIleGluHisHis 6
|||||
Db 195 TTCGAATTGACATCAT 178
RESULT 11
AL914932
LOCUS AL914932 272 bp mRNA linear EST 06-JUL-2004
DEFINITION AL914932 PJR-Z1+Z2 Danio rerio cDNA clone 147-D03-2, mRNA sequence.
ACCESSION AL914932
VERSION AL914932.1 GI:23180229
EST.
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE
AUTHORS 1 (bases 1 to 272)
Lo,J., Lee,S., Xu,M., Liu,F., Ruan,H., Eun,A., He,Y., Ma,W.,
Wang,W., Wen,Z. and Peng,J.
15000 unique zebrafish EST clusters and their future use in
microarray for profiling gene expression patterns during
embryogenesis
Genome Res. 13 (3), 455-466 (2003)
JOURNAL 22505427
MEDLINE

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PUBMED
COMMENT
    Contact: Peng J
    Lab of Functional Genomics
    Institute of Molecular and Cell Biology
    30 Medical Drive, Singapore, 117609, Singapore
    Email: pengj@imcb.a-star.edu.sg
    Clone requests: info@openbiosystems.com
    Open Biosystems,
    6705 Oodyssey Drive, Huntsville, AL 35806.
    Location/Qualifiers
    1..272
    /organism="Danio rerio"
    /mol_type="mRNA"
    /strain="local wildtype"
    /db_xref="taxon:7955"
    /clone="147-D03-2"
    /tissue.type="whole embryo or fish"
    /dev stage="mixed stages"
    /clone_lib="PUR-Z1+Z2"

FEATURES
    source
    Alignment Scores:
    Pred. No.: 1.52e+03 Length: 272
    Score: 36.00 Matches: 6
    Percent Similarity: 100.00% Conservative: 0
    Best Local Similarity: 100.00% Mismatches: 0
    Query Match: 100.00% Indels: 0
    DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AL914932 (1-272)

Qy 1 PheGlnIleGluHisHis 6
Db 23 TTCCAGATCGAGCATCAT 40

RESULT 12
BQ910596/c
LOCUS
DEFINITION BQ910596 291 bp mRNA linear EST 19-AUG-2002
clone QHA14K08, mRNA sequence.
ACCESSION BQ910596
VERSION BQ910596.1 GI:22309375
KEYWORDS EST.
SOURCE Helianthus annuus (common sunflower)
ORGANISM Helianthus annuus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.
REFERENCE
1 (bases 1 to 291)
Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,
Ellison,P., Kolman,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,
Lai,Z., Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Armstrong Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QH_CA_Contig578, see http://cgdb.ucdavis.edu/
for details.
Plate: QHA14 row: K column: 08.
Location/Qualifiers
1..291
/organism="Helianthus annuus"
/mol_type="mRNA"
/cultivar="RH801"
/db_xref="taxon:4232"

FEATURES
    source
    Alignment Scores:
    Pred. No.: 1.65e+03 Length: 291
    Score: 36.00 Matches: 6
    Percent Similarity: 100.00% Conservative: 0
    Best Local Similarity: 100.00% Mismatches: 0
    Query Match: 100.00% Indels: 0
    DB: 5 Gaps: 0

US-10-029-756-20 (1-6) x BQ910596 (1-291)

Qy 1 PheGlnIleGluHisHis 6
Db 281 TTCCAAATTGAACATCAT 264

RESULT 13
CK855086/c
LOCUS
DEFINITION CK855086 298 bp mRNA linear EST 08-MAR-2004
SWBL3CAW35B12SK Wuchereria bancrofti L3 cDNA (SAW96MLW-WBL3)
Wuchereria bancrofti cDNA clone SWBL3CAW35B12 5', mRNA sequence.
ACCESSION CK855086
VERSION CK855086.1 GI:45243709
KEYWORDS EST.
SOURCE Wuchereria bancrofti
ORGANISM Wuchereria bancrofti
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Wuchereria.
REFERENCE
1 (bases 1 to 298)
Williams,S.A.
Genes Expressed in L3 infective stage larvae of Wuchereria
bancrofti
Unpublished (1999)
Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers
1..298
/organism="Wuchereria bancrofti"
/mol_type="mRNA"
/db_xref="taxon:6293"
/clone="SWBL3CAW35B12"
/dev stage="L3 infective stage larvae"
/lab_host="XLI-Blue MRP"
/clone_lib="Wuchereria bancrofti L3 cDNA (SAW96MLW-WBL3)"
/notes="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2:
Xho I; Lymphatic filarial nematode parasite of humans.
mRNA was prepared from approximately 8,000 L3 isolated
from mosquitoes in Cairo, Egypt and converted to
double-stranded cDNA using reverse transcriptase and
oligo(dT) followed by RNase H and DNA pol I. The library
has 1.0 x 10E6 independent recombinants and the average

```

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/clone="QHA14K08"
/lab_host="E.Coli"
/clone_lib="QH ABCDI sunflower RH801"
/notes="Vector: pBRCNASTAB; The library was constructed
from 11 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG_TISSUE=shoots environmental stress
TAG_LIB=QH ABCDI sunflower RH801
TAG_SEQ=TCGCAACGGG"

ORIGIN
Alignment Scores:
Pred. No.: 1.65e+03 Length: 291
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-029-756-20 (1-6) x BQ910596 (1-291)

Qy 1 PheGlnIleGluHisHis 6
Db 281 TTCCAAATTGAACATCAT 264

RESULT 13
CK855086/c
LOCUS
DEFINITION CK855086 298 bp mRNA linear EST 08-MAR-2004
SWBL3CAW35B12SK Wuchereria bancrofti L3 cDNA (SAW96MLW-WBL3)
Wuchereria bancrofti cDNA clone SWBL3CAW35B12 5', mRNA sequence.
ACCESSION CK855086
VERSION CK855086.1 GI:45243709
KEYWORDS EST.
SOURCE Wuchereria bancrofti
ORGANISM Wuchereria bancrofti
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Wuchereria.
REFERENCE
1 (bases 1 to 298)
Williams,S.A.
Genes Expressed in L3 infective stage larvae of Wuchereria
bancrofti
Unpublished (1999)
Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: pBluescript SK.
Location/Qualifiers
1..298
/organism="Wuchereria bancrofti"
/mol_type="mRNA"
/db_xref="taxon:6293"
/clone="SWBL3CAW35B12"
/dev stage="L3 infective stage larvae"
/lab_host="XLI-Blue MRP"
/clone_lib="Wuchereria bancrofti L3 cDNA (SAW96MLW-WBL3)"
/notes="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2:
Xho I; Lymphatic filarial nematode parasite of humans.
mRNA was prepared from approximately 8,000 L3 isolated
from mosquitoes in Cairo, Egypt and converted to
double-stranded cDNA using reverse transcriptase and
oligo(dT) followed by RNase H and DNA pol I. The library
has 1.0 x 10E6 independent recombinants and the average

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insert size is ~300 bp. The library was constructed by Michelle. Lizotte-Waniewski. The library is available from Dr.S.A.Williams, email: genome@smith.edu."

ORIGIN

Alignment Scores:
Pred. No.: 1.7e+03 Length: 298
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-029-756-20 (1-6) x CK855086 (1-298)

Qy 1 PheGlnIleGluHisHis 6

Db 177 TTTCATATCGAACACCAT 160

RESULT 14

CG091494 300 bp DNA linear GSS 20-AUG-2003
LOCUS PUIMK80TB ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTa0616N15,
DEFINITION genomic survey sequence.
ACCESSION CG091494
VERSION CG091494.1 GI:33973788
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 300)

REFERENCE
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.

TITLE Maize Genomics Consortium

JOURNAL Unpublished (2003)

COMMENT Other GSSs: PUIMK80TD

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: IR

Class: sheared ends.

FEATURES
source

1. .300
Location/Qualifiers
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTa0616N15"
/clone_lib="ZM 0.6 1.0 KB"
/note="vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"

ORIGIN

Alignment Scores:
Pred. No.: 1.71e+03 Length: 300
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-029-756-20 (1-6) x CG091494 (1-300)

Qy 1 PheGlnIleGluHisHis 6

Db 129 TTCCAGATTGACACCAT 112

RESULT 15

AL914933/c

LOCUS

DEFINITION AL914933 PJR-Z1+Z2 Danio rerio cDNA clone 127-F03-2, mRNA sequence.

ACCESSION AL914933

VERSION AL914933.1 GI:23180230

KEYWORDS EST.

SOURCE Danio rerio (zebrafish)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 305)

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Peng J

Lab of Functional Genomics

Institute of Molecular and Cell Biology

30 Medical Drive, Singapore, 117609, Singapore

Email: pengj@imcb.a-star.edu.sg

Clone requests: info@openbiosystems.com

Open Biosystems,

6705 Odyssey Drive, Huntville, AL 35806.

FEATURES
source

1. .305
Location/Qualifiers

/organism="Danio rerio"

/mol_type="mRNA"

/strain="local wildtype"

/db_xref="taxon:7955"

/clone="127-F03-2"

/tissue_type="whole embryo or fish"

/dev_stage="mixed stages"

/clone_lib="PJR-Z1+Z2"

ORIGIN

Alignment Scores:

Pred. No.: 1.75e+03 Length: 305

Score: 36.00 Matches: 6

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AL914933 (1-305)

Qy 1 PheGlnIleGluHisHis 6

Db 141 TTCCAGATCGACCATCAT 124

RESULT 16

CG091498

LOCUS

DEFINITION

PUIMK80TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTa0616N15,

ACCESSION CG091498

VERSION CG091498.1 GI:33973792

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 307)

REFERENCE

AUTHORS

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.

TITLE

Maize Genomics Consortium

```
JOURNAL Unpublished (2003)
COMMENT Other_GSSs: PUIMK807B
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.

FEATURES
source
  Location/Qualifiers
    1..307
      /organism="Zea mays"
      /mol_type="genomic DNA"
      /strain="B73"
      /db_xref="taxon:4577"
      /clone="ZM8BTA0616N15"
      /clone_lib="ZM_0.6-1.0 kb"
      /note="Vector: PCR4-TOPO; Site_1: EcoRI; 0.6-1.0 kb high
      Cot selected genomic DNA library"

ORIGIN
Alignment Scores:
Pred. No.: 1.76e+03 Length: 307
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-029-756-20 (1-6) x CG091498 (1-307)

Qy 1 PheGlnIleGluHisHis 6
Db 165 TTCAGATTGAGCACCAT 182

RESULT 17
CR464551/c 309 bp mRNA linear EST 01-JUL-2004
LOCUS LIONp463C10369 3', mRNA sequence.
DEFINITION
ACCESSION CR464551
VERSION CR464551.1 GI:49596900
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 309)
AUTHORS Henrich,J., Hermanns,J., Kranz,H., Loebbert,R., Schlueter,T.,
Schuette,D., Weindel,M., Heil,O., Ebert,L., Neubert,P., Peters,M.,
Radelof,U., Schneider,D. and Korn,B.
Rat ArrayTAG CDNA
Unpublished (2004)
CONTACT: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
RP: CAGGAACAGCTATGAC.

FEATURES
Location/Qualifiers
  1..309
    /organism="Rattus norvegicus"
    /mol_type="mRNA"
    /db_xref="taxon:10116"
    /clone="LIONp463C10369"
    /lab_host="DH10B"
    /clone_lib="Rat pBluescript Lion"

source
  1..309
    /organism="Rattus norvegicus"
    /mol_type="mRNA"
    /db_xref="taxon:10116"
    /clone="LIONp463C10369"
    /lab_host="DH10B"
    /clone_lib="Rat pBluescript Lion"

ORIGIN
Alignment Scores:
Pred. No.: 1.78e+03 Length: 309
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-029-756-20 (1-6) x CR464551 (1-309)

Qy 1 PheGlnIleGluHisHis 6
Db 306 TTCAGATTGAGCACCAC 289

RESULT 18
BI432070 316 bp mRNA linear EST 30-APR-2003
LOCUS EST534831 P. infestans-challenged potato leaf, compatible reaction
DEFINITION Solanum tuberosum cDNA clone PPCAL91 5' sequence, mRNA sequence.
ACCESSION BI432070
VERSION BI432070.1 GI:15256760
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 316)
AUTHORS Restrepo,S., Griffiths,H.M., Smart,C.D., Cho,J., Chienmingo,A.,
Bougril,O., Buell,C.R., Ronning,C.M., Fry,W.E. and Baker,B.
Generation of ESTs from Potato Leaves Challenged with Phytophthora
infestans, Compatible Interaction
Unpublished (2000)
CONTACT: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
This clone can be obtained from the University of Arizona Genomics
Institute. Orders can be made through URL:
http://genome.arizona.edu/orders/
Seq primer: M13F-R.

FEATURES
Location/Qualifiers
  1..316
    /organism="Solanum tuberosum"
    /mol_type="mRNA"
    /cultivar="kennebec"
    /db_xref="taxon:4113"
    /clone="PPCAL91"
    /tissue_type="leaf"
    /dev_stage="6 week old"
    /lab_host="SOLR"
    /clone_lib="P. infestans-challenged potato leaf,
    compatible reaction"
    /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
    XhoI; supplier: Cornell University, Fry lab; sequencing:
    The Institute for Genomic Research; Whole plants were
    challenged with 20,000 sporangia/ml of the compatible P.
    infestans isolate US 940480. Leaf tissue was collected at
    3, 6, 9, 12, 24, 48, 72 hours after inoculation and frozen
    in liquid nitrogen immediately upon removal. Kennebec
    plants showed first symptoms of infection at 48 hours
    after inoculation. NOTE: We cannot exclude the
    possibility that this sequence is actually derived from
    Phytophthora rather than potato."
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ORIGIN
Alignment Scores:
Pred. No.: 1.82e+03 Length: 316
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x B1432070 (1-316)

Qy 1 PheGlnIleGluHisHis 6
Db 196 TTTCAGATTGAGCATCAT 213

RESULT 19
LOCUS B1011761 317 bp mRNA linear EST 13-JUN-2001
DEFINITION CM3-EN0049-050201-714-c08 EN0049 Homo sapiens cDNA, mRNA sequence.
ACCESSION B1011761
VERSION B1011761.1 GI:14415832
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 317)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&tl2=CM3-EN0049-050201-714-c08&tl3=2001-02-05&tl4=1)
Seq primer: puc 18 forward
High quality sequence start: 28
High quality sequence stop: 317.
FEATURES
source
location/Qualifiers
1. 317
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="EN0049"
/note="Organ: lung normal; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORFES PCR (O.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
Alignment Scores:
Pred. No.: 1.83e+03 Length: 317
Score: 36.00 Matches: 6

```

```

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x B1011761 (1-317)

Qy 1 PheGlnIleGluHisHis 6
Db 195 TTTCAGATTGAGCACAC 212

RESULT 20
LOCUS CD552411 325 bp mRNA linear EST 11-JUN-2003
DEFINITION B0342D11-5 NIA Mouse E9.5 Whole Embryo cDNA Library (Long) Mus musculus cDNA clone NIA:B0342D11 IMAGE:30433102 5', mRNA sequence.
ACCESSION CD552411
VERSION CD552411.1 GI:31600142
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 325)
AUTHORS Piao,Y., KO,N.T., Lim,M.K. and Ko,M.S.H.
TITLE Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification method
JOURNAL Genome Res. 11 (9), 1553-1558 (2001)
MEDLINE 21429098
PUBMED 11544199
COMMENT Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: B0342 row: D column: 11
Seq primer: M13 Reverse
High quality sequence stop: 325
POLYA=No.
FEATURES
source
location/Qualifiers
1. 325
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="nia:EST:B0342D11-5"
/db_xref="taxon:10090"
/clone="NIA:B0342D11 IMAGE:30433102"
/tissue_type="E9.5 whole embryo"
/dev_stage="whole embryo including extraembryonic tissues at 9.5-days postcoitum"
/lab_host="DH10B"
/clone_lib="NIA Mouse E9.5 Whole Embryo cDNA Library (Long)"
/note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 16 embryos at 9.5-days postcoitum. Double-stranded cDNAs were synthesized with an Oligo(dT) primer (Invitrogen: 5'-pGACTAGTTCTAGATCGGAGCGCCGCTTTT-TTTT-3') from 6.1 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lone-linker LL-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into

```



```
library"
/mol_type="mRNA"
/strain="70-15"
/db_xref="taxon:105664"
/clone="mg1e1005D12f"
/dev_stage="Infection stage, 48hrs, Subtraction with healthy plant"
/clone_lib="Subtracted Rice blast Infection Stage cDNA library"
/notes="Vector: pBluescriptII SK(+) Vector; Rice blast infection stage mRNA population at 48 hrs after inoculation was subtracted with mRNA population of healthy plant."
```

ORIGIN

Alignment Scores: 1.97e+03 Length: 337
Pred. No.: 36.00 Matches: 6
Score: 36.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x AW070147 (1-337)

Qy 1 PheGlnIleGluHis 6
Db 93 TTCCAATCGAGCACCAT 76

RESULT 23

BQ329017/c
LOCUS BQ329017 341 bp mRNA linear EST 17-MAY-2002
DEFINITION CM3-EN0049-301000-436-c08 EN0049 Homo sapiens cDNA, mRNA sequence.
ACCESSION BQ329017
VERSION BQ329017.1 GI:20969093
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 341)
AUTHORS Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-EN0049-301000-436-c08&t3=2000-10-30&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 5
High quality sequence stop: 40.

FEATURES

source
1..341
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"

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/clone_lib="EN0049"  
/notes="Organ: lung normal; Vector: puc18; Site 1: SmaI;  
Site 2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."
```

ORIGIN

Alignment Scores: 2e+03 Length: 341
Pred. No.: 36.00 Matches: 6
Score: 36.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-029-756-20 (1-6) x BQ329017 (1-341)

Qy 1 PheGlnIleGluHis 6
Db 128 TTCAGATTGAGCACCAC 111

RESULT 24

BF926891/c
LOCUS BF926891 354 bp mRNA linear EST 19-JAN-2001
DEFINITION IL5-NT0228-041200-305-a08 NT0228 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF926891
VERSION BF926891.1 GI:12324619
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 354)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Sucher,F., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL5&t2=IL5-NT0228-041200-305-a08&t3=2000-12-04&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 353.

FEATURES

source
1..354
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NT0228"
/notes="Organ: nervous tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under low stringency conditions."

```

ORIGIN
Alignment Scores:
Pred. No.: 2.09e+03 Length: 354
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x BF926891 (1-354)

QY 1 PheGlnIleGluHis 6
Db 348 TTCCAGATTGACACCAC 331

RESULT 25
W67110 357 bp mRNA linear EST 14-JUN-1996
LOCUS me24h09.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA
DEFINITION clone IMAGE:388481 5', mRNA sequence.
ACCESSION W67110
VERSION W67110.1 GI:1375649
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 357)
Matra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lemon,G., Soares,B., Wilson,R. and
Waterson,K.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LBNL; contact the
IMAGE Consortium (info@image.lbnl.gov) for further information.
MGI:240313
Seq primer: ETPRimer
High quality sequence stop: 344.
Location/Qualifiers
1..357
/organism="Mus musculus"
/mol_type="mRNA"
/strain="G57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:388481"
/sex="unknown"
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
/clone_lib="Soares mouse embryo NbME13.5 14.5"
/notes="Vector: pTYT30-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer 15'
TGTTCACATCTGAATGGAGCGCGGAAATTTTTTTTTTTTTTTTTTTT
T 3'), on equal amounts of mRNA from 2 13.5dpc and 2
14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
State Univ. from 2 ]; double-stranded cDNA was ligated to
Eco RI adaptors (Pharmacia), digested with Not I and
cloned into the Not I and Eco RI sites of the modified
pTYT3 vector. Library went through one round of
normalization, and was constructed by Bento Soares and

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M.Fatima Bonaldo. "

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ORIGIN
Alignment Scores:
Pred. No.: 2.11e+03 Length: 357
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-029-756-20 (1-6) x W67110 (1-357)

QY 1 PheGlnIleGluHis 6
Db 322 TTCCAGATTGACACCAC 339

RESULT 26
BH635504 358 bp DNA linear GSS 14-FEB-2002
LOCUS 1008005D06.2BL_y1 1008 - RescueMu Grid 1 Zea mays genomic, genomic
DEFINITION survey sequence.
ACCESSION BH635504
VERSION BH635504.1 GI:18657741
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 358)
Walbot,V.
Maize genomic sequences found using engineered RescueMu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1008005 row: 24
Class: transposon-tagged.
Location/Qualifiers
1..358
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1008 - RescueMu Grid 1"
/notes="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site www.zmldb.iastate.edu and follow the links for
'RescueMu.' Grid 1 was grown at Berkeley in 2001. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

ORIGIN
Alignment Scores:
Pred. No.: 2.12e+03 Length: 358
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0

```

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-10-029-756-20 (1-6) x BHG35504 (1-358)

Qy 1 PheGlnIleGluHis 6
 |||||
 Db 273 TTTCATATAGACACAC 290

RESULT 27
 AI985774/c
 LOCUS
 DEFINITION w120c08.x1 NCI CGAP Utl1 Homo sapiens cDNA clone IMAGE:2508014 3' similar to TR:060427 O60427 BC269730_2.; mRNA sequence.

ACCESSION AI985774
 VERSION AI985774
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 360)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 1662 Std Error: 0.00
 Seq Primer: -40UP from Gibco
 High quality sequence stop: 165.
 Location/Qualifiers
 1. 360
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2508014"
 /tissue_type="well-differentiated endometrial adenocarcinoma, 7 pooled tumors"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Utl1"
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"

ORIGIN
 Alignment Scores:
 Pred. No.: 2.13e+03 Length: 360
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AI985774 (1-360)

Qy 1 PheGlnIleGluHis 6
 |||||
 Db 99 TTCCAGATTGACACCAT 82

RESULT 28
 BY671067
 LOCUS

DEFINITION BY671067 RIKEN full-length enriched, 14.5 days embryo df/df Rathke's pouches Mus musculus cDNA clone K820015K13 3', mRNA sequence.

ACCESSION BY671067.1 GI:27052615
 VERSION EST.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 368)
 Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Saito,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Bruscia,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Sempie,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Varadaraj,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shingawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
 Analysis of the mouse transcriptome based on functional annotation
 Of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 JOURNAL MEDLINE 22354683
 PUBMED 12466851
 COMMENT Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
 Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.: Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Michelle Brinkmeier and Sally Camper (Dept. Human Genetics University of Michigan Medical School 4301 MSRB 3 1500 W. Medical Center Dr. Ann Arbor, MI 48109-0638 USA) whose assistance we gratefully acknowledge.
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

Location/Qualifiers

1..368
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="K820015K13"
/tissue_type="Rathke's pouches"
/dev_stages="14.5 days embryo df/df"
/clone_libs="RIKEN full-length enriched, 14.5 days embryo df/df Rathke's pouches"

ORIGIN

Alignment Scores:
Pred. No.: 2.19e+03 Length: 368
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x BY671067 (1-368)

Oy 1 PheGlnIleGluHis 6
|||||
Db 56 TTCAGATTGACACCAC 73

RESULT 29

AW045920/c

LOCUS

DEFINITION AW045920 376 bp mRNA linear EST 18-SEP-1999
UI-M-BH1-aku-d-02-0-UI.s1 NIH_BMAP_M_S2 Mus musculus cDNA clone
UI-M-BH1-aku-d-02-0-UI 3', mRNA sequence.

ACCESSION AW045920

VERSION AW045920.1 GI:5906449

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 376)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

8889548

Contact: Chin, H

National Institute of Mental Health

6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD

20892-9643, USA

Tel: 301 443 1706

Fax: 301 443 9890

Email: mjest@mail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized amygdala library cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined.

Seg primer: M13 Forward

POLYA=Yes

FEATURES

Location/Qualifiers

1..376
/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clones="UI-M-BH1-aku-d-02-0-UI"

/dev_stages="27-32 days"

/lab_host="DH10B (Life Technologies)"

/clone_libs="NIH_BMAP_M_S2"

/note="Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The NIH BMAP_M_S2 library is a subtracted library derived from NIH_BMAP_M_S1, which in turn is a subtracted library derived from a mixture of normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus). The driver used for subtraction consisted of a pool of 5,000 clones from the NIH_BMAP_M_S1 library and a pool of 2,000 clones obtained from non-normalized and normalized mouse brain spinal cord libraries.

TAG_TISSUE=amygdala

TAG_LIB=NIH_BMAP_M_S2

TAG_SEQ=GTGAG"

ORIGIN

Alignment Scores:
Pred. No.: 2.25e+03 Length: 376
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x AW045920 (1-376)

Oy 1 PheGlnIleGluHis 6

|||||

Db 325 TTCAGATTGACACCAC 308

RESULT 30

BP652482

LOCUS

DEFINITION

BP652482 383 bp mRNA linear EST 27-JUN-2004

BP652482 mRNA sequence.

ACCESSION BP652482

VERSION BP652482.1 GI:49303952

KEYWORDS EST.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1 (bases 1 to 383)

AUTHORS

Seki, M., Narusaka, M., Kamiya, A., Ishida, J., Satou, M., Sakurai, T., Nakajima, M., Enju, A., Akiyama, K., Ono, Y., Muramatsu, M., Hayashizaki, Y., Kawai, J., Carninci, P., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A. and Shinozaki, K.
Functional annotation of a full-length Arabidopsis cDNA collection
Science 296 (5565), 141-145 (2002)

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Motoaki Seki

Plant Functional Genomics Research Group

RIKEN Genomic Sciences Center

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel: 81-298-36-4359

Fax: 81-298-36-3060

Email: msek@rtc.riken.go.jp

reversed clone; Please visit our web site

(<http://pfgc.gsc.riken.go.jp/>) for further details.

FEATURES

source

1..383

/organism="Arabidopsis thaliana"

/mol_type="mRNA"

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/db xref="taxon:3702"
/clone="RAFL19-93-E15"
/tissue_type="mixture of silique and flower"
/lab_host="DH10B"
/clone_lib="RAFL19"
/note="Site 1: BamHI; Site 2: SalI; Subtraction Library"

ORIGIN

Alignment Scores:
Pred. No.:      2.3e+03      Length:      383
Score:          36.00      Matches:      6
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:              2          Gaps:      0

US-10-029-756-20 (1-6) x BP652482 (1-383)

Oy      1 PheGlnIleGluHis 6
Db      247 TTCCAGATAGAACACCAC 264

RESULT 31
LOCUS   AW437559
DEFINITION 78918 MARC 1BOV Bos taurus cDNA 5', mRNA linear EST 25-APR-2001
ACCESSION AW437559
VERSION   AW437559.1 GI:6972865
KEYWORDS  EST.
SOURCE    Bos taurus (cow)
ORGANISM  Bos taurus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
          Bovinae; Bos.
REFERENCE 1 (bases 1 to 385)
AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
          Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
          Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
          Chitko-McKown,C.G., Petrea,G., Holt,I., Karamycheva,S., Liang,P.,
          Quackenbush,J. and Keefe,J.W.
          Sequence evaluation of four pooled-tissue normalized bovine cDNA
          libraries and construction of a gene index for cattle
JOURNAL   Genome Res. 11 (4), 626-630 (2001)
MEDLINE   21180013
PUBMED    11282378
COMMENT   Contact: Smith TPL
          USDA, ARS, US Meat Animal Research Center
          PO Box 166, Clay Center, NE 68933-0166, USA
          Tel: 402 762 4366
          Fax: 402 762 4390
          Email: smith@email.marc.usda.gov
          Single pass sequencing. Bases called and trimmed with phred
          v0.980904.e. Vector identified by cross_match with the -minscore 20
          and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCAGCG
Plate: 42 row: H column: 12
Seq primer: ATTAGGTGACACTATAG.

FEATURES
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1..385
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 1BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from lymph node, ovary,
fat, hypothalamus, and pituitary."

ORIGIN

Alignment Scores:
Pred. No.:      2.31e+03      Length:      385
Score:          36.00      Matches:      6
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:              2          Gaps:      0

US-10-029-756-20 (1-6) x AW437559 (1-385)

Oy      1 PheGlnIleGluHis 6
Db      8 TTCCAGATCGAGCACCACAT 25

RESULT 32
LOCUS   BM702968
DEFINITION UI-E-CLI-afe-f-03-0-UI.r1 UI-E-CLI Homo sapiens cDNA clone
ACCESSION BM702968
VERSION   BM702968.1 GI:19016226
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 386)
AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
          Normalization and subtraction: two approaches to facilitate gene
          discovery
JOURNAL   Genome Res. 6 (9), 791-806 (1996)
MEDLINE   97044477
PUBMED    8889548
COMMENT   Contact: Soares, MB
          Coordinated Laboratory for Computational Genomics
          University of Iowa
          375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
          Tel: 319 335 8250
          Fax: 319 335 9565
          Email: bento-soares@uiowa.edu
          Tissue Procurement: Dr. Gregg Hageman
          cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
          cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
          DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
          Clone Distribution: Researchers may obtain clones from Research
          Genetics (www.resgen.com).
          Seq primer: M13 Reverse.
          Location/Qualifiers
          1..386
          /organism="Homo sapiens"
          /mol_type="mRNA"
          /db_xref="taxon:9606"
          /clone="UI-E-CLI-afe-f-03-0-UI"
          /tissue_type="human retina"
          /dev_stage="adult"
          /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
          /clone_lib="UI-B-CLI"
          /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
          modified polylinker; Site 1: EcoR I; Site 2: Not I;
          UI-B-CLI is a normalized cDNA library containing the
          following tissue(s): retina. The library was constructed
          according to Bonaldo, Lennon and Soares, Genome Research,
          6:791-806, 1996. First strand cDNA synthesis was primed
          with an oligo-dT primer containing a Not I site. Double
          stranded cDNA was ligated to an EcoR I adaptor, digested
          with Not I, and cloned directionally into pT7T3-Pac
          vector. The oligonucleotide used to prime the synthesis of
          first-strand cDNA contains a library tag sequence that is
          located between the Not I site and the (dT)18 tail. The
          sequence tag for this library is CCGCG. This library was
          created for the program, Gene Discovery in the Visual
          System, supported by National Eye Institute (NEI)."
```

```

Alignment Scores:
Pred. No.: 2.32e+03
Score: 36.00
Length: 386
Matches: 6
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 100.00%
Indels: 0
DB: 4
Gaps: 0

US-10-029-756-20 (1-6) x BM702968 (1-386)

QY 1 PheGlnlleGluHis 6
DB 21 TTCACAGTCGACACAC 38

RESULT 33
LOCUS AA428359 387 bp mRNA linear EST 16-OCT-1997
DEFINITION zw32h10.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
IMAGE:771043 5' similar to WP:W08D2.4 CE06559 ;, mRNA sequence.
ACCESSION AA428359
VERSION AA428359.1 GI:2112346
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 387)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
CONTACT: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Putative full length read
The vector to vector length is 423
Seq primer: -28mi3 rev2 ET from Amerham
High quality sequence stop: 348.
FEATURES
source
1..387
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5980917"
/db_xref="taxon:9606"
/clone="IMAGE:771043"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares ovary tumor NbHOT"
/notes="Organ: ovary; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCACTGAAAGTGGAGCGCGGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M.Patima Bonaldo."
ORIGIN
Alignment Scores:
Pred. No.: 2.33e+03
Score: 36.00
Length: 387
Matches: 6
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 100.00%
Indels: 0
DB: 4
Gaps: 0

US-10-029-756-20 (1-6) x BM702968 (1-386)

QY 1 PheGlnlleGluHis 6
DB 21 TTCACAGTCGACACAC 38

RESULT 33
LOCUS AA428359 387 bp mRNA linear EST 16-OCT-1997
DEFINITION zw32h10.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
IMAGE:771043 5' similar to WP:W08D2.4 CE06559 ;, mRNA sequence.
ACCESSION AA428359
VERSION AA428359.1 GI:2112346
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 387)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
CONTACT: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Putative full length read
The vector to vector length is 423
Seq primer: -28mi3 rev2 ET from Amerham
High quality sequence stop: 348.
FEATURES
source
1..387
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5980917"
/db_xref="taxon:9606"
/clone="IMAGE:771043"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares ovary tumor NbHOT"
/notes="Organ: ovary; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCACTGAAAGTGGAGCGCGGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M.Patima Bonaldo."
ORIGIN
Alignment Scores:
Pred. No.: 2.33e+03
Score: 36.00
Length: 387
Matches: 6
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 100.00%
Indels: 0
DB: 4
Gaps: 0

US-10-029-756-20 (1-6) x AA428359 (1-387)

QY 1 PheGlnlleGluHis 6
DB 94 TTCACAGTCGACACAT 111

RESULT 34
LOCUS BH635847 387 bp DNA linear GSS 14-FEB-2002
DEFINITION 1008007E01.1EL_y1 1008 - RescueMu Grid I Zea mays genomic, genomic
survey sequence.
ACCESSION BH635847
VERSION BH635847.1 GI:18658084
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE 1 (bases 1 to 387)
AUTHORS Walbot,V.
TITLE Maize genomic sequences found using engineered RescueMu transposon
JOURNAL Unpublished (2001)
COMMENT Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1008007 row: 24
Class: transposon-tagged.
LOCATION/Qualifiers
1..387
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="adult"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1008 - RescueMu Grid I"
/notes="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site www.zmldb.iastate.edu and follow the links for
'RescueMu'. Grid I was grown at Berkeley in 2001. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."
ORIGIN
Alignment Scores:
Pred. No.: 2.33e+03
Score: 36.00
Length: 387
Matches: 6
Percent Similarity: 100.00%
Conservative: 0
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 100.00%
Indels: 0
DB: 8
Gaps: 0

US-10-029-756-20 (1-6) x BH635847 (1-387)

QY 1 PheGlnlleGluHis 6
DB 229 TTTCAAATAGACACAC 246

```



```

RESULT 35
BE097869/c
LOCUS
DEFINITION
UI-R-B01-aqc-h-02-0-UI.s1 UI-R-B01 Rattus norvegicus cDNA clone
UI-R-B01-aqc-h-02-0-UI 3', mRNA sequence.
ACCESSION
BE097869
VERSION
BE097869.1 GI:8488800
KEYWORDS
EST.
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 388)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
9704477
MEDLINE
8889548
PUBMED
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9585
Email: bento-soares@uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
normalized hypothalamus library cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA-Yes.
FEATURES
source
1..388
Location/Qualifiers
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-B01-aqc-h-02-0-UI"
/dev_stage="adult"
/lab_host="DHI0B (Life Technologies)"
/clone_lib="UI-R-B01"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The library
(UI-R-B01) is a subtracted library derived from a mixture
of the following tissues: thalamus, cerebellum,
hypothalamus, medulla, pons, midbrain, cerebral
corpus striatum and hippocampus. For a detailed
description of the library from which this clone was
derived, please visit our web site at
ratest.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)
TAG_TISSUE=hypothalamus
TAG_LIB=UI-R-B01
TAG_SEQ=GATGC"
ORIGIN
Alignment Scores:
Pred. No.: 2,346+03 Length: 388
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 2
US-10-029-756-20 (1-6) x BE097869 (1-388)

```

```

Qy 1 PheGlnIleGluHisHis 6
|||||
337 TTCCAGATTGACACCAC 320

RESULT 36
CB774012
LOCUS
DEFINITION
CB774012 393 bp mRNA linear EST 16-MAY-2003
MRPE4-00130-f3 5', mRNA sequence.
ACCESSION
CB774012
VERSION
CB774012.1 GI:29862403
KEYWORDS
EST.
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 393)
Angen EST Program.
Angen Rat EST Program
Unpublished (2003)
JOURNAL
Contact: Dan Fitzpatrick
Angen, Inc
One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00130 row: f column: 3.
FEATURES
source
1..393
Location/Qualifiers
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="mrpe4-00130-f3"
/tissue_type="placenta embryo"
/clone_lib="mrpe4 (10380)"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI;
placenta embryo day 17"
ORIGIN
Alignment Scores:
Pred. No.: 2,37e+03 Length: 393
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-10-029-756-20 (1-6) x CB774012 (1-393)

Qy 1 PheGlnIleGluHisHis 6
|||||
361 TTCCAGATTGACACCAC 378

RESULT 37
AA279631
LOCUS
DEFINITION
AA279631 398 bp mRNA linear EST 15-AUG-1997
z886h09.r1 NCI CGAP GCBI Homo sapiens cDNA clone IMAGE:704417 5',
similar to WP:W08D2.4 CE06559 ;, mRNA sequence.
ACCESSION
AA279631
VERSION
AA279631.1 GI:1921149
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 398)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
This clone is available royalty-free through LLNL ; contact the

```


IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 790 Std Error: 0.00
 Seq primer: -28mi3 rev2 ET from Amerham
 High quality sequence stop: 369.

FEATURES

source
 1..398
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:704417"
 /tissue_type="germinal center B cell"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP_GCB1"

/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, Igp-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer
 [5'-TGTTACCAATCTGAAGTGGAGCGCGCTCATTTTTTTTTTTT-3', 1. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Alignment Scores:
 Pred. No.: 2.41e+03 Length: 398
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AA279631 (1-398)

Qy 1 PheGlnIleGluHisHis 6
 Db 153 TTCAGATCGAGCACCAC 170

RESULT 38

BM716358
 LOCUS BM716358 402 bp mRNA linear EST 28-FEB-2002
 DEFINITION UI-E-C11-age-i-20-0-UI.r2 UI-E-C11 Homo sapiens cDNA clone
 UI-E-C11-age-i-20-0-UI 5', mRNA sequence.

ACCESSION BM716358.1 GI:19029616
 VERSION BM716358.1
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS 1 (bases 1 to 402)

Bonaldo, M.F., Lennon, G. and Soares, M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Dr. Gregg Hageman

cDNA Library prepared by: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

Cloning Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research

Genetics (www.resgen.com).
 Seq primer: M13 Reverse.

Location/Qualifiers

FEATURES

source

1..402

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clones="UI-E-C11-age-i-20-0-UI"

/tissue_type="RPE and Choroid"

/dev stage="adult"

/lab_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone_lib="UI-E-C11"

/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: Eco RI; Site 2: Not I;

UI-E-C11 is a normalized cDNA library containing the

following tissue(s): RPE and Choroid. The library was

constructed according to Bonaldo, Lennon and Soares,

Genome Research, 6:791-806, 1996. First strand cDNA

synthesis was primed with an oligo-dT primer containing a

Not I site. Double stranded cDNA was ligated to an EcoRI

adaptor, digested with Not I, and cloned directionally

into pT73-Pac vector. The oligonucleotide used to prime

the synthesis of first-strand cDNA contains a library tag

sequence that is located between the Not I site and the

(dT)18 tail. The sequence tag for this library is ACCGA.

This library was created for the program, Gene Discovery

in the Visual System, supported by National Eye Institute

(NEI)."

ORIGIN

Alignment Scores:
 Pred. No.: 2.44e+03 Length: 402
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x BM716358 (1-402)

Qy 1 PheGlnIleGluHisHis 6

Db 358 TTCAGATTGAGCACCAC 375

RESULT 39

BF079544

LOCUS BF079544 408 bp mRNA linear EST 18-OCT-2000

DEFINITION 230188 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.

ACCESSION BF079544

VERSION BF079544.1 GI:10873383

KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 408)

AUTHORS Fahrenkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J.,

Vallet, J., Wise, T., Rohrer, G.A., Pertea, G., Sultana, R.,

Quackenbush, J., and Keeler, J.W.

TITLE Porcine gene discovery by normalized cDNA-library sequencing and

EST cluster assembly

JOURNAL Mamm. Genome 13 (8), 475-478 (2002)

MEDLINE 22213789

PUBMED 12226715

COMMENT Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred

v0.980904.e. Vector identified by cross_match with the -minscore 18

and -mismatch 12 options.

PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCCTCAGTACGACG
 Plate: 46 row: G column: 17
 Seq primer: ATTAGGTGACATATAG.
 Location/Qualifiers
 1..408
 /organism="Sus scrofa"
 /mol_type="mRNA"
 /db_xref="taxon:9823"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="WARC 2PIC"

FEATURES

source

/note="vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
 Library made from pooled tissue from testis, ovary,
 endometrium, hypothalamus, pituitary, and placenta."

ORIGIN

Alignment Scores:
 Pred. No.: 2.48e+03 Length: 408
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x BF079544 (1-408)

Qy 1 PheGlnIleGluHis 6
 |||||
 Db 135 TTCCAGATTGAGCACCAC 152

RESULT 40

CB338121/c

LOCUS

DEFINITION kb62g09.y1 Brugia malayi L3 pAMP1 v2 Brugia malayi cDNA 5' similar
 to TR:O61388 O61388 DELTA6-FATTY-ACID-DESATURASE. [2] TR:Q23221 ;
 mRNA sequence.

ACCESSION

VERSION CB338121.1 GI:28940283

KEYWORDS

SOURCE EST.

ORGANISM

Brugia malayi
 Brugia malayi
 Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 Onchocercidae; Brugia.

REFERENCE

AUTHORS

1 (bases 1 to 408)
 McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
 Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,
 Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,
 Tsagariehvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
 Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,
 Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
 McCann,R., Waterston,R. and Wilson,R.
 The Washington Univ. Nematode EST Project, 1999
 Unpublished (1999)

TITLE

JOURNAL

COMMENT

Contact: McCarter JP
 The Washington Univ. Nematode EST Project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: est@watson.wustl.edu
 Nematodes were provided by Dr. Ben-Wen Li and Dr. Gary Weil of
 Washington University, St. Louis, MO (weillab@imgate.wustl.edu).
 Possible reversed clone: similarity on wrong strand
 Seq primer: -40RP from Gibco.

FEATURES

source

1..408
 /organism="Brugia malayi"
 /mol_type="mRNA"
 /db_xref="taxon:6279"
 /dev_stage="L3"
 /lab_host="DH10B"

/clone_lib="Brugia malayi L3 pAMP1 v2"
 /note="vector: pAMP1(Invitrogen); Site 1: NotI; Site 2:
 SalI; The library was constructed by Amy Rush, Claire
 Murphy and Dr. James McCarter at Washington University,
 St. Louis. The cDNA was made by using Dynabead oligo-dT
 priming (Dyna). PCR based library using a modified
 protocol from the SMART PCR cDNA Synthesis Kit from
 Clontech. Directionally cloned into the UDG sites of
 pAMP1. Nematodes were provided by Dr. Ben-Wen Li and Dr.
 Gary Weil of Washington University, St. Louis, MO
 (weillab@imgate.wustl.edu)."

ORIGIN

Alignment Scores:
 Pred. No.: 2.48e+03 Length: 408
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x CB338121 (1-408)

Qy 1 PheGlnIleGluHis 6

|||||
 Db 184 TTTCAGATTGAGCACCAC 167

RESULT 41

BP664452

LOCUS

DEFINITION BP664452 RAFL21 Arabidopsis thaliana cDNA clone RAFL21-12-G01 3',
 mRNA sequence.

ACCESSION

VERSION BP664452.1 GI:49315922

KEYWORDS

SOURCE EST.

ORGANISM

Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

AUTHORS

1 (bases 1 to 410)
 Seki,M., Narusaka,M., Kamiya,A., Ishida,J., Satou,M., Sakurai,T.,
 Nakajima,M., Enju,A., Akiyama,K., Ono,Y., Muramatsu,M.,
 Hayashizaki,Y., Kawai,J., Carninci,P., Itoh,M., Ishii,Y.,
 Arakawa,T., Shibata,K., Shinagawa,A. and Shinozaki,K.
 Functional annotation of a full-length Arabidopsis cDNA collection
 Science 296 (5565), 141-145 (2002)

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Motoaki Seki
 Plant Functional Genomics Research Group
 RIKEN Genomic Sciences Center
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-4359
 Fax: 81-298-36-9060

Email: mseki@tc.riken.go.jp
 reversed clone; please visit our web site
 (http://pfgweb.gsc.riken.go.jp/) for further details.

FEATURES

source

1..410
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /db_xref="taxon:3702"
 /clone="RAFL21-12-G01"
 /lab_host="DH10B"
 /clone_lib="RAFL21"

/note="Site 1: BamHI; Site 2: SalI; Subtraction Library.
 The sequence was obtained from samples subjected to
 various stress and plant hormones-treated"

ORIGIN

Alignment Scores:

Pred. No.: 2.5e+03 Length: 410

Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 5 Gaps: 0

US-10-029-756-20 (1-6) x BP664452 (1-410)

Qy 1 PheGlnIleGluHis 6

Db 331 TTTCAATCGACACAC 348

RESULT 42

CB803565 410 bp mRNA linear EST 16-MAY-2003
 LOCUS AMGNNUC:MRPE4-00118-B12-A mrpe4 (10380) Rattus norvegicus cDNA
 DEFINITION clone mrpe4-00118-b12 5', mRNA sequence.

ACCESSION CB803565

VERSION CB803565.1 GI:29918875

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

REFERENCE 1 (bases 1 to 410)

AUTHORS Angen EST Program.

TITLE Angen Rat EST Program

JOURNAL Unpublished (2003)

COMMENT Contact: Dan Fitzpatrick

Angen, Inc

One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA

Tel: 805 447-4881

Plate: 00118 row: b column: 12.

FEATURES

source
 1..410
 Location/Qualifiers
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /db_xref="taxon:10116"
 /clone="mrpe4-00118-b12"
 /tissue_type="placenta embryo"
 /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI;
 placenta embryo day 17"

ORIGIN

Alignment Scores:
 Pred. No.: 2.5e+03 Length: 410
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x CB803565 (1-410)

Qy 1 PheGlnIleGluHis 6

Db 328 TTCAGATTGACACAC 345

RESULT 43

BE019170 411 bp mRNA linear EST 06-JUN-2000
 LOCUS BE019170
 DEFINITION bb49d08.y1 NIH MGC 17 Homo sapiens cDNA clone IMAGE:3009999 5',
 similar to TR:060427 060427 BC269730 2. i, mRNA sequence.

ACCESSION BE019170

VERSION BE019170.1 GI:8279231

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 411)

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Other ESTs: bb49d08.x1

Contact: Robert Strausberg, Ph.D.

Email: sgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

image.llnl.gov/image/html/iresources.shtml

Seq primer: -40RP from Gibco

High quality sequence stop: 282.

FEATURES

source

1..411

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3009999"

/tissue_type="rhabdomyosarcoma"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_17"

/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;

Site_2: XhoI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Size-selected >500bp

for average insert size 1.8kb. Library constructed by

Ling Hong in the laboratory of Gerald M. Rubin (University

of California, Berkeley) using ZAP-cDNA synthesis kit

(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

US-10-029-756-20 (1-6) x BE019170 (1-411)

Qy 1 PheGlnIleGluHis 6

Db 229 TTCAGATTGACACCAT 246

RESULT 44

BQ491147/c

LOCUS BQ491147

DEFINITION BQ491147

ACCESSION BQ491147

VERSION BQ491147.1 GI:24434615

KEYWORDS EST.

SOURCE

ORGANISM

Paracoccidioides brasiliensis

Eukaryota; Fungi; Ascomycota;

Onygenales; mitosporic Onygenales;

Paracoccidioides.

REFERENCE 1 (bases 1 to 413)

AUTHORS

Goldman,G.H., dos Reis Marques,E.,

Bernardes,L.A., Qutapin,A.C.,

Seniglini,C.P., de Oliveira,R.C.,

Puccia,R., Batista,W.L.,

Bogossian,A.P., Tekala,F.,

Goldman,M.H.

Expressed sequence tag analysis of the human pathogen

Paracoccidioides brasiliensis yeast phase: identification of

putative homologues of Candida albicans virulence and pathogenicity

genes

Eukaryot. Cell 2 (1), 34-48 (2003)

Contact: Gustavo Henrique Goldman

Laboratory of Molecular Biology

Universidade de Sao Paulo - USP - FCFRP
Av do Cafe S/N, CEP: 14040-903, Ribeirao Preto - SP, Brazil
Email: ggoldman@usp.br.

FEATURES

Location/Qualifiers

1. .413
/organism="Paracoccidoides brasiliensis"
/mol_type="mRNA"
/db_xref="taxon:121759"
/clone_lib="PB0001"

ORIGIN

Alignment Scores:
Pred. No.: 2.52e+03 Length: 413
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-029-756-20 (1-6) x BQ491147 (1-413)

Qy 1 PheGlnIleGluHisHis 6

Db 170 TTCCAGATTGACATCAT 153

RESULT 45

BB783485
LOCUS BB783485 RIKEN full-length enriched, brain CRL-1443 BC3H1 CDNA Mus
DEFINITION musculus CDNA clone G43008K22 3', mRNA sequence.

ACCESSION BB783485

VERSION BB783485.1 GI:16951981

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 414)

Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,

Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K.,

Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,

Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R.,

Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N.,

Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,

Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,

Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A.,

Muramatsu,M. and Hayashizaki,Y.

RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
2001)

Unpublished (2001)

JOURNAL

COMMENT

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsr.riken.jp, URL:http://genome.gsc.riken.jp/

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,

Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,

Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,

Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.

and Hayashizaki,Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,

Sugahara,Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.

e mouse tissues.

FEATURES

source

Location/Qualifiers
1. .414
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C3H"
/db_xref="taxon:10090"
/clone="G43008K22"
/tissue_type="brain"
/cell_line="CRL-1443 BC3H1"
/clone_lib="RIKEN full-length enriched, brain CRL-1443
BC3H1 CDNA"

ORIGIN

Alignment Scores:
Pred. No.: 2.52e+03 Length: 414
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x BB783485 (1-414)

Qy 1 PheGlnIleGluHisHis 6

Db 29 TTCCAGATTGACACCAC 46

RESULT 46

AU283982/c

LOCUS AU283982

DEFINITION AU283982 Molgula tectiformis library Molgula tectiformis cDNA clone

MT08B2G01R 5', mRNA sequence.

ACCESSION AU283982.1 GI:26023516

KEYWORDS EST.

SOURCE Molgula tectiformis

ORGANISM Molgula tectiformis

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;

Stolidobranchia; Molguliidae; Molgula.

1 (bases 1 to 416)

Takada,N., Murakami,S.D., Swalla,B.J. and Satch,N.

EST analysis of tailless ascidian M. tectiformis

Unpublished (2002)

Contact: Seiko D. Murakami

Graduate School of Science, Department of Zoology

Kyoto University

Sakyo-ku, Kyoto 606-8502, Japan

Tel: 81-75-753-4095

Fax: 81-75-705-1113

Email: seiko@ascidian.zool.kyoto-u.ac.jp.

Location/Qualifiers

1. .416

/organism="Molgula tectiformis"

/mol_type="mRNA"

/db_xref="taxon:30286"

/clones="MT08B2G01R"

/clone_lib="Molgula tectiformis library"

Alignment Scores:

Pred. No.: 2.54e+03 Length: 416

Score: 36.00 Matches: 6

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AU283982 (1-416)

```

OY      1 PheGlnIleGluHis 6
DB      410 TTCCAAATCGAACACCAT 393

RESULT 47
LOCUS   AA430733
DEFINITION zw20g08.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
IMAGE:769886 5' similar to WP:W08D2.4 CE06559 ;, mRNA sequence.
ACCESSION AA430733
VERSION   AA430733
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens

REFERENCE
AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
          Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
          Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
          White,Y., Wylie,T., Waterston,R. and Wilson,R.
          WashU-Merck EST Project 1997
          Unpublished (1997)
          Contact: Wilson RK
          Washington University School of Medicine
          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
          Tel: 314 286 1800
          Fax: 314 286 1810
          Email: est@watson.wustl.edu
          This clone is available royalty-free through LLNL ; contact the
          IMAGE Consortium (info@image.llnl.gov) for further information.
          Seq primer: -28ml3 rev2 ET from Amersham.

FEATURES
source
1..418
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5973761"
/db_xref="taxon:9606"
/clone="IMAGE:769886"
/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares ovary tumor NbHOT"
/note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAGTGGAGCGCGGTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7T3 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."

ORIGIN
Alignment Scores:
Pred. No.: 2.55e+03 Length: 418
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AA430733 (1-418)

OY      1 PheGlnIleGluHis 6
DB      95 TTCCAGATTGACACCAT 112

RESULT 48
LOCUS   AA488546
DEFINITION ab37g09.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone

IMAGE:843040 5' similar to WP:W08D2.4 CE06559 ;, mRNA sequence.
ACCESSION AA488546
VERSION   AA488546
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens

REFERENCE
AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
          Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
          Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
          White,Y., Wylie,T., Waterston,R. and Wilson,R.
          WashU-NCI human EST Project
          Unpublished (1997)
          Contact: Wilson RK
          Washington University School of Medicine
          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
          Tel: 314 286 1800
          Fax: 314 286 1810
          Email: est@watson.wustl.edu
          This clone is available royalty-free through LLNL ; contact the
          IMAGE Consortium (info@image.llnl.gov) for further information.
          Insert Length: 656 Std Error: 0.00
          Seq primer: -28ml3 rev1 ET from Amersham
          High quality sequence stop: 359.
          Location/Qualifiers
            1..418
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:843040"
              /sex="female"
              /dev_stage="HeLa S3 cell line"
              /lab_host="SOLR (kanamycin resistant)"
              /clone_lib="Stratagene HeLa cell s3 937216"
              /note="Vector: pBluescript SK-; Site_1: SmaI; Site_2:
              XhoI; Cloned unidirectionally. Primer: Oligo dT. HeLa S3
              epithelioid carcinoma cells grown to semi-confluency
              without induction. Average insert size: 1.5 kb; Uni-ZAP XR
              Vector. -5' adaptor sequence: 5' GAATTCGGCAGG 3' -3'
              adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

ORIGIN
Alignment Scores:
Pred. No.: 2.55e+03 Length: 418
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AA488546 (1-418)

OY      1 PheGlnIleGluHis 6
DB      246 TTCCAGATTGACACCAT 263

RESULT 49
LOCUS   CB764557
DEFINITION AMGNNUC:MRPE4-00118-B11-A mrpe4 (10380) Rattus norvegicus cDNA
clone mrpe4-00118-b11 5', mRNA sequence.
ACCESSION CB764557
VERSION   CB764557
KEYWORDS  EST.
SOURCE    Rattus norvegicus (Norway rat)
ORGANISM  Rattus norvegicus

REFERENCE
AUTHORS   Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
          Rattus norvegicus
          Rattus norvegicus
          Rattus norvegicus
          Rattus.
          1 (bases 1 to 419)
          Amgen EST Program.

```

```

TITLE      Angen Rat EST Program
JOURNAL    Unpublished (2003)
COMMENT    Contact: Dan Fitzpatrick
          Angen, Inc
          One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
          Tel: 805 447-4881
          Plate: 00118 row: b column: 11.
FEATURES   Location/Qualifiers
            source
              1..419
                /organism="Rattus norvegicus"
                /mol_type="mRNA"
                /db_xref="taxon:10116"
                /clone="mrpe4-00118-b11"
                /tissue_type="placenta embryo"
                /clone_lib="mrpe4 (10380)"
                /note="vector: pSPOR1; Site_1: SalI; Site_2: NotI;
                placenta embryo day 17"

ORIGIN
Alignment Scores:
Pred. No.:      2.56e+03      Length:      419
Score:          36.00         Matches:      6
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:     100.00%     Indels:      0
DB:              6           Gaps:       0

US-10-029-756-20 (1-6) x CB764557 (1-419)

Qy      1 PheGlnIleGluHisHis 6
      |||||
Db      317 TTCCAGATTGAACACCAC 334

RESULT 50
AW297013/c      420 bp mRNA linear EST 16-JAN-2000
LOCUS          UI-H-BW0-ajf-d-04-0-UI-s1 NCI CGAP_Sub6 Homo sapiens cDNA clone
DEFINITION     IMAGE:2731447 3', mRNA sequence.
ACCESSION     AW297013
VERSION       AW297013.1 GI:6703649
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 420)
              NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
              National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
              Tumor Gene Index
              Unpublished (1997)
              Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-remail.nih.gov
              The sequence contained an oligo-dt track that was present in the
              oligonucleotide that was used to prime the synthesis of first
              strand cDNA and therefore this may represent a bonafide poly A
              tail. cDNA library preparation: M.B. Soares Lab Clone distribution:
              NCI-CGAP clone distribution information can be found through the
              I.M.A.G.E. Consortium/BLN at:
              www-bio.lnl.gov/bbrp/image/image.html
              Seq primer: M13 Forward
              POLYA=Yes.
FEATURES   Location/Qualifiers
            1..420
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /clone="IMAGE:2731447"
              /lab_host="DH10B (Life Technologies)"
              /clone_lib="NCI-CGAP Sub6"
              /note="vector: p7T3D-pac (Pharmacia) with a modified
              polylinker; Site 1: Not I; Site 2: Eco RI; NCI CGAP Sub6
              is a subtracted library derived from BW, which consists of
              a mixture of four normalized libraries: NCI_CGAP_Brn50,

```

```

NCI CGAP Lul3, NCI CGAP Ov18, GBC1. The NCI CGAP Sub6
library had 7 million recombinants. A single-stranded DNA
preparation of BW was used as a tracer in a subtractive
hybridization with a driver comprising: the IMAGE pool
(NCI_CGAP_Kid3 pool 1 LLAM 3334-3337, 3682-3683,
3798-3803 (IMAGE Clones 132376-1323911,
1456008-1456775, 1500552-1502855); NCI CGAP Kid5 pool 1
LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE Clones
1323912-1325831, 1471368-1472903, 1492104-1493255);
NCI_CGAP_Lu5 pool 1 LLAM 3575-3582, 3851-3854 (IMAGE
Clones 1414920-1417991, 1520904-1522439); NCI_CGAP_CC4
pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE
Clones 1257096-1258631, 1469064-1470983,
1475592-1476743); NCI CGAP Pr22 pool 1 LLAM 2457-2459,
2758-2759, 3062-3068 (IMAGE Clones 985608-986759,
1101192-1101959, 1217928-1220615); NCI_CGAP_Co10 pool 1
LLAM 2644-2653, 2871-2872 (IMAGE Clones
1057416-1061255, 1144584-1145351). (50% of the driver
population), plus a pool of 3,840 arrayed clones from
NCI CGAP Sub1 (IMAGE Clones 2708616-2710535) and
NCI_CGAP_Sub2 (IMAGE Clones 2710536-2712455) (20% of
the driver population), plus a pool of 11,136 clones from
NCI_CGAP_Sub3 (IMAGE Clones 2712456-2723591) (30% of
the driver population). Subtraction was performed as
previously described [Bonaldo, Lennon & Soares (1996):
Normalization and Subtraction: Two Approaches To
Facilitate Gene Discovery. Genome Research 6, 791-806.
TAG_TISSUE=lung
TAG_LIB=NCI_CGAP-Lul3
TAG_SEQ=GCCGG"

```

ORIGIN

```

Alignment Scores:
Pred. No.:      2.57e+03      Length:      420
Score:          36.00         Matches:      6
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:     100.00%     Indels:      0
DB:              2           Gaps:       0

```

US-10-029-756-20 (1-6) x AW297013 (1-420)

Qy 1 PheGlnIleGluHisHis 6

|||||

Db 414 TTCCAGATTGAACACCAC 397

RESULT 51

CF140245

LOCUS

DEFINITION UI-HF-CB0-abg-h-09-0-UI.r1 NIH_MGC_210 Homo sapiens cDNA clone

CF140245

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 421)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Tim Ratliff

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/humanfl.html>
 Seq primer: pYX-5.

FEATURES

source
 Location/Qualifiers

1..421
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3097937"
 /tissue_type="CNCAP(3)T-225 cell line"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_lib="NIH MGC 210"

/note="Organ: Prostate; Vector: pT7T3 Pac; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into pT7T3 Pac vector. The library tag sequence located between the Not I site and the polyA tail is CCCAC. Tissue was provided by Tim Ratliff."

ORIGIN

Alignment Scores:
 Pred. No.: 2.58e+03 Length: 421
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-10-029-756-20 (1-6) x CF140245 (1-421)

Qy 1 PheGlnIleGluHis 6
 |||||
 Db 198 TTCCAGATTGAGCACCAC 215

RESULT 52

CO707465/c
 LOCUS
 DEFINITION DG32-82122 DG32-liver Canis familiaris cDNA 3', mRNA linear EST 26-JUL-2004
 ACCESSION CO707465
 VERSION CO707465.1 GI:50656167
 KEYWORDS EST.
 SOURCE Canis familiaris (dog)

ORGANISM
 Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 Schluter,T., Hermanns,J., Weindel,M., Schuette,D., Kranz,H.,
 Henrich,J. and Loebeert,R.
 Dog arrayTAG cDNA clone collection
 Unpublished (2004)
 Contact: Thomas Schluter
 LION Bioscience AG
 Walhoferstrasse 98, D-69123 Heidelberg, Germany
 Tel: +49 6221 4038 150
 Fax: +49 6221 4038 290
 Email: Thomas.Schluter@lionbioscience.com.

Location/Qualifiers

1..421
 /organism="Canis familiaris"
 /mol_type="mRNA"
 /strain="Beagle"
 /db_xref="taxon:9615"
 /tissue_type="liver"
 /dev_stage="adult"
 /lab_host="DH10B"

FEATURES

source
 Location/Qualifiers

1..421
 /organism="Canis familiaris"
 /mol_type="mRNA"
 /strain="Beagle"
 /db_xref="taxon:9615"
 /tissue_type="liver"
 /dev_stage="adult"
 /lab_host="DH10B"

/clone_lib="DG32-liver"
 /note="Organ: liver; Vector: Dog pBluescript LION"

ORIGIN

Alignment Scores:
 Pred. No.: 2.58e+03 Length: 421
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-10-029-756-20 (1-6) x CO707465 (1-421)

Qy 1 PheGlnIleGluHis 6
 |||||
 Db 294 TTCCAGATTGAGCACCAC 277

RESULT 53

CB762663
 LOCUS
 DEFINITION AMGNNUC:NRHW1-00304-E12-A W rat hypo+pit (10478) Rattus norvegicus cDNA clone nrhw1-00304-e12 5', mRNA sequence.
 ACCESSION CB762663
 VERSION CB762663.1 GI:29851054
 KEYWORDS EST.
 SOURCE Rattus norvegicus (Norway rat)

ORGANISM
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 Angen EST Program.
 Angen Rat EST Program
 Unpublished (2003)
 Contact: Dan Fitzpatrick
 Angen, Inc
 One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
 Tel: 805 447-4881
 Plate: 00304 row: e column: 12.

FEATURES

source
 Location/Qualifiers

1..423
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /db_xref="taxon:10116"
 /clone="nrhw1-00304-e12"
 /tissue_type="hypo+pit"
 /clone_lib="W rat hypo+pit (10478)"
 /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; W rat hypo+pit Wistar rat"

ORIGIN

Alignment Scores:
 Pred. No.: 2.59e+03 Length: 423
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x CB762663 (1-423)

Qy 1 PheGlnIleGluHis 6
 |||||
 Db 279 TTCCAGATTGAGCACCAC 296

RESULT 54

AV615350/c
 LOCUS
 DEFINITION AV615350 Bos taurus adipocyte cell line Bos taurus cDNA clone
 ACCESSION AV615350
 VERSION AV615350.1 GI:9751020

```

KEYWORDS
SOURCE      Bos taurus (cow)
ORGANISM    Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1 (bases 1 to 429)
AUTHORS    Takasuga,A., Hirotsune,S., Itoh,R., Jitohzono,A., Suzuki,H., Aso,H.
            and Sugimoto,Y.
TITLE      Establishment of a high throughput EST sequencing system using
            poly(A) tail-removed cDNA libraries and determination of 36,000
            bovine ESTs
JOURNAL     Nucleic Acids Res. 29 (22), E108 (2001)
MEDLINE     21570554
PUBMED      11713328
COMMENT     Contact: Yoshikazu Sugimoto
            Animal Genetics Division
            Shirakawa Institute of Animal Genetics
            Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
            Tel: 81-248-25-5641
            Fax: 81-248-25-5725
            Email: kazusugi@ococa.ocn.ne.jp
            Single pass sequencing.
            This clone was obtained from a polyA-deleted cDNA library.
FEATURES
            source
                1..429
                Location/Qualifiers
                    /organism="Bos taurus"
                    /mol_type="mRNA"
                    /db_xref="taxon:9913"
                    /clone="E1AD011C10"
                    /cell_type="an adipocyte cell line"
                    /lab_host="DH10B"
                    /clone_lib="Bos taurus adipocyte cell line"
                    /note="vector: pZri; Site_1: SalI; Site_2: NotI; Poly A
                    was deleted from a NotI site"
ORIGIN
Alignment Scores:
Pred. No.:      2.64e+03      Length:      429
Score:          36.00         Matches:      6
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             1            Gaps:        0

US-10-029-756-20 (1-6) x AV615350 (1-429)

Qy      1 PheGlnIleGluHisHis 6
      |||||
Db      204 TTCCAGATTGAGCACCAT 187

RESULT 55
W53753      Mus musculus
LOCUS       md12f10.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA
DEFINITION  clone IMAGE:368203 5' similar to PIR:S54809 S54809 delta 6
            deaturase - Spirulina platensis ;, mRNA sequence.
ACCESSION   W53753
VERSION     W53753.1 GI:1357588
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 429)
REFERENCE   1 (bases 1 to 429)
AUTHORS    Maria,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wyllie,T., Lemon,G., Soares,B., Wilson,R. and
            Waterston,R.
            The WashU-HHMI Mouse EST Project
            Unpublished (1996)
            Contact: Marra M/Mouse EST Project

```

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WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:229635
Possible reversed clone: similarity on wrong strand
Seq primer: ETPRimer
High quality sequence stop: 346.
FEATURES
            source
                1..429
                Location/Qualifiers
                    /organism="Mus musculus"
                    /mol_type="mRNA"
                    /strain="C57BL/6J"
                    /db_xref="taxon:10090"
                    /clone="IMAGE:368203"
                    /sex="unknown"
                    /tissue_type="embryo"
                    /dev_stage="13.5-14.5dpc total fetus"
                    /lab_host="DH10B"
                    /clone_lib="Soares mouse embryo NbME13.5 14.5"
                    /note="vector: pT7T3D-Pac (Pharmacia) with a modified
                    polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
                    was primed with a Not I - oligo(dT) primer [5',
                    TGTTACCAATCTGAAGTGGAGCGCGCGGAAATTTTCTTTTCTTTTCTTTT
                    T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
                    14.5dpc embryos [total RNA provided by Minoru Ko, Wayne
                    State Univ., from 2 ]; double-stranded cDNA was ligated to
                    Eco RI adaptors (Pharmacia), digested with Not I and
                    cloned into the Not I and Eco RI sites of the modified
                    pT7T3 vector. Library went through one round of
                    normalization, and was constructed by Bento Soares and
                    M.Fatima Bonaldo. "
ORIGIN
Alignment Scores:
Pred. No.:      2.64e+03      Length:      429
Score:          36.00         Matches:      6
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    100.00%      Indels:      0
DB:             7            Gaps:        0

US-10-029-756-20 (1-6) x W53753 (1-429)

Qy      1 PheGlnIleGluHisHis 6
      |||||
Db      322 TTCCAGATTGAGCACCAC 339

RESULT 56
BE763399/c  430 bp      mRNA      linear      EST 19-SEP-2000
LOCUS       RCO-NT0036-010600-031-d05 NT0036 Homo sapiens cDNA, mRNA sequence.
DEFINITION  BE763399
ACCESSION   BE763399
VERSION     BE763399.1 GI:10193323
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 430)
REFERENCE   1 (bases 1 to 430)
AUTHORS    Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
            Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
            Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
JOURNAL

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MEDLINE
20202663
10737800
PUBMED
COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil

Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?c1=8t2-RC0-NT0036-010
600-031-d05&t3=2000-06-01&t4=1)

Seq primer: puc 18 forward
High quality sequence start: 10
High quality sequence stop: 430.

FEATURES
source

1..430
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="NT0036"

/note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Alignment Scores:
Pred. No.: 2.64e+03 Length: 430
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x BE763399 (1-430)

Qy 1 PheGlnIleGluHisHie 6

Db 39 TTCACATCGAGCACAC 22

RESULT 57

BG302890/c

LOCUS

DEFINITION BG302890 430 bp mRNA linear EST 23-FEB-2001
IMAGE:3816388 3' similar to TR:095864 095864 DELTA-6 FATTY ACID
DESATURASE. 1, mRNA sequence.

ACCESSION BG302890

VERSION BG302890.1 GI:13109417

KEYWORDS EST.

SOURCE

ORGANISM

Danio rerio (zebrafish)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

REFERENCE

AUTHORS

1 (bases 1 to 430)
Sugano, S., Kawakami, K., Johnson, S., Li, F., Marra, M., Eddy, S.,
Hillier, L., Clifton, S., Allen, M., Gibbons, M., Jost, S., Kucaba, T.,
Martin, J., Pape, D., Steptoe, M., Underwood, K., Theising, B.,
Ritter, E., Bowers, Y., Wylie, T., Waterston, R. and Wilson, R.
WASHU Zebrafish EST Project 1999

TITLE

JOURNAL

COMMENT

Contact: S.L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu

Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA
Sequencing by: Washington University Genome Sequencing Center Clone
distribution information can be found through the I.M.A.G.E.

Consortium/LLNL, send email to: info@image.llnl.gov
Trace considered overall poor quality

Seq primer: 17 from Gibco

High quality sequence stop: 1.

FEATURES

source

1..430
Location/Qualifiers
/organism="Danio rerio"

/mol_type="mRNA"

/strain="AB"

/db_xref="taxon:7955"

/clones="IMAGE:3816388"

/sex="mixed (one male and one female, including

unfertilized eggs)"

/dev_stage="adult"

/lab_host="DH10B (phage resistant)"

/clone_lib="Sugano Kawakami zebrafish DR"

/note="Vector: pME18S-FL3; Site 1: DraIII (CACTGTGTG);

Site 2: DraIII (CACCATGTG); 1st strand cDNA was primed

with an oligo(dT) primer [ATGTGGCTTTTITTTTTTTT];

double-stranded cDNA was ligated to a DraIII adaptor

[TGTGGCTTACTG], digested and cloned into distinct DraIII

sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site

CACCATGTG). XhoI should be used to isolate the cDNA

insert. Size selection was performed to exclude fragments

<1.5kb. Library constructed by Dr. Sumio Sugano

(University of Tokyo Institute of Medical Science) and

kindly donated by Dr. Koichi Kawakami. Custom primers for

sequencing: 5' end primer CTTCTGCTCTAAAGTGG and 3' end

primer CGACCTGCAGCTCGACACA."

ORIGIN

Alignment Scores:
Pred. No.: 2.64e+03 Length: 430
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x BG302890 (1-430)

Qy 1 PheGlnIleGluHisHie 6

Db 190 TTCACATCGAGCATCAT 173

RESULT 58

AA003204

LOCUS

DEFINITION

AA003204

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WASHU-HMI Mouse EST Project

Washington University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:261385

Seq primer: BTPprimer
 High quality sequence stop: 358.
 Location/Qualifiers
 1. .431

FEATURES

source

/organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:426833"
 /sex="unknown"
 /tissue_type="embryo"
 /dev_stage="13.5-14.5dpc total fetus"
 /lab_host="DH10B"
 /clone_lib="Soares mouse embryo NbME13.5 14.5"
 /note="Vector: pTT3D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was primed with a Not I - oligo(dT) primer [5',
 TGTTCACCAATCTGAAGTCGGAGCGCGCGGAATTTTTTTTTTTTTTTT
 T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
 14.5dpc embryos (total RNA provided by Minoru Ko, Wayne
 State Univ., from 2); double-stranded cDNA was ligated to
 Eco RI adaptors (Pharmacia), digested with Not I and
 cloned into the Not I and Eco RI sites of the modified
 pTT73 vector. Library went through one round of
 normalization, and was constructed by Bento Soares and
 M.Patima Bonaldo."

ORIGIN

Alignment Scores:
 Pred. No.: 2.65e+03 Length: 431
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AA003204 (1-431)

Qy 1 PheGlnIleGluHisHis 6
 Db 288 TTCAGATTGAACACCAC 305

RESULT 59

BE763432/c 435 bp mRNA linear EST 19-SEP-2000
 LOCUS RCO-NT00036-100700-032-e08 NT0036 Homo sapiens cDNA, mRNA sequence.

DEFINITION BE763432
 ACCESSION BE763432.1 GI:10193356
 VERSION BE763432.1
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 435)

REFERENCE 1 (bases 1 to 435)
 AUTHORS Nagai M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P.,
 Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
 Brunsstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,
 O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Simpson, A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800

COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil

Tel: +55-11-2704922
 Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=et2=RCO-NT0036-100
 700-032-e08&t3=2000-07-10&t4=1)

Seq primer: puc 18 forward
 High quality sequence stop: 14
 High quality sequence start: 435.

FEATURES

source

1. .435
 /location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="NT0036"
 /note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN

Alignment Scores:
 Pred. No.: 2.68e+03 Length: 435
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x BE763432 (1-435)

Qy 1 PheGlnIleGluHisHis 6
 Db 42 TTCAGATCGACACCAC 25

RESULT 60

AA049958

LOCUS AA049958 436 bp mRNA linear EST 09-SEP-1996
 DEFINITION mJ3809.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA
 Clone IMAGE:478432 5', mRNA sequence.

ACCESSION AA049958

VERSION AA049958.1 GI:1529629

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 436)

REFERENCE 1 (bases 1 to 436)
 AUTHORS Marra M., Hallier L., Allen M., Bowles M., Dietrich N., Dubuque, T.,
 Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellendberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.

TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)

COMMENT Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:289176

Seq primer: -28M13 rev2 from Amersham
 High quality sequence stop: 430.
 Location/Qualifiers
 1..436
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CS7BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:478432"
 /sex="unknown"
 /tissue_type="embryo"
 /dev_stage="13.5-14.5dpc total fetus"
 /lab_host="DH10B"
 /clone_lib="Soares mouse embryo NMB13.5 14.5"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAGTGGAGCGCGGGAATTTTTTTTTTTTTTTT T 3'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Alignment Scores:
 Pred. No.: 2.69e+03 Length: 436
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AA049958 (1-436)

Qy 1 PheGlnIleGluHis 6
 |||||
 Db 289 TTCCAGATTGACACCAC 306

RESULT 61

AL047548
 LOCUS
 DEFINITION DKFZp586D0421_r1 586 (synonym: hutel) Homo sapiens cDNA clone
 DKFZp586D0421, mRNA sequence.

ACCESSION AL047548.1 GI:4728544
 VERSION AL047548.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 440)

AUTHORS Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
 EST (Ottenwaelder, et al.)

TITLE Unpublished (1999)

JOURNAL Contact: MIPS

COMMENT MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by MediGenomix (Martinsried/Germany) within the cDNA
 sequencing consortium of the German Genome Project. No s1 sequence
 available.

This clone (DKFZp586D0421) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

Location/Qualifiers
 1..440

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="DKFZp586D0421"
 /tissue_type="uterus"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="586 (synonym: hutel)"
 /note="Vector: pSport1; Site_1: NotI; Site_2: SalI/MluI"

ORIGIN

Alignment Scores:
 Pred. No.: 2.72e+03 Length: 440
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AL047548 (1-440)

Qy 1 PheGlnIleGluHis 6
 |||||
 Db 29 TTCCAGATTGACACCAC 46

RESULT 62

CD618243/c

LOCUS

DEFINITION CD618243 441 bp mRNA linear EST 12-JAN-2004

ACCESSION CD618243

VERSION CD618243.1 GI:40266508

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 441)

AUTHORS Fu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.

TITLE Circular rapid amplification of cDNA ends for high-throughput

JOURNAL extension cloning of partial genes

COMMENT Genomics 84 (1), 205-210 (2004)

Contact: Fu GK

Incyte Genomics, Inc.

3160 Porter Dr., Palo Alto, CA 94304, USA

Tel: 6508454102

Email: gfu@incyte.com.

Location/Qualifiers

1..441

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone_lib="FLP"

/note="Vector: pDrive Cloning Vector"

ORIGIN

Alignment Scores:
 Pred. No.: 2.72e+03 Length: 441
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x CD618243 (1-441)

Qy 1 PheGlnIleGluHis 6
 |||||
 Db 432 TTCCAGATTGACACCAC 415

RESULT 63

CN959568

LOCUS

DEFINITION 7068_100133_85 Fundulus heteroclitus Liver

EST 08-JUN-2004

linear

442 bp mRNA

Fundulus heteroclitus

```

cDNA, mRNA sequence.
CN959568
CN959568.1 GI:48441157
EST.
SOURCE Fundulus heteroclitus (killifish)
ORGANISM Fundulus heteroclitus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Cyprinodontiformes; Fundulidae; Fundulus.
1 (bases 1 to 442)
Crawford,D.L., Oleksiak,M.F., Kolell,K.J., Paschall,J., VanWye,J.,
Roach,J.L. and Whitehead,J.A.
Fundulus Functional Genomics: EST Database for Teleost Fish
Unpublished (2004)
Contact: Crawford, Douglas L.
Marine Genomics - Crawford Lab
Rosenstiel School of Marine and Atmospheric Science - University of
Miami
4600 Rickenbacker Causeway, Miami, FL 33149-1098 USA
Tel: 305 361 4121
Email: dcrawford@rsmas.miami.edu
Database Web Interface
http://genomics.rsmas.miami.edu/funnybase/super_craw3/
Plate: 100133 row: D column: 11.

FEATURES             source
    source
    1..442
    /organism="Fundulus heteroclitus"
    /mol_type="mRNA"
    /db_xref="taxon:8078"
    /tissue_type="Liver"
    /clone_lib="Fundulus Heteroclitus Liver"
    /note="Organ: Liver"

ORIGIN
Alignment Scores:      2.73e+03      Length:      442
Pred. No.:            36.00          Matches:      6
Score:                100.00%        Conservative:  0
Percent Similarity:   100.00%        Mismatches:   0
Best Local Similarity: 100.00%        Indels:       0
Query Match:         100.00%        Gaps:         0
DB:                  7

US-10-029-756-20 (1-6) x CN962628 (1-442)

Qy      1 PheGlnIleGluHis 6
Db      195 TTTCAAATCGACCAT 212

RESULT 65
CN966615
LOCUS   CN966615
DEFINITION 14112_100293_58 Fundulus Heteroclitus Liver Fundulus heteroclitus
          cDNA similar to Delta-5/delta-6 fatty acid desaturase (BC 1.14.19,
          mRNA sequence.
          CN966615
          VERSION CN966615.1 GI:48448204
          KEYWORDS EST.
          SOURCE Fundulus heteroclitus (killifish)
          ORGANISM Fundulus heteroclitus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
          Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
          Cyprinodontiformes; Fundulidae; Fundulus.
          1 (bases 1 to 442)
          Crawford,D.L., Oleksiak,M.F., Kolell,K.J., Paschall,J., VanWye,J.,
          Roach,J.L. and Whitehead,J.A.
          Fundulus Functional Genomics: EST Database for Teleost Fish
          Unpublished (2004)
          Contact: Crawford, Douglas L.
          Marine Genomics - Crawford Lab
          Rosenstiel School of Marine and Atmospheric Science - University of
          Miami
          4600 Rickenbacker Causeway, Miami, FL 33149-1098 USA
          Tel: 305 361 4121
          Email: dcrawford@rsmas.miami.edu
          Database Web Interface
          http://genomics.rsmas.miami.edu/funnybase/super_craw3/
          Plate: 100293 row: G column: 8.

FEATURES             source
    source
    1..442
    /organism="Fundulus heteroclitus"
    /mol_type="mRNA"
    /db_xref="taxon:8078"
    /tissue_type="Liver"
    /clone_lib="Fundulus Heteroclitus Liver"
    /note="Organ: Liver"

ORIGIN
Alignment Scores:      2.73e+03      Length:      442
Pred. No.:            36.00          Matches:      6
Score:                100.00%        Conservative:  0
Percent Similarity:   100.00%        Mismatches:   0
Best Local Similarity: 100.00%        Indels:       0
Query Match:         100.00%        Gaps:         0
DB:                  7

US-10-029-756-20 (1-6) x CN959568 (1-442)

Qy      1 PheGlnIleGluHis 6
Db      255 TTTCAAATCGACCAT 272

RESULT 64
CN962628
LOCUS   CN962628
DEFINITION 10125_100235_27 Fundulus Heteroclitus Liver Fundulus heteroclitus
          cDNA similar to Delta-5/delta-6 fatty acid desaturase (BC 1.14.19,
          mRNA sequence.
          CN962628
          VERSION CN962628.1 GI:48444217
          KEYWORDS EST.
          SOURCE Fundulus heteroclitus (killifish)
          ORGANISM Fundulus heteroclitus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
          Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
          Cyprinodontiformes; Fundulidae; Fundulus.
          1 (bases 1 to 442)
          Crawford,D.L., Oleksiak,M.F., Kolell,K.J., Paschall,J., VanWye,J.,
          Roach,J.L. and Whitehead,J.A.
          Fundulus Functional Genomics: EST Database for Teleost Fish
          Unpublished (2004)
          Contact: Crawford, Douglas L.
          Marine Genomics - Crawford Lab
          Rosenstiel School of Marine and Atmospheric Science - University of
          Miami

```

Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-10-029-756-20 (1-6) x CN966615 (1-442)

Qy 1 PheGlnIleGluHisHis 6
 |||||
 Db 217 TTTCAAATCGAACCAT 234

RESULT 66
 AA310580

LOCUS AA310580 443 bp mRNA linear EST 19-APR-1997
 DEFINITION EST191401 Jurkat T-cells V Homo sapiens cDNA 5' end, mRNA sequence.
 ACCESSION AA310580
 VERSION AA310580.1 GI:1962927
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 443)
 AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Pritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.-Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.B., Kunsch,C., Hungjun,J., Li,H., Meisner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
 TITLE Initial assessment of human gene diversity and expression patterns
 based upon 83 million nucleotides of cDNA sequence
 JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
 MEDLINE 96026280
 PUBMED 7566098
 COMMENT Other ESTs: THCI52140
 Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
 Seq primer: M13 Reverse.

FEATURES
 source
 1. 443
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="ATCC (inhost):156619"
 /db_xref="taxon:9606"
 /cell_type="T-lymphocyte"
 /clone_lib="Jurkat T-cells V"
 /notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"

ORIGIN
 Alignment Scores: 2.74e+03 Length: 443
 Pred. No.: 36.00 Matches: 6
 Score: 100.00%
 Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AA310580 (1-443)

Qy 1 PheGlnIleGluHisHis 6
 |||||
 Db 149 TTCCAGATTGAGCACCAT 166

RESULT 67
 BF750956/c

LOCUS BF750956 444 bp mRNA linear EST 10-JAN-2001
 DEFINITION RCI-BN0414-021100-021-h03 BN0414 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF750956
 VERSION BF750956.1 GI:12077632
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 444)
 AUTHORS Dias Neto,E., Garcia Correa,R., Vertovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
 TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC1&t2=RC1-BN0414-021100-021-h03&t3=2000-11-02&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence start: 18
 High quality sequence stop: 443.

FEATURES
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 1. 444
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="BN0414"
 /notes="Organ: breast normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORFESTS PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
 Alignment Scores: 2.75e+03 Length: 444
 Pred. No.: 36.00 Matches: 6
 Score: 100.00%
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x BF750956 (1-444)

```

QY      1 PheGlnIleGluHis 6
Db      379 TTCCAGATTCGACAC 362

RESULT 68
BF890295
LOCUS   BF890295          444 bp    mRNA    linear    EST 25-APR-2001
DEFINITION 21915 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  BF890295
VERSION     BF890295.1  GI:12281825
KEYWORDS   EST.
SOURCE     Bos taurus (cow)
ORGANISM   Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE  1 (bases 1 to 444)
AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
          Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
          Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
          Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F.,
          Quackenbush,J. and Keefe,J.W.
          Sequence evaluation of four pooled-tissue normalized bovine cDNA
          libraries and construction of a gene index for cattle
          Genome Res. 11 (4), 626-630 (2001)
JOURNAL   21180013
MEDLINE   11282978
COMMENT   Contact: Smith TPL
          USDA, ARS, US Meat Animal Research Center
          PO Box 166, Clay Center, NE 68933-0166, USA
          Tel: 402 762 4366
          Fax: 402 762 4390
          Email: smith@email.marc.usda.gov
          Single pass sequencing. Bases called and alt trimmed with phred
          v0.980904.e. Vector identified by cross_match with the -minscore 18
          and -minmatch 12 options.
          PCR Primers
          FORWARD: AGGAAACAGCTATGACCAT
          BACKWARD: GTTTCACAGTCACGACG
          Plate: 57 row: G column: 16
          Seq primer: ATTTAGGTGACACTATAG.
FEATURES   source
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            /mol_type="mRNA"
            /db_xref="taxon:9913"
            /tissue_type="pooled"
            /lab_host="DH10B"
            /clone_lib="MARC 3BOV"
            /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
            Library made from pooled tissue from marrow, alveolar
            macrophage, ovary, fetal semitendinosus muscle, and fetal
            longissimus muscle."
ORIGIN
Alignment Scores:          2.75e+03          Length:          444
Pred. No.:                36.00             Matches:          6
Percent Similarity:       100.00%            Conservative:    0
Best Local Similarity:    100.00%            Mismatches:     0
Query Match:              100.00%            Indels:         0
DB:                        2                 Gaps:           0

US-10-029-756-20 (1-6) x BF890295 (1-444)

QY      1 PheGlnIleGluHis 6
Db      101 TTCCAGATTCGACAC 118

RESULT 69
BQ101252
LOCUS   BQ101252          444 bp    mRNA    linear    EST 29-APR-2002
DEFINITION 21915 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION  BQ101252
VERSION     BQ101252.1  GI:20134236
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 444)
AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
          Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
          Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
          Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
          Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarisvilli,R.,
          Williams,T., Jackson,Y. and Bowers,Y.
          Endocrine Pancreas Consortium
          Unpublished (2000)
          Other ESTs: ij25h11.xl
          Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
          Endocrine Pancreas Consortium
          Harvard University, Howard Hughes Medical Institute
          Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
          MA 02138
          Tel: 617-495-1812
          Fax: 617-495-8557
          Email: dmelton@bioh.harvard.edu
          Library was constructed by Dr. Douglas Melton DNA sequencing by:
          Washington University Genome Sequencing Center This clone is
          available royalty-free through LNL; please contact the IMAGE
          consortium (info@image.llnl.gov) for further information
          Putative full length read
          vector to vector length is 547
          Seq primer: -40RP from Gibco.
FEATURES   source
            1..444
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:6135813"
            /sex="Both"
            /tissue_type="Islets of Langerhans"
            /dev_stage="Adult"
            /lab_host="DH10B"
            /clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
            /note="Organ: Pancreas; Vector: pSPORT1; Site 1: Not 1;
            Site 2: Sal 1; Starting library constructed using
            SuperScript Plasmid Library kit (Life Technologies). cDNA
            made by oligo-dT priming. Size-selected by column
            fractionation; average insert size 1.08 kb. Library was
            amplified once on solid support and plasmid DNA from
            library made from Bernaldo, Lennon, and Soares 1996 Genome
            Research 6:791-806; 0.5 microgram single-stranded library
            plasmid DNA was mixed with 5 micrograms PCR product
            representing library inserts and hybridized to an Ecot of
            20. Single-stranded (unhybridized) plasmids were isolated
            by hydroxyapatite chromatography and used to make this
            library."
ORIGIN
Alignment Scores:          2.75e+03          Length:          444
Pred. No.:                36.00             Matches:          6
Percent Similarity:       100.00%            Conservative:    0
Best Local Similarity:    100.00%            Mismatches:     0
Query Match:              100.00%            Indels:         0
DB:                        5                 Gaps:           0

US-10-029-756-20 (1-6) x BQ101252 (1-444)

QY      1 PheGlnIleGluHis 6

```

```

DEFINITION ij25h11.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
cDNA clone IMAGE:6135813 5' similar to TR:Q9Y5Q0 Q9Y5Q0 DELTA-6
FATTY ACID DESATURASE. ;, mRNA sequence.

```

```

ACCESSION  BQ101252
VERSION     BQ101252.1  GI:20134236
KEYWORDS   EST.
SOURCE     Homo sapiens (human)

```

```

ORGANISM   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE  1 (bases 1 to 444)
AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
          Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,
          Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
          Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
          Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarisvilli,R.,
          Williams,T., Jackson,Y. and Bowers,Y.
          Endocrine Pancreas Consortium
          Unpublished (2000)

```

```

TITLE      Other ESTs: ij25h11.xl
JOURNAL
COMMENT    Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
          Endocrine Pancreas Consortium
          Harvard University, Howard Hughes Medical Institute
          Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
          MA 02138
          Tel: 617-495-1812
          Fax: 617-495-8557
          Email: dmelton@bioh.harvard.edu

```

```

          Library was constructed by Dr. Douglas Melton DNA sequencing by:
          Washington University Genome Sequencing Center This clone is
          available royalty-free through LNL; please contact the IMAGE
          consortium (info@image.llnl.gov) for further information
          Putative full length read
          vector to vector length is 547
          Seq primer: -40RP from Gibco.

```

```

FEATURES   source
            1..444
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:6135813"
            /sex="Both"
            /tissue_type="Islets of Langerhans"
            /dev_stage="Adult"
            /lab_host="DH10B"
            /clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
            /note="Organ: Pancreas; Vector: pSPORT1; Site 1: Not 1;
            Site 2: Sal 1; Starting library constructed using
            SuperScript Plasmid Library kit (Life Technologies). cDNA
            made by oligo-dT priming. Size-selected by column
            fractionation; average insert size 1.08 kb. Library was
            amplified once on solid support and plasmid DNA from
            library made from Bernaldo, Lennon, and Soares 1996 Genome
            Research 6:791-806; 0.5 microgram single-stranded library
            plasmid DNA was mixed with 5 micrograms PCR product
            representing library inserts and hybridized to an Ecot of
            20. Single-stranded (unhybridized) plasmids were isolated
            by hydroxyapatite chromatography and used to make this
            library."

```

```

ORIGIN
Alignment Scores:          2.75e+03          Length:          444
Pred. No.:                36.00             Matches:          6
Percent Similarity:       100.00%            Conservative:    0
Best Local Similarity:    100.00%            Mismatches:     0
Query Match:              100.00%            Indels:         0
DB:                        5                 Gaps:           0

US-10-029-756-20 (1-6) x BQ101252 (1-444)

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```

QY      1 PheGlnIleGluHis 6

```

```

Db      45  |||||||TTCCAGATCGAGCACAC 62
RESULT 70
LOCUS   BG412193
DEFINITION
OV2_39_A06.b1_A002 Ovary 2 (OV2) Sorghum bicolor cDNA, mRNA
sequence.
ACCESSION
VERSION  BG412193
KEYWORDS  BG412193.1  GI:13317746
SOURCE    Sorghum bicolor (sorghum)
ORGANISM  Sorghum bicolor
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE
AUTHORS  Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and
Pratt,L.H.
TITLE     An EST database from Sorghum: ovaries of varying immature stages
JOURNAL   Unpublished (2000)
COMMENT   Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Seq primer: JEN REV
High quality sequence stop: 444
POLYA=No.

FEATURES
source
1..445
/organism="Sorghum bicolor"
/mol_type="mRNA"
/db_xref="taxon:4558"
/clone_lib="Ovary 2 (OV2)"
/note="Organ: Mix of ovaries of varying immature stages
from 8-week-old plants; Vector: pBluescript II from Lambda
Zap II; Site 1: XhoI; Site 2: EcoRI; The library was made
from Poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."

ORIGIN
Alignment Scores:
Pred. No.: 2.75e+03 Length: 445
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x BG412193 (1-445)

Qy      1  PheGlnIleGluHisHis 6
|||||
Db      187 TTCCAGATTGAGCACCAT 204

RESULT 71
LOCUS   AA488410/c
DEFINITION
ab37909.g1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone
IMAGE:843040 3' similar to WP.W08D2.4 CE06559 ;, mRNA sequence.
ACCESSION
VERSION  AA488410
KEYWORDS  AA488410.1  GI:2215841
SOURCE    EST.
Homo sapiens (human)
ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS  Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,

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Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wyllie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert length: 656 Std Error: 0.00
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 440.

FEATURES
source
1..446
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:843040"
/sex="female"
/dev_stage="HeLa S3 cell line"
/lab_host="SOUR (kanamycin resistant)"
/clone_lib="Stratagene HeLa cell s3 937216"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; Cloned unidirectionally. Primer: Oligo dt. HeLa S3
epithelioid carcinoma cells grown to semi-confluency
without induction. Average insert size: 1.5 kb; Uni-ZAP XR
Vector. -5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3'
adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTT 3'"

ORIGIN
Alignment Scores:
Pred. No.: 2.76e+03 Length: 446
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AA488410 (1-446)

Qy      1  PheGlnIleGluHisHis 6
|||||
Db      328 TTCCAGATTGAGCACCAT 311

RESULT 72
LOCUS   CB841818
DEFINITION
M15E-2428 MOUSE EMBRYONIC DAY 15.5 EYE Mus musculus cDNA 5', mRNA
sequence.
ACCESSION
VERSION  CB841818
KEYWORDS  CB841818.1  GI:34373088
SOURCE    EST.
Mus musculus (house mouse)
ORGANISM  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS  Yu,J., Farjo,R., MacNee,S.P., Baehr,W., Stambolian,D.E. and
Swaroop,A.
TITLE     Annotation and analysis of 10,000 expressed sequence tags from
developing mouse eye and adult retina
JOURNAL   Genome Biol. 4 (10), R65 (2003)
MEDLINE   22881944
PUBMED    14519200
Contact: Swaroop, A.
Department of Ophthalmology and Visual Sciences
Kellogg Eye Center, University of Michigan
540 KEC, 1000 Wall St., Ann Arbor, MI 48105, USA
Tel: 734 615 2246
Fax: 734 647 0228

```

FEATURES
source
Email: swaroop@umich.edu.
Location/Qualifiers
1. .446
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="eye"
/clone_lib="MOUSE EMBRYONIC DAY 15.5 EYE"
/note="Vector: pSPORT1"

ORIGIN

Alignment Scores:
Pred. No.: 2.76e+03 Length: 446
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x CB841818 (1-446)

Qy 1 PheGlnIleGluHis 6
|||||
Db 160 TTCAGATTGAACACCAC 177

RESULT 73

CK345055/c
LOCUS
DEFINITION CK345055 447 bp mRNA linear EST 22-DEC-2003
L0034F07-3 NIA Mouse E12.5 Female Mesonephros and Gonads cDNA
Library Mus musculus cDNA clone L0034F07 3', mRNA sequence.

ACCESSION CK345055
VERSION CK345055.1 GI:40300668
KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE
AUTHORS Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
TITLE Construction of long-transcript enriched cDNA libraries from
submicrogram amounts of total RNAs by a universal PCR amplification
method

Genome Res. 11 (9), 1553-1558 (2001)

JOURNAL
MEDLINE 21429098

PUBMED 11544199

COMMENT Contact: Dawood B. Dudekula

Laboratory of Genetics

National Institute on Aging/National Institutes of Health

333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA

Email: cdna@gsun.grc.nia.nih.gov

Plate: L0034 row: F column: 07

Seq primer: -21M13 Forward

High quality sequence stop: 447

POLYA=Yes.

Location/Qualifiers

1. .447

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="niaEST:L0034F07-3"

/db_xref="taxon:10090"

/clone="L0034F07"

/sex="female"

/dev_stage="12.5dpc"

/lab_host="DH10B"

/clone_lib="NIA Mouse E12.5 Female Mesonephros and Gonads
cDNA Library"

/note="Vector: pSPORT1 (Gibco/BRL Life Technology);
Site 1: SalI; Site 2: NotI; Total RNAs were extracted from
2 Mesonephros. The double-stranded cDNA was synthesized
by Gibco's kit with an Oligo(dT) primer (NotI
primer-adaptor from Gibco/BRL)

[5'-PGACTAGTCTTAGATCGGCGCGCCCTTTTTTTTTTTT-3'] from

3.42ug of total RNA . The double-stranded cDNAs were treated with T4 DNA polymerase and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker L1-Sal3 (include SalI sequence). The cDNAs were purified by phenol/chloroform and separated from free linkers by Centricon 100. Then, cDNAs were amplified by long-range high fidelity PCR using Takara's Ex Taq polymerase. Then, the cDNAs were purified by phenol/chloroform and by Centricon 100. The cDNAs were digested with SalI and NotI enzymes. Then, the cDNAs were size selected by Gibco's Size Fractionation Column. The cDNAs were cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by chemical method. The library was constructed by Xiaohong Wang."

ORIGIN

Alignment Scores:
Pred. No.: 2.77e+03 Length: 447
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-029-756-20 (1-6) x CK345055 (1-447)

Qy 1 PheGlnIleGluHis 6
|||||
Db 266 TTCAGATTGAGCACCAC 249

RESULT 74

BF890281
LOCUS BF890281 449 bp mRNA linear EST 25-APR-2001
DEFINITION 231897 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.

ACCESSION BF890281

VERSION BF890281.1 GI:12281811

KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM

Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.

1 (bases 1 to 449)

REFERENCE
AUTHORS Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chitko-McKown, C.G., Perlea, G., Holt, I., Karamycheva, S., Liang, F.,
Quackenbush, J. and Keefe, J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA

libraries and construction of a gene index for cattle

Genome Res. 11 (4), 626-630 (2001)

JOURNAL 21180013

MEDLINE 11282978

PUBMED 11282978

COMMENT

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred

v0.980904.e. Vector identified by cross_match with the -minscore 18

and -minmatch 12 options.

PCR Primers

FORWARD: AGGAAACAGCTATGACCAT

BACKWARD: GTTTCCAGTCACGACG

Plate: 57 row: D column: 16

Seq primer: ATTTAGGTGACACTATAG.

Location/Qualifiers

1. .449

/organism="Bos taurus"

/mol_type="mRNA"

/db_xref="taxon:9913"

/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 3BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."

ORIGIN

Alignment Scores:

Pred. No.: 2.78e+03 Length: 449
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x BF890281 (1-449)

Qy 1 PheGlnileGluHisHis 6

Db 92 TTCCAGATCGAGCACCAT 109

RESULT 75

BF002756/c

LOCUS

DEFINITION BF002756 449 bp mRNA linear EST 06-OCT-2000
similar to TR:O60427 O60427 BC269730.2.1, mRNA sequence.

ACCESSION BF002756

VERSION BF002756.1

KEYWORDS EST.

SOURCE BF002756.1 GI:10703031

ORGANISM Homo sapiens (human)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE 1 (Bases 1 to 449)

JOURNAL NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL, send email to:

info@image.llnl.gov

Seq primer: -40UP from Gibco.

Location/Qualifiers

1..449

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3310877"

/sex="male"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="NCI CGAP Pr28"

/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)

with a modified polylinker; Plasmid DNA from the

normalized library NCI CGAP Pr22 was prepared, and as

circles were made in vitro. Following HAP purification,

this DNA was used as tracer in a subtractive hybridization

reaction. The driver was PCR-amplified cDNAs from a pool

of 5,000 clones made from the same library (cloneIDs

985608-986759, 1101192-1101959, and 1217928-1220615).

Subtraction by Bento Soares and M. Fatima Bonaldo."

ORIGIN

Alignment Scores:

Qy 1 PheGlnileGluHisHis 6

Db 92 TTCCAGATCGAGCACCAT 109

Pred. No.: 2.78e+03 Length: 449
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x BF002756 (1-449)

Qy 1 PheGlnileGluHisHis 6

Db 348 TTCCAGATCGAGCACCAT 331

RESULT 76

AA531459

LOCUS

DEFINITION

AA531459 452 bp mRNA linear EST 20-AUG-1997

similar to TR:G1040729 G1040729 CYTOCHROME B5 CONTAINING FUSION

PROTEIN.1, mRNA sequence.

ACCESSION AA531459

VERSION AA531459.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

TITLE 1 (Bases 1 to 452)

JOURNAL NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: W. Marston Linehan, M.D., Rodrigo F. Chuvaqui,

M.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

DNA Sequencing by: Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www.bio.llnl.gov/bbrp/image/image.html

Insert Length: 977 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 395.

Location/Qualifiers

1..452

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:997172"

/sex="male"

/tissue_type="invasive prostate tumor"

/lab_host="DH10B"

/clone_lib="NCI CGAP Pr10"

/note="Organ: prostate; Vector: pAMP10; mRNA made from

invasive prostate tumor, cDNA made by oligo-dt priming.

Non-directionally cloned. Size-selected on agarose gel,

average insert size 600 bp. Library made by D. Krizman,

NIH."

ORIGIN

Alignment Scores:

Pred. No.: 2.81e+03 Length: 452
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AA531459 (1-452)

Qy 1 PheGlnileGluHisHis 6

Db 1 TTCCAGATCGAGCACCAT 109

Db 359 TTCCAGATCGAGCACCAC 376
 RESULT 77
 BY260760
 LOCUS
 DEFINITION
 cDNA clone K330303J05 5', mRNA sequence. EST 10-DEC-2002
 BY260760
 ACCESSION
 VERSION
 BY260760.1 GI:26442272
 KEYWORDS
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 455)
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nikaudo, I., Osato, N., Saito, R., Suzuki, H., Yamana, K.,
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
 Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,
 Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,
 Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V.,
 Ciothlav, C., Corbani, L. E., Cousins, S., Dalia, E., Dragani, T. A.,
 Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
 Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
 Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,
 Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,
 Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,
 Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
 Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G.,
 Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,
 Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M.,
 Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K.,
 Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,
 Verardo, R., Wagner, L. G., Wahlestedt, C., Wang, Y., Watanabe, Y.,
 Wells, C., Wilming, L. G., Wyszynski, B., Zhu, Y., Zimmer, A., Carninci, P.,
 Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
 Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
 Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
 Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
 Itoh, M., Kagawa, I., Miyazumi, A., Sakai, K., Sasaki, D., Shibata, K.,
 Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
 Rogers, J., Birney, E. and Hayashizaki, Y.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
 Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
 Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
 Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
 Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
 Hayashizaki, Y. Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome

Encyclopædia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Tissues were provided by Michela Fagiolini and Takao K. Hensch (
 Laboratory for Neuronal Circuit Development Brain Science Institute
 RIKEN 2-1 Hiroasawa, Wako-shi, Saitama 351-0198 Japan) whose
 assistance we gratefully acknowledge. Please visit our web site
 (http://genome.gsc.riken.go.jp) for further details.

FEATURES
 Location/Qualifiers
 1. 455
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="K330303J05"
 /tissue_type="visual cortex"
 /clone_lib="RIKEN full-length enriched, visual cortex"

ORIGIN
 Alignment Scores:
 Pred. No.: 2.83e+03 Length: 455
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 5 Gaps: 0
 US-10-029-756-20 (1-6) x BY260760 (1-455)

Qy 1 PheGlnIleGluHisHis 6
 |||||
 17 TTCCAGATTCGAGCACCAC 34

Db
 RESULT 78
 BF917591
 LOCUS
 DEFINITION
 IL3-UT01114-211200-360-E07 UT0114 Homo sapiens cDNA, mRNA sequence.
 BF917591
 ACCESSION
 VERSION
 BF917591.1 GI:12309049
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 458)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,
 Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F.,
 Goldman, G. H., Carvalho, A. F., Matsukuma, A., Baia, G. S., Simpson, D. H.,
 Brunstein, A., deOliveira, P. S., Bucher, P., Jongeneel, C. V.,
 O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and
 Simpson, A. J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE
 20202663
 PUBMED
 10737800
 COMMENT
 Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-UT0114-
 211200-360-E07&t3=2000-12-21&t4=1)
 Seq primer: puc 18 forward
 High quality sequence stop: 457.
 Location/Qualifiers
 1. 458

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="UT0114"

/note="Organ: uterus_tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Alignment Scores:
Pred. No.: 2.85e+03 Length: 458
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x BF917591 (1-458)

Qy 1 PheGlnIleGluHis 6
|||||
Db 87 TTTCAAATAGAACACCAC 104

RESULT 79

BF917881
LOCUS BF917881 458 bp mRNA linear EST 18-JAN-2001
DEFINITION IL3-UT0114-221200-360-E07 UT0114 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF917881
VERSION BF917881.1 GI:12309339
KEYWORDS EST.
SOURCE Homo sapiens (human)

REFERENCE 1 (bases 1 to 458)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
COMMENT

TITLE

LABORATORY OF CANCER GENETICS

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil

Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=IL3&t2=IL3-UT0114-
221200-360-E07&t3=2000-12-22&t4=1)

Seq primer: puc 18 forward
High quality sequence stop: 457.
Location/Qualifiers

FEATURES

source

1. 458
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="UT0114"
/note="Organ: uterus_tumor; Vector: puc18; Site_1: SmaI;

ORIGIN

Alignment Scores:
Pred. No.: 2.85e+03 Length: 458
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x BF917881 (1-458)

Qy 1 PheGlnIleGluHis 6
|||||
Db 87 TTTCAAATAGAACACCAC 104

RESULT 80

BF059742
LOCUS BF059742 458 bp mRNA linear EST 15-JUN-2001
DEFINITION IL3-UT0114-080101-360-E07 UT0114 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF059742
VERSION BF059742.1 GI:14467269
KEYWORDS EST.
SOURCE Homo sapiens (human)

REFERENCE 1 (bases 1 to 458)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=IL3&t2=IL3-UT0114-
080101-360-E07&t3=2001-01-08&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 457.
Location/Qualifiers

1. 458
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="UT0114"

FEATURES

source

1. 458
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="UT0114"
/note="Organ: uterus_tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Alignment Scores:
 Pred. No.: 2.85e+03 Length: 458
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x BI059742 (1-458)

Oy 1 PheGlnlleGluHisHis 6

|||||

Db 87 TTTCATAGACACAC 104

RESULT 81
 CN006019
 LOCUS ip37f09.g1 Brain - Cerebellum Library (DOGE8T8) Canis familiaris
 DEFINITION cDNA clone ip37f09, mRNA sequence.
 ACCESSION CN006019
 VERSION CN006019.1 GI:45770167
 KEYWORDS EST.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 458)
 AUTHORS Balija,V., Nascimento,L.U. and McCombie,W.R.
 TITLE ESTs from Canis familiaris cerebellum (dog)
 JOURNAL Unpublished (2004)
 COMMENT Contact: W. Richard McCombie
 Lita Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org
 Plate: ip37 row: f column: 09
 High quality sequence stop: 458.

FEATURES

source
 1..458
 /organism="Canis familiaris"
 /mol_type="mRNA"
 /db_xref="taxon:9615"
 /clone="ip37f09"
 /sex="Unknown"
 /tissue_type="Cerebellum"
 /dev_stage="3 month old normal canine"
 /lab_host="XLI0 Gold"
 /clone_lib="Brain - Cerebellum Library (DOGE8T8)"
 /note="Organ: Brain; Vector: pBluescript II SK; Site: 1:
 EcoRI; Site 2: XhoI; Library constructed using pBluescript
 XR kit from Stratagene. Cloned cDNA was size selected
 between 1-3 kb. Mark Haskins VMD, PhD, Pathology and
 Medical Genetics, School of Veterinary Medicine,
 University of Pennsylvania, 3800 Spruce Street,
 Philadelphia, PA 19104-6051"

ORIGIN

Alignment Scores:
 Pred. No.: 2.85e+03 Length: 458
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-10-029-756-20 (1-6) x CN006019 (1-458)

Oy 1 PheGlnlleGluHisHis 6

|||||

Db

RESULT 82
 BM721986/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BM721986 461 bp mRNA linear EST 01-MAR-2002
 UI-E-E00-ahw-e-22-0-UI.r1 UI-E-E00 Homo sapiens cDNA clone
 UI-E-E00-ahw-e-22-0-UI 5', mRNA sequence.
 BM721986
 BM721986.1 GI:19042251
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 461)
 Bernaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
 97044477
 8889548
 COMMENT Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: bento-soares@uiowa.edu
 Tissue Procurement: Dr. Gregg Hageman
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Researchers may obtain clones from Research
 Genomics (www.resgen.com).
 The following repetitive elements were found in this cDNA
 sequence: 85-159, >MIR#SINE/MIR
 Seq primer: M13 Reverse.

FEATURES

source
 1..461
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-E-E00-ahw-e-22-0-UI"
 /tissue_type="fetal eye"
 /dev_stage="fetal"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-E-E00"
 /note="Organ: eye; Vector: pTTT3-Pac (Pharmacia) with a
 modified polylinker; Site 1: EcoR I; Site 2: Not I;
 UI-E-E00 is a cDNA library containing the following
 tissue(s): fetal eye. The library was constructed
 according to Bernaldo, Lennon and Soares, Genome Research,
 6:791-806, 1996. First strand cDNA synthesis was primed
 with an oligo-dT primer containing a Not I site. Double
 stranded cDNA was ligated to an EcoR I adaptor, digested
 with Not I, and cloned directionally into pTTT3-Pac
 vector. The oligonucleotide used to prime the synthesis of
 first-strand cDNA contains a library tag sequence that is
 located between the Not I site and the (dT)18 tail. The
 sequence tag for this library is GCGGTATACC. This library
 was created for the program, Gene Discovery in the Visual
 System, supported by National Eye Institute (NEI)."

ORIGIN

Alignment Scores:
 Pred. No.: 2.87e+03 Length: 461
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x BM721986 (1-461)

```

QY      1 PheGlnlleGluHis 6
DB      248 TTTCAATTGACATCAT 231

RESULT 83
LOCUS   CA902069/c
DEFINITION   CA902069 463 bp mRNA linear EST 27-DEC-2002
               PCS20399 Scarlet Runner Bean Suspensor Region Triplex2 Phaseolus
               coccineus cDNA 5' similar to MPPI attachment factor 1, mRNA
               sequence.
ACCESSION   CA902069
VERSION     CA902069.1 GI:27389061
KEYWORDS    EST.
SOURCE      Phaseolus coccineus
ORGANISM    Phaseolus coccineus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Phaseolus.
REFERENCE   1 (bases 1 to 463)
AUTHORS    Bui,A.O., Le,B.H., Weterings,K., Bi,Y.-P., Choi,J.-S.,
            McElroy,K.E., Choi,P.S., Harada,J.J., Fischer,R.L. and
            Goldberg,R.B.
TITLE      Gene Activity in Different Regions of a Post-Fertilization Plant
            Embryo by EST Analysis
JOURNAL    Unpublished (2002)
COMMENT    Contact: Goldberg, R.B.
            Department of Molecular, Cell, & Developmental Biology
            University of California, Los Angeles
            621 Charles E. Young Drive South, Los Angeles, CA 90095-1606, USA
            Tel: 310 825 3270
            Fax: 310 825 8201
            Email: bobg@ucla.edu
            Seq primer: 5' Triplex
            POLYA=No.

FEATURES             Location/Qualifiers
     source           1..463
                     /organism="Phaseolus coccineus"
                     /mol_type="mRNA"
                     /cultivar="Hammond's Dwarf Scarlet"
                     /db_xref="taxon:3986"
                     /dev_stage="6-days post-pollination"
                     /clone_lib="Scarlet Runner Bean Suspensor Region Triplex2"
                     /note="Organ: Suspensor Region of Globular-Stage Embryos;
                     Vector: Triplex2; Site 1: SfiIA; Site 2: SfiIB; Suspensor
                     regions were micro-dissected from globular-stage embryos
                     six days after pollination from greenhouse-grown plants
                     [Weterings et al., Plant Cell 13, 2409-2425 (2001)].
                     Double-stranded cDNA was synthesized from suspensor mRNA
                     using the SMART cDNA Library Construction Kit according to
                     the manufacturer (Clontech). The suspensor cDNA fragments
                     were directionally ligated into the SfiI restriction site
                     of the lambda Triplex2 vector (Clontech), and the
                     recombinant cDNAs were transformed into E. coli XL1-Blue
                     cells (Clontech). Suspensor cDNA plasmids used for
                     directional sequencing were obtained by in vivo excision
                     from the lambda Triplex2 recombinants in E. coli BM25.8
                     cells (Clontech)."
```

```

ORIGIN
Alignment Scores: 2.89e+03 Length: 463
Pred. No.: 36.00 Matches: 6
Score: 100.00% Conservatives: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 6 Gaps: 0
DB:

US-10-029-756-20 (1-6) x CA902069 (1-463)
QY      1 PheGlnlleGluHis 6
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```

```

DB      414 TTTCAGATAGACATCAT. 397

RESULT 84
LOCUS   CD430143
DEFINITION   CD430143 465 bp mRNA linear EST 03-JUN-2003
               clone ETH1_17_D05_A002 3', mRNA sequence.
ACCESSION   CD430143
VERSION     CD430143.1 GI:31345786
KEYWORDS    EST.
SOURCE      Sorghum bicolor (sorghum)
ORGANISM    Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Sorghum.
            1 (bases 1 to 465)
AUTHORS    Cordonnier-Pratt,M.-M., Wentzel,V., Suzuki,Y., Sugano,S.,
            Klein,R.R., Liang,C., Sun,F., Sullivan,R., Shah,M., Salzman,R.,
            Chua Tan,N., Gonzalez,M., Lane,S., Miller,V., Nanda,P.,
            Olaseinde,O., Eastman,A. and Pratt,L.H.
TITLE      An EST database from Sorghum: 1-aminocyclopropane-1-carboxylic acid
            (ACC)-treated seedlings
JOURNAL    Unpublished (2003)
COMMENT    Other ESTs: ETH1_17_D05_g1_A002
            Contact: Cordonnier-Pratt MM
            Laboratory for Genomics and Bioinformatics
            The University of Georgia, Department of Plant Biology
            Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
            Tel: 706 542 1860
            Fax: 706 583 0210
            Email: mmpratt@uga.edu
            Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
            the Human Genome Center, University of Tokyo Institute of Medical
            Science; plant material and RNA prepared at Texas A & M University;
            sequencing done in the Laboratory for Genomics and Bioinformatics,
            University of Georgia. Sequence ends have been trimmed to exclude
            vector and regions below Phred quality 16. Three-prime sequences
            are presented as their reverse complement and have been trimmed to
            exclude polyA.
            Seq primer: Sug3 (CGACCTGCAGCTCGAGCACA)
            POLYA=Yes.

FEATURES             Location/Qualifiers
     source           1..465
                     /organism="Sorghum bicolor"
                     /mol_type="mRNA"
                     /cultivar="BTx623"
                     /db_xref="taxon:4558"
                     /clone_lib="ETH1_17_D05_A002"
                     /lab_hosts="DH10B-T1 phage-resistant E. coli"
                     /note="Vector: pME18S-FL3; Site 1: XhoI; Site 2: XhoI; The
                     library was prepared from polyA+ RNA from seedlings grown
                     in hydroponic culture. At 8 days of age, medium was
                     supplemented with 0.5 mM 1-aminocyclopropane-1-carboxylic
                     acid (ACC) to induce endogenous ethylene (ETH) production.
                     Roots and shoots were harvested after 27 and 72 hr and
                     material from both time points was combined prior to RNA
                     isolation. Double-stranded cDNA was cloned
                     unidirectionally into different DraIII sites of the
                     pME18S-FL3 vector (5-prime DraIII site is CACTGTGTG,
                     3-prime DraIII site is CACCATGTG). XhoI excises the cDNA
                     insert."
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```

ORIGIN
Alignment Scores: 2.9e+03 Length: 465
Pred. No.: 36.00 Matches: 6
Score: 100.00% Conservatives: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 6 Gaps: 0
DB:

US-10-029-756-20 (1-6) x CD430143 (1-465)

```

```

Qy 1 PheGlnIleGluHisHis 6
Db 66 TTCAGATTGAGCACCAT 83

RESULT 85
CV520815/c
LOCUS
DEFINITION 0899P00502.xl D11 Mimulus guttatus library 2 Mimulus guttatus cDNA
clone 0899P00502.xl D11, mRNA sequence.
ACCESSION CV520815
VERSION CV520815.1 GI:53847347
KEYWORDS EST.
SOURCE Mimulus guttatus (spotted monkey flower)
ORGANISM Mimulus guttatus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Lamiales; Gentianales; Mimuleae;
Mimulus.
REFERENCE 1 (bases 1 to 465)
AUTHORS Willis,J., Vision,T., Dietrich,P.S. and Allen,A.
TITLE Mimulus guttatus cDNA sequence
JOURNAL Unpublished (2004)
COMMENT Contact: Willis J
Department of Biology
Duke University
072-A Biological Sciences Science Drive, Durham, NC 27708, USA
Tel: 919 660 7340
Fax: 919 660 7293
Email: jwillis@duke.edu
Plate: 0089P0050 row: 11 column: D
Seq primer: T7
High quality sequence start: 15
High quality sequence stop: 692.
Location/Qualifiers
FEATURES
source
1..465
/organism="Mimulus guttatus"
/mol_type="mRNA"
/db_xref="taxon:4155"
/clone="0899P00502.xl D11"
/clone_lib="Mimulus guttatus library 2"
/notes="Vector: pGEM-T Easy; a Mimulus guttatus cDNA library"
ORIGIN
Alignment Scores:
Pred. No.: 2.9e+03 Length: 465
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-10-029-756-20 (1-6) x CV520815 (1-465)

Qy 1 PheGlnIleGluHisHis 6
Db 417 TTCAGATTCGAGCACCAT 400

RESULT 86
AA478552/c
LOCUS
DEFINITION zw95hi2.s1 Soares total_fetus Nb2HF8_9w Homo sapiens cDNA clone
IMAGE:784775 3', mRNA sequence.
ACCESSION AA478552
VERSION AA478552.1 GI:2207186
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 469)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,

```

Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997

TITLE JOURNAL COMMENT

Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 459.

FEATURES

Location/Qualifiers
source
1..469
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5982393"
/db_xref="taxon:9606"
/clone="IMAGE:784775"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/clone_lib="Soares total_fetus Nb2HF8_9w"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
total_fetus material with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAGTGGAGCGCGCTTAATTTTTTTTTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Alignment Scores:
Pred. No.: 2.93e+03 Length: 469
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x AA478552 (1-469)

Qy 1 PheGlnIleGluHisHis 6
Db 409 TTCAGATTGAGCACCAC 392

RESULT 87

AA490669
LOCUS
DEFINITION UI-M-BH3-ast-g-05-0-UI.s1 NIH BMAP M.S4 Mus musculus cDNA clone
UI-M-BH3-ast-g-05-0-UI 3', mRNA sequence.
ACCESSION AA490669
VERSION AA490669.1 GI:7060940
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 470)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548

COMMENT

Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD

20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: MEST@mail.nih.gov

The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized brain stems library cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements
Seq primer: M13 Forward
POLYA-Yes.

FEATURES

Location/Qualifiers

1..470
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clones="UI-M-BH3-ast-g-05-0-UI"
/dev_stages="27-32 days"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NIH BMAP M_S4"
/note="Vector: pRTT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The NIH_BMAP_M_S4 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hippocampus) after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: NIH_BMAP_M_S4, NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1, NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library (NIH_BMAP_M_S4) was constructed as follows: PCR amplified cDNA inserts from NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1 clones from which 3' ESTs had been derived was used as a driver in a hybridization with a pool of the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1 libraries in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the NIH_BMAP_M_S4 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)

TAG_TISSUE=brain-stems
TAG_LIB=NIH_BMAP_M_S4
TAG_SEQ=TCATG"

ORIGIN

Alignment Scores:
Pred. No.: 2.94e+03 Length: 470
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x AW490669 (1-470)

Qy 1 PheGlnIleGluHis 6
|||||
Db 300 TTCAGATTGAACACCAC 317

RESULT 88

BF706865

LOCUS 281517 MARC 3BOV Bos taurus cDNA 5', mRNA linear EST 25-APR-2001

DEFINITION BF706865

ACCESSION BF706865

VERSION BF706865.1

KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus

REFERENCE 1 (bases 1 to 473)

AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T., Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett,G.L., Heaton,M.P., Laegreid,W.M., Rohrer,G.A., Chitko-McKown,C.G., Perte,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and Keale,J.W.

TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

JOURNAL Genome Res. 11 (4), 626-630 (2001)

MEDLINE 21180013

PUBMED 11282978

COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCACGACG

Plate: 79 row: 0 column: 2

Seq primer: ATTAGTGACACTAG.

Location/Qualifiers

1..473

/organism="Bos taurus"

/mol_type="mRNA"

/db_xref="taxon:9913"

/tissue_type="pooled"

/lab_host="DH10B"

/clone_lib="MARC 3BOV"

/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinous muscle, and fetal longissimus muscle."

ORIGIN

Alignment Scores:

Pred. No.: 2.96e+03 Length: 473

Score: 36.00 Matches: 6

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x BF706865 (1-473)

Qy 1 PheGlnIleGluHis 6

|||||

Db 199 TTCAGATCGACCCAT 216

RESULT 89

BE756742

LOCUS 210977 MARC 2BOV Bos taurus cDNA 5', mRNA linear EST 25-APR-2001

DEFINITION BE756742

ACCESSION BE756742

VERSION BE756742.1

KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus

REFERENCE
AUTHORS
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
 1 (bases 1 to 474)

TITLE
 Smith, T.P.L., Grossee, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

JOURNAL
MEDLINE
PUBMED
 Genome Res. 11 (4), 626-630 (2001)
 21180013
 11282978

COMMENT
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTTCCCAGTCACGACG
 Plate: 59 row: C column: 24
 Seq primer: ATTAGGTGACACTATAG.
 Location/Qualifiers
 1. 474
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 2BOV"
 /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from testis, thymus, semitendinosus muscle, longissimus muscle, pancreas, adrenal, and endometrium."

FEATURES
 source
 1. 474

ORIGIN
 Alignment Scores:
 Pred. No.: 2.97e+03 Length: 474
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x BE756742 (1-474)

Qy
 1 PheGlnIleGluHisHis 6
 |||||

Db
 122 TTCCAGATCGAGCACCAT 139

RESULT 90
 BF890300
 LOCUS
 DEFINITION RH122_41_D11.g1_A003 Rhizome2 (RH122) Sorghum propinquum cDNA, mRNA
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Sorghum propinquum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE
AUTHORS
 1 (bases 1 to 477)
 Cordonnier-Pratt, M.-M., Gingle, A., Paterson, A., Sudman, M. and Pratt, L.H.
 An EST database from Sorghum: Sorghum propinquum rhizomes Unpublished (2000)
 Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmpratt@uga.edu

TITLE
 Quackenbush, J. and Keele, J.W.
 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle

JOURNAL
MEDLINE
PUBMED
 Genome Res. 11 (4), 626-630 (2001)
 21180013
 11282978

COMMENT
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTTCCCAGTCACGACG
 Plate: 57 row: H column: 16
 Seq primer: ATTAGGTGACACTATAG.
 Location/Qualifiers
 1. 477
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 3BOV"
 /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinosus muscle, and fetal longissimus muscle."

FEATURES
 source
 1. 477

ORIGIN
 Alignment Scores:
 Pred. No.: 2.99e+03 Length: 477
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x BF890300 (1-477)

Qy
 1 PheGlnIleGluHisHis 6
 |||||

Db
 119 TTCCAGATCGAGCACCAT 136

RESULT 91
 BG158520
 LOCUS
 DEFINITION RH122_41_D11.g1_A003 Rhizome2 (RH122) Sorghum propinquum cDNA, mRNA
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Sorghum propinquum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE
AUTHORS
 1 (bases 1 to 477)
 Cordonnier-Pratt, M.-M., Gingle, A., Paterson, A., Sudman, M. and Pratt, L.H.
 An EST database from Sorghum: Sorghum propinquum rhizomes Unpublished (2000)
 Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmpratt@uga.edu

Seq primer: PolyTwix
High quality sequence start: 115
High quality sequence stop: 476
POLYA=No.

FEATURES

Location/Qualifiers
1..477

/organism="Sorghum propinquum"
/mol_type="mRNA"
/db_xref="taxon:132711"
/clone_lib="Rhizome2 (RHIZ2)"
/note="Organ: Rhizomes; Vector: pBluescript II from Lambda Zap II; Site 1: XhoI; Site 2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."

ORIGIN

Alignment Scores:
Pred. No.: 2.99e+03 Length: 477
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x BG158520 (1-477)

QY 1 PheGlnIleGluHis 6
|||||
DB 58 TTCCAGATTGACCAT 75

RESULT 92

BM689101
LOCUS BM689101 477 bp mRNA linear EST 28-FEB-2002
DEFINITION UI-E-CQ1-act-b-04-0-UI.r1 UI-E-CQ1 Homo sapiens cDNA clone
UI-E-CQ1-act-b-04-0-UI 5', mRNA sequence.

ACCESSION BM689101
VERSION BM689101.1 GI:19002359
KEYWORDS EST.

SOURCE

ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS 1 (bases 1 to 477)
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 9704477
PubMed 889548

COMMENT

Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565

Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.regen.com).

Seq primer: M13 Reverse.

FEATURES

Location/Qualifiers
1..477
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-E-CQ1-act-b-04-0-UI"
/tissue_type="optic nerve"
/dev_stages="adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-E-CQ1"

/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoRI; Site 2: Not I; UI-E-CQ1 is a normalized cDNA library containing the following tissue(s): optic nerve. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoRI adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CCATTAAAGTG. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."

ORIGIN

Alignment Scores:
Pred. No.: 2.99e+03 Length: 477
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x BM689101 (1-477)

QY 1 PheGlnIleGluHis 6
|||||
DB 126 TTCCAGATCGAGCACCAC 143

RESULT 93

CD343234
LOCUS CD343234 480 bp mRNA linear EST 29-MAY-2003
DEFINITION EctStee66f08.y1 Eimeria tenella M5-6 Excised cDNA Eimeria tenella
cDNA 5' similar to TR:O15902 O15902 ACTIN DEPOLYMERIZING FACTOR. ;
mRNA sequence.

ACCESSION CD343234
VERSION CD343234.1 GI:31134855

KEYWORDS

SOURCE Eimeria tenella
ORGANISM Eimeria tenella

Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
Eimeria.

REFERENCE 1 (bases 1 to 480)

AUTHORS

Liberator, P., Diaz, C., Tang, K., Marra, M., Hillier, L., Kucaba, T.,
Martin, J., Wylie, T., Underwood, K., Steptoe, M., Theising, B.,
Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D.,
Harvey, N., Schurk, R., Ritter, E., Kohn, S., Florence, N., Shin, T.,
Jackson, Y., Cardenas, M., McCann, R., Waterston, R., Wilson, R. and
Sibley, D.

WashU-Merck Eimeria tenella project

TITLE

UNPUBLISHED (1999)

JOURNAL

COMMENT Contact: David Sibley, Ph.D.

WashU-Merck Eimeria tenella project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Contact David Sibley (toxoeat@borcim.wustl.edu) for further

information relating to organism, libraries, or clone availability.

Seq primer: -40RP from Gibco

High quality sequence stop: 304.

Location/Qualifiers

1..480

/organism="Eimeria tenella"

/mol_type="mRNA"

/db_xref="taxon:5802"

/dev_stages="L5L8"

/lab_host="E.coli DH10B (Genetec, Inc)"

/clone_lib="Eimeria tenella M5-6 Excised cDNA"

/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Sporozoites were obtained from in vitro sporulated and excysted oocysts of E. tenella grown in chickens. cDNA containing a xhoi site. Following second strand synthesis, EcoRI adapters were ligated to the cDNA and products were size-selected on sephacryl S500. The cDNA were ligated to EcoRI/XhoI prepared lambda ZapII (Stratagene). The primary library was mass excised using ExAssist helper phage (Stratagene). The phagemids were precipitated with PEG 8000, extracted with phenol/chloroform and electroporated into DH10B cells. The library may contain a small percentage of host or bacterial contaminants. Library materials provided by: Paul Liberator, Merck Research Labs Library constructed by: Paul Liberator, Merck Research Labs."

ORIGIN

Alignment Scores:
 Pred. No.: 3.02e+03 Length: 480
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-10-029-756-20 (1-6) x CD343234 (1-480)

Qy 1 PheGlnIleGluHisHis 6
 |||||
 Db 316 TTCAGATTGAGCACCAT 333

RESULT 94

BF654535
 LOCUS 278752 MARC 3BOV Bos taurus cDNA 5' mRNA linear EST 25-APR-2001
 DEFINITION
 ACCESSION BF654535
 VERSION BF654535.1 GI:11919667
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus

REFERENCE
 AUTHORS Smith, R.P.L., Grossee, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Caeas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Perte, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
 TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
 JOURNAL Genome Res. 11 (4), 626-630 (2001)
 MEDLINE 21180013
 PUBMED 11282978

COMMENT
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@mail.marc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCCTCAGTCACGACG
 Plate: 71 row: G column: 19
 Seq primer: ATTTAGGTGACACTATAG.
 Location/Qualifiers
 1. .487
 /organism="Bos taurus"
 /mol_type="mRNA"

FEATURES
 source

/db xref="taxon:9913"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 3BOV"
 /notes="vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
 Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinosus muscle, and fetal longissimus muscle."

ORIGIN

Alignment Scores:
 Pred. No.: 3.07e+03 Length: 487
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x BF654535 (1-487)

Qy 1 PheGlnIleGluHisHis 6
 |||||
 Db 215 TTCAGATCGAGCACCAT 232

RESULT 95

AW231075
 LOCUS u070e04.y1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:2647902 5'
 DEFINITION similar to TR:095864 095864 DELTA-6 FATTY ACID DESATURASE. ;, mRNA
 ACCESSION AW231075
 VERSION AW231075.1 GI:6560307
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS 1 (bases 1 to 489)
 TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 COMMENT Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapsb@mail.nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html

MG1:1028354

Seq primer: -40RP from Gibco
 High quality sequence stop: 434.

FEATURES
 source

1. .489
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="FVB/N"
 /db xref="taxon:10090"
 /tissue_type="tumor, biopsy sample"
 /dev_stage="3 months, virgin"
 /lab_host="DH10B"
 /clone_lib="NCI_CGAP Mam1"
 /notes="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Library constructed by Life Technologies. Investigator
 providing samples: Gilbert Smith, NIH"

ORIGIN

Alignment Scores:

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Pred. No.: 3.08e+03 Length: 489
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x AW231075 (1-489)

Qy 1 PheGlnlleGluHis 6
Db 260 TTCCAGATTGAGCACCAC 277

RESULT 96
BQ499479/c
LOCUS BQ499479 489 bp mRNA linear EST 31-OCT-2002
DEFINITION EST08704 Pb0001 Paracoccidioides brasiliensis cDNA, mRNA sequence.
ACCESSION BQ499479
VERSION BQ499479.1 GI:24452790
KEYWORDS EST.
SOURCE Paracoccidioides brasiliensis
ORGANISM Paracoccidioides brasiliensis
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Ongyenes; mitosporic Ongyenes; Paracoccidioides.

REFERENCE
AUTHORS Goldman, G.H., dos Reis Marques, E., Duarte Ribeiro, D.C., de Souza
Bernardes, L.A., Quiapin, A.C., Vitorelli, P.M., Savoldi, M.,
Semighini, C.P., de Oliveira, R.C., Nunes, L.R., Travassos, L.R.,
Puccia, R., Batista, W.L., Ferreira, L.E., Moreira, J.C.,
Bogossian, A.P., Tekia, F., Nobrega, M.P., Nobrega, F.G. and
Goldman, M.H.
TITLE Expressed sequence tag analysis of the human pathogen
Paracoccidioides brasiliensis yeast phase: identification of
putative homologues of Candida albicans virulence and pathogenicity
genes
JOURNAL Eukaryot. Cell 2 (1), 34-48 (2003)
COMMENT Contact: Gustavo Henrique Goldman
Laboratory of Molecular Biology
Universidade de Sao Paulo - USP - FCFRP
Av do Cafe S/N, CEP: 14040-903, Ribeirao Preto - SP, Brazil
Email: ggoldman@usp.br

FEATURES
source
1. 489
Location/Qualifiers
/organism="Paracoccidioides brasiliensis"
/mol_type="mRNA"
/db_xref="taxon:121759"
/clone_lib="PB0001"

ORIGIN
Alignment Scores:
Pred. No.: 3.08e+03 Length: 489
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-10-029-756-20 (1-6) x BQ499479 (1-489)

Qy 1 PheGlnlleGluHis 6
Db 157 TTCCAGATTGAGCATCAT 140

RESULT 97
BQ774199
LOCUS BQ774199 490 bp mRNA linear EST 25-APR-2001
DEFINITION BQ774199 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BQ774199
VERSION BQ774199.1 GI:12122099
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 490)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,
Casas, E., Wray, J.E., White, J., Cho, J., Fahrrenkrug, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chitko-McKown, C.G., Pettea, G., Holt, I., Karamycheva, S., Liang, F.,
Quackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
Genome Res. 11 (4), 626-630 (2001)
21180013
11282978
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCAGTCAGCAG
Plate: 83 row: F column: 6
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
1. 490
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 3BOV"
Notes=Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."

ORIGIN
Alignment Scores:
Pred. No.: 3.09e+03 Length: 490
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x BQ774199 (1-490)

Qy 1 PheGlnlleGluHis 6
Db 300 TTCCAGATTGAGCACCAT 317

RESULT 98
BQ097454/c
LOCUS BQ097454 492 bp mRNA linear EST 12-JUN-2000
DEFINITION UI-R-B01-apx-f-12-0-UI.s1 UI-R-B01 Rattus norvegicus cDNA clone
UI-R-B01-apx-f-12-0-UI 3', mRNA sequence.
ACCESSION BQ097454
VERSION BQ097454.1 GI:8488385
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 492)
Bonaldo, M.P., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL

```

```

MEDLINE 97044477
PUBMED 8989548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road , 4156 MBBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
normalized hypothalamus library cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA=Yes.

FEATURES
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    1. .492
    /organism="Rattus norvegicus"
    /mol_type="mRNA"
    /strain="Sprague-Dawley"
    /db_xref="taxon:10116"
    /clone="UI-R-B01-afx-f-12-0-UI"
    /dev_stage="adult"
    /lab_host="DHI08 (Life Technologies)"
    /clone_lib="UI-R-B01"
    /note="Vector: p7T3D-Pac (Pharmacia) with a modified
    polylinker; Site 1: Not I; Site 2: Eco RI; The library
    (UI-R-B01) is a subcloned library derived from a mixture
    of the following tissues: thalamus, cerebellum,
    hypothalamus, medulla, pons, midbrain, cerebral cortex,
    corpus striatum and hippocampus. For a detailed
    description of the library from which this clone was
    derived, please visit our web site at
    ratest.eng.uiowa.edu. The subtraction has been previously
    described in (Bonaldo, Lennon and Soares, Genome Research
    6:791-806, 1996)
    TAG_TISSUE=hypothalamus
    TAG_LIB=UI-R-B01
    TAG_SEQ=GATGC"

ORIGIN
Alignment Scores:
Pred. No.: 3.11e+03 Length: 492
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x BE097454 (1-492)

Qy 1 PheGlnIleGluHisHis 6
Db 337 TTCCAGATTGACACCAC 320

RESULT 99
CR305637 496 bp DNA linear GSS 01-MAR-2004
LOCUS Medicago truncatula BAC ends cultivar Jemalong A17 of Medicago
DEFINITION truncatula, genomic survey sequence.
ACCESSION CR305637
VERSION CR305637.1 GI:44851781
KEYWORDS GSS.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.

```

```

REFERENCE 1 (bases 1 to 496)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (25-FEB-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
FEATURES
    Location/Qualifiers
    source
    1. .496
    /organism="Medicago truncatula"
    /mol_type="genomic DNA"
    /cultivar="Jemalong A17"
    /db_xref="taxon:3880"
    /clone_lib="MTE1"
    /note="Vector: pIndigoBAC ; Site 1: EcoRI ; Site 2: EcoRI
    ; Deballe F. and Chalhou B.-genoscope sequence ID :
    mte1-25M12FML"

ORIGIN
Alignment Scores:
Pred. No.: 3.14e+03 Length: 496
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-029-756-20 (1-6) x CR305637 (1-496)

Qy 1 PheGlnIleGluHisHis 6
Db 16 TTTCAATTCGATCAT 33

RESULT 100
CR305637/c 501 bp mRNA linear EST 26-JUL-2004
LOCUS DG32-106d16 DG32-liver Canis familiaris cDNA 3', mRNA sequence.
DEFINITION
ACCESSION CO696980
VERSION CO696980.1 GI:50645534
KEYWORDS EST.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 501)
AUTHORS Schlueter, T., Hermanns, J., Weindel, M., Schuetter, D., Kranz, H.,
Henrich, J. and Loebbert, R.
TITLE Dog arrayTAG cDNA clone collection
JOURNAL Unpublished (2004)
COMMENT Contact: Thomas Schlueter
LION bioscience AG
Waldhoferstrasse 98, D-69123 Heidelberg, Germany
Tel: +49 6221 4038 150
Fax: +49 6221 4038 290
Email: Thomas.Schlueter@lionbioscience.com.
FEATURES
    Location/Qualifiers
    source
    1. .501
    /organism="Canis familiaris"
    /mol_type="mRNA"
    /strain="Beagle"
    /db_xref="taxon:9615"
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    /dev_stage="adult"
    /lab_host="DHI08"
    /clone_lib="DG32-liver"
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ORIGIN
Alignment Scores:
Pred. No.: 3.18e+03 Length: 501
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

```

DB: 7 Gaps: 0

US-10-029-756-20 (1-6) x CO696980 (1-501)

Qy 1 PheGlnIleGluHis 6

Db 292 TTCCAGATTGACCAT 275

Search completed: June 8, 2005, 15:13:56
Job time : 2534.16 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 8, 2005, 11:36:25 ; Search time 91.5789 Seconds

(without alignments)
107.204 Million cell updates/sec

Title: US-10-029-756-20

Perfect score: 36

Sequence: 1 FQIEHH 6

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10029756/runat_07062005_122751_28805/app_query.fasta_1.597
-DB=Issued Patents NA -QWTF=fastap -SUPPLX=p2n.rn1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=dlosum62 -TRANS=human40.cdi
-LIST=1000 -OUTALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=100
-MODE=LOCAL -DOUFTW=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10029756@cgn 1 1 177 @runat 07062005_122751_28805 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | No. | Score | Query Match | Length | ID | Description |
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| 1 | 36 | 100.0 | 266 | 4 | US-09-313-294A-3256 | Sequence 3256, Ap |
| 2 | 36 | 100.0 | 291 | 4 | US-09-313-294A-1966 | Sequence 1966, Ap |
| 3 | 36 | 100.0 | 347 | 4 | US-09-702-705-355 | Sequence 355, App |
| 4 | 36 | 100.0 | 347 | 4 | US-09-736-457-355 | Sequence 355, App |
| 5 | 36 | 100.0 | 347 | 4 | US-09-614-144B-355 | Sequence 355, App |
| 6 | 36 | 100.0 | 347 | 4 | US-09-671-325-355 | Sequence 355, App |
| 7 | 36 | 100.0 | 347 | 4 | US-09-589-184-355 | Sequence 355, App |
| 8 | 36 | 100.0 | 347 | 4 | US-09-658-824-355 | Sequence 355, App |
| 9 | 36 | 100.0 | 372 | 4 | US-09-710-279-1855 | Sequence 1855, Ap |
| 10 | 36 | 100.0 | 405 | 3 | US-09-134-001C-1672 | Sequence 1672, Ap |
| 11 | 36 | 100.0 | 449 | 3 | US-09-439-261-38 | Sequence 38, Appl |
| 12 | 36 | 100.0 | 449 | 3 | US-09-227-613-37 | Sequence 37, Appl |

| | | | | | | |
|----|----|-------|--------|---|----------------------|--------------------|
| 13 | 36 | 100.0 | 473 | 3 | US-09-439-261-37 | Sequence 37, Appl |
| 14 | 36 | 100.0 | 473 | 3 | US-09-227-613-36 | Sequence 36, Appl |
| 15 | 36 | 100.0 | 655 | 3 | US-09-439-261-3 | Sequence 3, Appl |
| 16 | 36 | 100.0 | 655 | 3 | US-09-227-613-3 | Sequence 3, Appl |
| 17 | 36 | 100.0 | 864 | 3 | US-09-439-261-12 | Sequence 12, Appl |
| 18 | 36 | 100.0 | 864 | 3 | US-09-227-613-13 | Sequence 13, Appl |
| 19 | 36 | 100.0 | 876 | 4 | US-09-248-796A-2259 | Sequence 2259, Ap |
| 20 | 36 | 100.0 | 1132 | 4 | US-09-710-279-4425 | Sequence 4425, Ap |
| 21 | 36 | 100.0 | 1320 | 4 | US-09-769-863-28 | Sequence 28, Appl |
| 22 | 36 | 100.0 | 1335 | 3 | US-09-439-261-1 | Sequence 1, Appl |
| 23 | 36 | 100.0 | 1335 | 3 | US-09-227-613-1 | Sequence 1, Appl |
| 24 | 36 | 100.0 | 1478 | 4 | US-09-148-545-63 | Sequence 63, Appl |
| 25 | 36 | 100.0 | 1684 | 2 | US-08-831-570-1 | Sequence 1, Appl |
| 26 | 36 | 100.0 | 1684 | 2 | US-08-831-575-1 | Sequence 1, Appl |
| 27 | 36 | 100.0 | 1685 | 1 | US-08-366-779-1 | Sequence 4, Appl |
| 28 | 36 | 100.0 | 1685 | 1 | US-08-789-936-4 | Sequence 4, Appl |
| 29 | 36 | 100.0 | 1685 | 3 | US-08-934-254-4 | Sequence 4, Appl |
| 30 | 36 | 100.0 | 1685 | 4 | US-09-685-775-4 | Sequence 4, Appl |
| 31 | 36 | 100.0 | 1686 | 3 | US-09-439-261-6 | Sequence 6, Appl |
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| 33 | 36 | 100.0 | 1717 | 4 | US-09-048-888-2 | Sequence 2, Appl |
| 34 | 36 | 100.0 | 1758 | 4 | US-09-949-016-4904 | Sequence 4904, Ap |
| 35 | 36 | 100.0 | 1843 | 3 | US-09-439-261-7 | Sequence 7, Appl |
| 36 | 36 | 100.0 | 1843 | 3 | US-09-227-613-7 | Sequence 7, Appl |
| 37 | 36 | 100.0 | 1928 | 4 | US-08-048-888-4 | Sequence 4, Appl |
| 38 | 36 | 100.0 | 2016 | 4 | US-09-148-545-119 | Sequence 119, App |
| 39 | 36 | 100.0 | 2257 | 3 | US-09-439-261-8 | Sequence 8, Appl |
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| 41 | 36 | 100.0 | 2540 | 4 | US-09-023-655-295 | Sequence 295, App |
| 42 | 36 | 100.0 | 3158 | 4 | US-09-949-016-4613 | Sequence 4613, Ap |
| 43 | 36 | 100.0 | 4103 | 4 | US-09-710-279-4180 | Sequence 4180, Ap |
| 44 | 36 | 100.0 | 15595 | 4 | US-09-949-016-16077 | Sequence 16077, A |
| 45 | 36 | 100.0 | 26684 | 4 | US-09-949-016-15109 | Sequence 15109, A |
| 46 | 36 | 100.0 | 26684 | 4 | US-09-949-016-15110 | Sequence 15110, A |
| 47 | 36 | 100.0 | 26684 | 4 | US-09-949-016-17409 | Sequence 17409, A |
| 48 | 36 | 100.0 | 26684 | 4 | US-09-949-016-17410 | Sequence 17410, A |
| 49 | 36 | 100.0 | 175265 | 4 | US-09-949-016-16089 | Sequence 16089, A |
| 50 | 35 | 97.2 | 5593 | 4 | US-09-672-265-7 | Sequence 7, Appl |
| 51 | 35 | 97.2 | 6216 | 3 | US-09-415-522-5 | Sequence 5, Appl |
| 52 | 34 | 94.4 | 33 | 2 | US-08-834-655-14 | Sequence 14, Appl |
| 53 | 34 | 94.4 | 33 | 3 | US-08-834-033A-22 | Sequence 22, Appl |
| 54 | 34 | 94.4 | 33 | 3 | US-08-363-574-14 | Sequence 14, Appl |
| 55 | 34 | 94.4 | 33 | 3 | US-09-363-576-14 | Sequence 14, Appl |
| 56 | 34 | 94.4 | 315 | 4 | US-09-489-039A-5096 | Sequence 5096, Ap |
| 57 | 34 | 94.4 | 447 | 3 | US-08-836-075A-3 | Sequence 3, Appl |
| 58 | 34 | 94.4 | 447 | 3 | US-08-836-075A-7 | Sequence 7, Appl |
| 59 | 34 | 94.4 | 601 | 4 | US-09-949-016-202174 | Sequence 202174, A |
| 60 | 34 | 94.4 | 601 | 4 | US-09-949-016-202175 | Sequence 202175, A |
| 61 | 34 | 94.4 | 601 | 4 | US-09-949-016-202176 | Sequence 202176, A |
| 62 | 34 | 94.4 | 1365 | 4 | US-09-578-063-34 | Sequence 34, Appl |
| 63 | 34 | 94.4 | 1702 | 3 | US-08-934-254-26 | Sequence 26, Appl |
| 64 | 34 | 94.4 | 1702 | 4 | US-09-685-775-26 | Sequence 26, Appl |
| 65 | 34 | 94.4 | 1980 | 4 | US-09-578-063-33 | Sequence 33, Appl |
| 66 | 34 | 94.4 | 2688 | 4 | US-09-489-039A-5328 | Sequence 5328, Ap |
| 67 | 34 | 94.4 | 6876 | 4 | US-08-956-171E-186 | Sequence 186, App |
| 68 | 34 | 94.4 | 6876 | 4 | US-08-781-986A-186 | Sequence 186, App |
| 69 | 34 | 94.4 | 99580 | 4 | US-09-949-016-17411 | Sequence 17411, A |
| 70 | 34 | 94.4 | 421491 | 4 | US-09-949-016-12805 | Sequence 12805, A |
| 71 | 34 | 94.4 | 421494 | 4 | US-09-949-016-14060 | Sequence 14060, A |
| 72 | 33 | 91.7 | 249 | 3 | US-09-134-001C-2030 | Sequence 2030, Ap |
| 73 | 33 | 91.7 | 306 | 4 | US-09-248-796A-9501 | Sequence 9501, Ap |
| 74 | 33 | 91.7 | 601 | 4 | US-09-949-016-160344 | Sequence 160344, A |
| 75 | 33 | 91.7 | 601 | 4 | US-09-949-016-160345 | Sequence 160345, A |
| 76 | 33 | 91.7 | 1122 | 4 | US-09-902-540-9255 | Sequence 9255, Ap |
| 77 | 33 | 91.7 | 1281 | 4 | US-09-857-583B-3 | Sequence 3, Appl |
| 78 | 33 | 91.7 | 1461 | 4 | US-09-857-583B-1 | Sequence 1, Appl |
| 79 | 33 | 91.7 | 1617 | 2 | US-08-834-655-1 | Sequence 1, Appl |
| 80 | 33 | 91.7 | 1617 | 3 | US-08-834-033A-1 | Sequence 1, Appl |
| 81 | 33 | 91.7 | 1617 | 3 | US-09-363-574-1 | Sequence 1, Appl |
| 82 | 33 | 91.7 | 1617 | 3 | US-09-363-526-1 | Sequence 1, Appl |
| 83 | 33 | 91.7 | 1617 | 3 | US-09-330-235-17 | Sequence 17, Appl |
| 84 | 33 | 91.7 | 1980 | 4 | US-09-710-279-1595 | Sequence 1595, Ap |
| 85 | 33 | 91.7 | 2073 | 3 | US-09-134-001C-2101 | Sequence 2101, Ap |

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|-----|----|------|---------|---|----------------------|--------------------|-------|----|------|---------|---|---------------------|--------------------|
| 86 | 33 | 91.7 | 3004 | 4 | US-09-710-279-4299 | Sequence 4299, Ap | c 159 | 31 | 86.1 | 2514 | 4 | US-09-489-039A-2214 | Sequence 2214, Ap |
| 87 | 33 | 91.7 | 3177 | 4 | US-09-710-279-3717 | Sequence 3717, Ap | 160 | 31 | 86.1 | 2517 | 3 | US-08-985-908-25 | Sequence 25, Appl |
| 88 | 33 | 91.7 | 3320 | 4 | US-09-710-279-3649 | Sequence 3649, Ap | 161 | 31 | 86.1 | 2517 | 3 | US-08-985-908-30 | Sequence 30, Appl |
| 89 | 33 | 91.7 | 3459 | 4 | US-09-016-434-1363 | Sequence 1363, Ap | c 162 | 31 | 86.1 | 2968 | 4 | US-09-527-058-6 | Sequence 6, Appl |
| 90 | 33 | 91.7 | 3643 | 4 | US-09-710-279-4011 | Sequence 4011, Ap | c 163 | 31 | 86.1 | 3623 | 4 | US-09-918-309A-23 | Sequence 23, Appl |
| 91 | 33 | 91.7 | 10322 | 4 | US-09-902-540-989 | Sequence 989, App | c 164 | 31 | 86.1 | 3910 | 4 | US-09-990-337-1 | Sequence 1, Appl |
| 92 | 33 | 91.7 | 15249 | 4 | US-08-956-171E-102 | Sequence 102, App | c 165 | 31 | 86.1 | 3984 | 3 | US-08-961-527-176 | Sequence 176, App |
| 93 | 33 | 91.7 | 15249 | 4 | US-08-781-986A-102 | Sequence 102, App | c 166 | 31 | 86.1 | 5183 | 1 | US-08-459-568-3 | Sequence 3, Appl |
| 94 | 33 | 91.7 | 30053 | 4 | US-09-949-016-16231 | Sequence 16231, A | c 167 | 31 | 86.1 | 5183 | 2 | US-08-399-411-3 | Sequence 3, Appl |
| 95 | 33 | 91.7 | 48974 | 3 | US-08-920-422-17 | Sequence 17, Appl | c 168 | 31 | 86.1 | 5426 | 4 | US-09-814-915A-8 | Sequence 8, Appl |
| 96 | 33 | 91.7 | 69752 | 4 | US-09-949-016-14094 | Sequence 14094, A | c 169 | 31 | 86.1 | 5444 | 4 | US-09-566-921-114 | Sequence 114, App |
| 97 | 33 | 91.7 | 767677 | 4 | US-09-949-016-12147 | Sequence 12147, A | c 170 | 31 | 86.1 | 5868 | 3 | US-08-516-859A-3 | Sequence 3, Appl |
| 98 | 33 | 91.7 | 767677 | 4 | US-09-949-016-17361 | Sequence 17361, A | c 171 | 31 | 86.1 | 5868 | 3 | US-09-586-472-3 | Sequence 3, Appl |
| 99 | 33 | 91.7 | 786431 | 4 | US-09-751-389-3 | Sequence 3, Appl | c 172 | 31 | 86.1 | 5868 | 3 | US-09-528-706-3 | Sequence 3, Appl |
| 100 | 33 | 91.7 | 1664976 | 4 | US-08-916-421B-1 | Sequence 1, Appl | c 173 | 31 | 86.1 | 5907 | 4 | US-09-976-594-892 | Sequence 892, App |
| 101 | 33 | 91.7 | 1664976 | 4 | US-09-692-570-1 | Sequence 1, Appl | c 174 | 31 | 86.1 | 5989 | 4 | US-09-949-016-5099 | Sequence 5099, App |
| 102 | 32 | 88.9 | 480 | 4 | US-09-621-976-13994 | Sequence 13994, A | c 175 | 31 | 86.1 | 6173 | 4 | US-09-949-016-5511 | Sequence 5511, App |
| 103 | 32 | 88.9 | 525 | 4 | US-09-134-000C-2245 | Sequence 2245, Ap | c 176 | 31 | 86.1 | 6173 | 4 | US-09-949-016-5512 | Sequence 5512, App |
| 104 | 32 | 88.9 | 558 | 4 | US-09-583-110-2141 | Sequence 2141, Ap | c 177 | 31 | 86.1 | 6416 | 3 | US-09-136-574A-2 | Sequence 2, Appl |
| 105 | 32 | 88.9 | 594 | 4 | US-09-583-110-2142 | Sequence 2142, Ap | c 178 | 31 | 86.1 | 6766 | 4 | US-09-527-058-1 | Sequence 1, Appl |
| 106 | 32 | 88.9 | 601 | 4 | US-09-949-016-69962 | Sequence 69962, A | c 179 | 31 | 86.1 | 15442 | 4 | US-09-949-016-16689 | Sequence 16689, A |
| 107 | 32 | 88.9 | 601 | 4 | US-09-949-016-76381 | Sequence 76381, A | c 180 | 31 | 86.1 | 16520 | 4 | US-09-949-016-14710 | Sequence 14710, A |
| 108 | 32 | 88.9 | 601 | 4 | US-09-949-016-76382 | Sequence 76382, A | c 181 | 31 | 86.1 | 16520 | 4 | US-09-949-016-15394 | Sequence 15394, A |
| 109 | 32 | 88.9 | 601 | 4 | US-09-949-016-169370 | Sequence 169370, A | c 182 | 31 | 86.1 | 17862 | 4 | US-09-902-540-1130 | Sequence 1130, App |
| 110 | 32 | 88.9 | 601 | 4 | US-09-949-016-189213 | Sequence 189213, A | c 183 | 31 | 86.1 | 25048 | 4 | US-09-902-540-1239 | Sequence 1239, App |
| 111 | 32 | 88.9 | 603 | 4 | US-09-489-039A-3641 | Sequence 3641, Ap | c 184 | 31 | 86.1 | 26103 | 4 | US-09-949-016-16841 | Sequence 16841, A |
| 112 | 32 | 88.9 | 609 | 4 | US-09-107-433-1114 | Sequence 1114, Ap | c 185 | 31 | 86.1 | 29555 | 4 | US-08-956-171B-206 | Sequence 206, App |
| 113 | 32 | 88.9 | 921 | 4 | US-09-252-931A-16185 | Sequence 16185, A | c 186 | 31 | 86.1 | 29555 | 4 | US-08-781-986A-206 | Sequence 206, App |
| 114 | 32 | 88.9 | 1011 | 4 | US-09-252-931A-16405 | Sequence 16405, A | c 187 | 31 | 86.1 | 40123 | 4 | US-08-311-731A-137 | Sequence 137, App |
| 115 | 32 | 88.9 | 1149 | 4 | US-09-328-352-355 | Sequence 355, App | c 188 | 31 | 86.1 | 41941 | 4 | US-09-949-016-17380 | Sequence 17380, A |
| 116 | 32 | 88.9 | 2868 | 3 | US-09-228-866-4 | Sequence 4, Appl | c 189 | 31 | 86.1 | 42394 | 4 | US-09-949-016-12752 | Sequence 12752, A |
| 117 | 32 | 88.9 | 2868 | 4 | US-10-101-464A-4 | Sequence 4, Appl | c 190 | 31 | 86.1 | 42395 | 4 | US-09-949-016-15115 | Sequence 15115, A |
| 118 | 32 | 88.9 | 14273 | 3 | US-08-961-527-40 | Sequence 40, Appl | c 191 | 31 | 86.1 | 42672 | 4 | US-09-949-016-17253 | Sequence 17253, A |
| 119 | 32 | 88.9 | 35047 | 4 | US-09-949-016-13965 | Sequence 13966, A | c 192 | 31 | 86.1 | 42672 | 4 | US-09-949-016-17254 | Sequence 17254, A |
| 120 | 32 | 88.9 | 43348 | 4 | US-09-949-016-17157 | Sequence 17157, A | c 193 | 31 | 86.1 | 46118 | 4 | US-09-949-016-17003 | Sequence 17003, A |
| 121 | 32 | 88.9 | 85963 | 4 | US-09-949-016-13804 | Sequence 13804, A | c 194 | 31 | 86.1 | 57267 | 4 | US-09-949-016-13789 | Sequence 13789, A |
| 122 | 32 | 88.9 | 121384 | 4 | US-09-949-016-16944 | Sequence 16944, A | c 195 | 31 | 86.1 | 58844 | 4 | US-09-949-016-13769 | Sequence 13769, A |
| 123 | 32 | 88.9 | 177293 | 4 | US-09-949-016-16513 | Sequence 16513, A | c 196 | 31 | 86.1 | 75126 | 4 | US-09-949-016-13300 | Sequence 13300, A |
| 124 | 31 | 86.1 | 228 | 4 | US-09-248-796A-13200 | Sequence 13200, A | c 197 | 31 | 86.1 | 88268 | 4 | US-09-949-016-14178 | Sequence 14178, A |
| 125 | 31 | 86.1 | 407 | 4 | US-09-621-976-10889 | Sequence 10889, A | c 198 | 31 | 86.1 | 101015 | 4 | US-09-949-016-16981 | Sequence 16981, A |
| 126 | 31 | 86.1 | 421 | 4 | US-09-513-999C-492 | Sequence 492, App | c 199 | 31 | 86.1 | 113379 | 4 | US-09-949-016-17561 | Sequence 17561, A |
| 127 | 31 | 86.1 | 426 | 4 | US-09-513-999C-25721 | Sequence 25721, A | c 200 | 31 | 86.1 | 113379 | 4 | US-09-949-016-17562 | Sequence 17562, A |
| 128 | 31 | 86.1 | 429 | 4 | US-09-471-276-717 | Sequence 717, App | c 201 | 31 | 86.1 | 178883 | 4 | US-09-949-016-12733 | Sequence 12733, A |
| 129 | 31 | 86.1 | 435 | 4 | US-09-540-236-1152 | Sequence 1152, Ap | c 202 | 31 | 86.1 | 178884 | 4 | US-09-949-016-13039 | Sequence 13039, A |
| 130 | 31 | 86.1 | 531 | 4 | US-10-101-464A-229 | Sequence 229, App | c 203 | 31 | 86.1 | 181429 | 4 | US-09-949-016-12372 | Sequence 12372, A |
| 131 | 31 | 86.1 | 594 | 4 | US-09-543-681A-1140 | Sequence 1140, Ap | c 204 | 31 | 86.1 | 181430 | 4 | US-09-949-016-15772 | Sequence 15772, A |
| 132 | 31 | 86.1 | 601 | 4 | US-09-949-016-37235 | Sequence 37235, A | c 205 | 31 | 86.1 | 191433 | 4 | US-09-949-016-16144 | Sequence 16144, A |
| 133 | 31 | 86.1 | 601 | 4 | US-09-949-016-107262 | Sequence 107262, A | c 206 | 31 | 86.1 | 194790 | 4 | US-09-949-016-15393 | Sequence 15393, A |
| 134 | 31 | 86.1 | 601 | 4 | US-09-949-016-107263 | Sequence 107263, A | c 207 | 31 | 86.1 | 246230 | 4 | US-09-949-016-17019 | Sequence 17019, A |
| 135 | 31 | 86.1 | 601 | 4 | US-09-949-016-128774 | Sequence 128774, A | c 208 | 31 | 86.1 | 246230 | 4 | US-09-949-016-17020 | Sequence 17020, A |
| 136 | 31 | 86.1 | 601 | 4 | US-09-949-016-128775 | Sequence 128775, A | c 209 | 31 | 86.1 | 246230 | 4 | US-09-949-016-17021 | Sequence 17021, A |
| 137 | 31 | 86.1 | 601 | 4 | US-09-949-016-141959 | Sequence 141959, A | c 210 | 31 | 86.1 | 246230 | 4 | US-09-949-016-17022 | Sequence 17022, A |
| 138 | 31 | 86.1 | 724 | 4 | US-09-976-594-894 | Sequence 894, App | c 211 | 31 | 86.1 | 246444 | 4 | US-09-949-016-13113 | Sequence 13113, A |
| 139 | 31 | 86.1 | 918 | 4 | US-09-328-352-1742 | Sequence 1742, Ap | c 212 | 31 | 86.1 | 260286 | 4 | US-09-949-016-17037 | Sequence 17037, A |
| 140 | 31 | 86.1 | 1023 | 4 | US-09-583-110-13 | Sequence 13, Appl | c 213 | 31 | 86.1 | 260293 | 4 | US-09-949-016-12106 | Sequence 12106, A |
| 141 | 31 | 86.1 | 1038 | 4 | US-09-107-433-1513 | Sequence 1513, Ap | c 214 | 31 | 86.1 | 300402 | 4 | US-09-949-016-13632 | Sequence 13632, A |
| 142 | 31 | 86.1 | 1065 | 4 | US-09-248-796A-333 | Sequence 333, App | c 215 | 31 | 86.1 | 312474 | 4 | US-09-949-016-17434 | Sequence 17434, A |
| 143 | 31 | 86.1 | 1161 | 4 | US-09-902-540-2751 | Sequence 2751, Ap | c 216 | 31 | 86.1 | 363032 | 4 | US-09-949-016-12415 | Sequence 12415, A |
| 144 | 31 | 86.1 | 1175 | 4 | US-09-270-767-12320 | Sequence 12320, A | c 217 | 31 | 86.1 | 363033 | 4 | US-09-949-016-15794 | Sequence 15794, A |
| 145 | 31 | 86.1 | 1296 | 4 | US-09-527-058-5 | Sequence 5, Appl | c 218 | 31 | 86.1 | 387902 | 4 | US-09-949-016-14543 | Sequence 14543, A |
| 146 | 31 | 86.1 | 1428 | 4 | US-09-520-781-15 | Sequence 15, Appl | c 219 | 31 | 86.1 | 421883 | 4 | US-09-949-016-12557 | Sequence 12557, A |
| 147 | 31 | 86.1 | 1464 | 4 | US-09-489-039A-2216 | Sequence 2216, Ap | c 220 | 31 | 86.1 | 451925 | 4 | US-09-949-016-12896 | Sequence 12896, A |
| 148 | 31 | 86.1 | 1563 | 4 | US-09-328-352-3325 | Sequence 3325, Ap | c 221 | 31 | 86.1 | 451925 | 4 | US-09-949-016-17305 | Sequence 17305, A |
| 149 | 31 | 86.1 | 1704 | 4 | US-09-107-532A-3076 | Sequence 3076, Ap | c 222 | 31 | 86.1 | 4403765 | 3 | US-09-103-840A-2 | Sequence 2, Appl |
| 150 | 31 | 86.1 | 1782 | 4 | US-09-134-000C-1981 | Sequence 1981, Ap | c 223 | 31 | 86.1 | 4411529 | 3 | US-09-103-840A-2 | Sequence 2, Appl |
| 151 | 31 | 86.1 | 1834 | 1 | US-09-248-796A-5237 | Sequence 5237, Ap | c 224 | 30 | 83.3 | 29 | 3 | US-09-439-261-52 | Sequence 52, Appl |
| 152 | 31 | 86.1 | 1834 | 1 | US-08-297-633A-1 | Sequence 1, Appl | c 225 | 30 | 83.3 | 30 | 4 | US-09-857-583B-6 | Sequence 6, Appl |
| 153 | 31 | 86.1 | 1834 | 1 | US-08-485-721-8 | Sequence 8, Appl | c 226 | 30 | 83.3 | 34 | 1 | US-08-422-101-16 | Sequence 16, Appl |
| 154 | 31 | 86.1 | 1834 | 2 | US-08-392-935-8 | Sequence 8, Appl | c 227 | 30 | 83.3 | 34 | 1 | US-08-422-091-16 | Sequence 16, Appl |
| 155 | 31 | 86.1 | 1834 | 5 | PCT-US93-08325-1 | Sequence 1, Appl | c 228 | 30 | 83.3 | 34 | 2 | US-08-422-092-16 | Sequence 16, Appl |
| 156 | 31 | 86.1 | 1834 | 5 | PCT-US93-08326-8 | Sequence 8, Appl | c 229 | 30 | 83.3 | 34 | 3 | US-08-422-093-16 | Sequence 16, Appl |
| 157 | 31 | 86.1 | 2460 | 4 | US-09-614-221A-419 | Sequence 419, App | c 230 | 30 | 83.3 | 34 | 3 | US-08-422-112-16 | Sequence 16, Appl |
| 158 | 31 | 86.1 | 2465 | 4 | US-09-774-528-180 | Sequence 180, App | c 231 | 30 | 83.3 | 47 | 3 | US-09-146-054-7 | Sequence 7, Appl |

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| C 232 | 30 | 83.3 | 47 | 3 | US-09-664-977A-7 | Sequence 7, Appli | c 305 | 30 | 83.3 | 841 | 3 | US-08-639-075A-110 | Sequence 110, Ap |
| C 233 | 30 | 83.3 | 270 | 3 | US-09-146-054-B | Sequence 8, Appli | c 306 | 30 | 83.3 | 841 | 3 | US-09-012-431-110 | Sequence 36, Appl |
| C 234 | 30 | 83.3 | 270 | 3 | US-09-664-977A-8 | Sequence 8, Appli | c 307 | 30 | 83.3 | 841 | 3 | US-09-032-215-36 | Sequence 38, Appl |
| C 235 | 30 | 83.3 | 274 | 4 | US-09-313-294A-1061 | Sequence 1061, Ap | c 308 | 30 | 83.3 | 841 | 3 | US-09-032-215-38 | Sequence 110, App |
| C 236 | 30 | 83.3 | 291 | 4 | US-09-636-215-823 | Sequence 823, App | c 309 | 30 | 83.3 | 841 | 3 | US-09-012-692-110 | Sequence 110, App |
| C 237 | 30 | 83.3 | 291 | 4 | US-09-685-166A-823 | Sequence 823, App | c 310 | 30 | 83.3 | 841 | 3 | US-08-906-613-110 | Sequence 110, App |
| C 238 | 30 | 83.3 | 291 | 4 | US-09-679-426-823 | Sequence 823, App | c 311 | 30 | 83.3 | 841 | 5 | PCT-US95-14442A-110 | Sequence 10399, A |
| C 239 | 30 | 83.3 | 291 | 4 | US-09-759-143-823 | Sequence 823, App | c 312 | 30 | 83.3 | 892 | 4 | US-09-270-767-10399 | Sequence 10399, A |
| C 240 | 30 | 83.3 | 291 | 4 | US-09-651-236-823 | Sequence 823, App | c 313 | 30 | 83.3 | 909 | 4 | US-09-252-991A-9793 | Sequence 9793, A |
| C 241 | 30 | 83.3 | 294 | 3 | US-08-816-977-22 | Sequence 22, Appl | c 314 | 30 | 83.3 | 938 | 2 | US-08-879-128-1 | Sequence 1, Appli |
| C 242 | 30 | 83.3 | 294 | 4 | US-09-334-477-22 | Sequence 22, Appl | c 315 | 30 | 83.3 | 938 | 4 | US-09-270-767-14547 | A |
| C 243 | 30 | 83.3 | 311 | 4 | US-09-313-294A-4963 | Sequence 4963, Ap | c 316 | 30 | 83.3 | 963 | 4 | US-09-489-039A-6389 | Sequence 6389, Ap |
| C 244 | 30 | 83.3 | 318 | 3 | US-09-134-001C-2370 | Sequence 2370, Ap | c 317 | 30 | 83.3 | 963 | 4 | US-09-270-767-13650 | Sequence 13650, A |
| C 245 | 30 | 83.3 | 363 | 4 | US-09-513-999C-2130 | Sequence 2130, Ap | c 318 | 30 | 83.3 | 987 | 4 | US-09-270-767-13650 | Sequence 49, Appl |
| C 246 | 30 | 83.3 | 390 | 4 | US-09-252-991A-12635 | Sequence 12635, A | c 319 | 30 | 83.3 | 987 | 4 | US-09-734-237B-49 | Sequence 51, Appl |
| C 247 | 30 | 83.3 | 394 | 4 | US-09-270-767-1270 | Sequence 1270, Ap | c 320 | 30 | 83.3 | 1035 | 4 | US-09-107-532A-2395 | Sequence 2395, Ap |
| C 248 | 30 | 83.3 | 394 | 4 | US-09-270-767-16552 | Sequence 16552, A | c 321 | 30 | 83.3 | 1035 | 4 | US-09-489-039A-44 | Sequence 44, Appl |
| C 249 | 30 | 83.3 | 489 | 4 | US-09-902-540-3331 | Sequence 3331, Ap | c 322 | 30 | 83.3 | 1107 | 4 | US-09-328-352-268 | Sequence 268, App |
| C 250 | 30 | 83.3 | 502 | 3 | US-09-889-595-5 | Sequence 5, Appli | c 323 | 30 | 83.3 | 1149 | 4 | US-09-466-965-41 | Sequence 41, Appl |
| C 251 | 30 | 83.3 | 502 | 4 | US-09-899-595-5 | Sequence 5, Appli | c 324 | 30 | 83.3 | 1173 | 4 | US-09-328-352-1474 | Sequence 1474, Ap |
| C 252 | 30 | 83.3 | 524 | 4 | US-09-270-767-4224 | Sequence 4224, Ap | c 325 | 30 | 83.3 | 1176 | 4 | US-09-925-637-7 | Sequence 7, Appli |
| C 253 | 30 | 83.3 | 524 | 4 | US-09-270-767-19506 | Sequence 19506, A | c 326 | 30 | 83.3 | 1233 | 4 | US-09-248-796A-3104 | Sequence 3104, Ap |
| C 254 | 30 | 83.3 | 540 | 3 | US-09-134-001C-1275 | Sequence 1275, Ap | c 327 | 30 | 83.3 | 1236 | 4 | US-09-543-681A-3232 | Sequence 3232, Ap |
| C 255 | 30 | 83.3 | 553 | 4 | US-09-281-646B-27 | Sequence 27, Appl | c 328 | 30 | 83.3 | 1236 | 4 | US-09-248-796A-10287 | Sequence 10287, A |
| C 256 | 30 | 83.3 | 561 | 4 | US-09-489-039A-4949 | Sequence 4949, Ap | c 329 | 30 | 83.3 | 1272 | 4 | US-09-583-110-397 | Sequence 397, App |
| C 257 | 30 | 83.3 | 578 | 3 | US-09-222-938A-26 | Sequence 26, Appl | c 330 | 30 | 83.3 | 1308 | 4 | US-09-107-433-1386 | Sequence 1396, Ap |
| C 258 | 30 | 83.3 | 601 | 4 | US-09-949-016-22412 | Sequence 22412, A | c 331 | 30 | 83.3 | 1338 | 4 | US-09-902-540-13965 | Sequence 4085, Ap |
| C 259 | 30 | 83.3 | 601 | 4 | US-09-949-016-24507 | Sequence 24507, A | c 332 | 30 | 83.3 | 1347 | 4 | US-09-252-991A-7495 | Sequence 7495, Ap |
| C 260 | 30 | 83.3 | 601 | 4 | US-09-949-016-51085 | Sequence 51085, A | c 333 | 30 | 83.3 | 1352 | 2 | US-08-415-593-44 | Sequence 44, Appl |
| C 261 | 30 | 83.3 | 601 | 4 | US-09-949-016-54591 | Sequence 54591, A | c 334 | 30 | 83.3 | 1353 | 4 | US-09-710-279-4394 | Sequence 4394, Ap |
| C 262 | 30 | 83.3 | 601 | 4 | US-09-949-016-54623 | Sequence 54623, A | c 335 | 30 | 83.3 | 1362 | 4 | US-09-769-863-13 | Sequence 13, Appl |
| C 263 | 30 | 83.3 | 601 | 4 | US-09-949-016-54655 | Sequence 54655, A | c 336 | 30 | 83.3 | 1380 | 3 | US-08-968-563-5 | Sequence 5, Appli |
| C 264 | 30 | 83.3 | 601 | 4 | US-09-949-016-76601 | Sequence 76601, A | c 337 | 30 | 83.3 | 1380 | 3 | US-08-969-683A-5 | Sequence 1, Appli |
| C 265 | 30 | 83.3 | 601 | 4 | US-09-949-016-89795 | Sequence 89795, A | c 338 | 30 | 83.3 | 1380 | 3 | US-09-297-928-1 | Sequence 1, Appli |
| C 266 | 30 | 83.3 | 601 | 4 | US-09-949-016-92365 | Sequence 92365, A | c 339 | 30 | 83.3 | 1380 | 4 | US-09-641-652-53 | Sequence 53, Appl |
| C 267 | 30 | 83.3 | 601 | 4 | US-09-949-016-119020 | Sequence 119020, A | c 340 | 30 | 83.3 | 1382 | 3 | US-09-257-584-1 | Sequence 1, Appli |
| C 268 | 30 | 83.3 | 601 | 4 | US-09-949-016-119056 | Sequence 119056, A | c 341 | 30 | 83.3 | 1464 | 4 | US-09-543-681A-1013 | Sequence 1013, Ap |
| C 269 | 30 | 83.3 | 601 | 4 | US-09-949-016-119092 | Sequence 119092, A | c 342 | 30 | 83.3 | 1467 | 4 | US-09-252-991A-13323 | Sequence 13323, A |
| C 270 | 30 | 83.3 | 601 | 4 | US-09-949-016-119128 | Sequence 119128, A | c 343 | 30 | 83.3 | 1512 | 4 | US-09-270-767-15148 | Sequence 15148, A |
| C 271 | 30 | 83.3 | 601 | 4 | US-09-949-016-119164 | Sequence 119164, A | c 344 | 30 | 83.3 | 1534 | 3 | US-08-858-207A-93 | Sequence 93, Appl |
| C 272 | 30 | 83.3 | 601 | 4 | US-09-949-016-119200 | Sequence 119200, A | c 345 | 30 | 83.3 | 1538 | 4 | US-09-902-540-8912 | Sequence 8912, Ap |
| C 273 | 30 | 83.3 | 601 | 4 | US-09-949-016-120890 | Sequence 120890, A | c 346 | 30 | 83.3 | 1590 | 4 | US-09-252-991A-6393 | Sequence 6393, Ap |
| C 274 | 30 | 83.3 | 601 | 4 | US-09-949-016-141604 | Sequence 141604, A | c 347 | 30 | 83.3 | 1599 | 4 | US-09-252-991A-7144 | Sequence 7144, Ap |
| C 275 | 30 | 83.3 | 601 | 4 | US-09-949-016-141605 | Sequence 141605, A | c 348 | 30 | 83.3 | 1707 | 4 | US-09-252-991A-6156 | Sequence 6156, Ap |
| C 276 | 30 | 83.3 | 601 | 4 | US-09-949-016-150795 | Sequence 150795, A | c 349 | 30 | 83.3 | 1740 | 4 | US-09-902-540-1944 | Sequence 1944, Ap |
| C 277 | 30 | 83.3 | 601 | 4 | US-09-949-016-150796 | Sequence 150796, A | c 350 | 30 | 83.3 | 1799 | 3 | US-09-222-938A-24 | Sequence 24, Appl |
| C 278 | 30 | 83.3 | 601 | 4 | US-09-949-016-150797 | Sequence 150797, A | c 351 | 30 | 83.3 | 1920 | 3 | US-09-294-894-1 | Sequence 1, Appli |
| C 279 | 30 | 83.3 | 601 | 4 | US-09-949-016-152431 | Sequence 152431, A | c 352 | 30 | 83.3 | 1936 | 2 | US-09-139-424-3 | Sequence 3, Appli |
| C 280 | 30 | 83.3 | 601 | 4 | US-09-949-016-152417 | Sequence 152417, A | c 353 | 30 | 83.3 | 2022 | 4 | US-09-252-991A-7351 | Sequence 7351, Ap |
| C 281 | 30 | 83.3 | 601 | 4 | US-09-949-016-175365 | Sequence 175365, A | c 354 | 30 | 83.3 | 2030 | 3 | US-08-706-216-3 | Sequence 3, Appli |
| C 282 | 30 | 83.3 | 601 | 4 | US-09-949-016-180637 | Sequence 180637, A | c 355 | 30 | 83.3 | 2030 | 4 | US-09-650-284B-3 | Sequence 3, Appli |
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| C 284 | 30 | 83.3 | 601 | 4 | US-09-949-016-192413 | Sequence 192413, A | c 357 | 30 | 83.3 | 2115 | 4 | US-08-956-171B-604 | Sequence 604, App |
| C 285 | 30 | 83.3 | 606 | 4 | US-09-621-976-110398 | Sequence 10398, A | c 358 | 30 | 83.3 | 2115 | 4 | US-08-781-986A-604 | Sequence 604, App |
| C 286 | 30 | 83.3 | 612 | 4 | US-09-134-000C-3066 | Sequence 3066, App | c 359 | 30 | 83.3 | 2130 | 4 | US-09-252-991A-10734 | Sequence 10734, A |
| C 287 | 30 | 83.3 | 675 | 4 | US-09-636-215-822 | Sequence 822, App | c 360 | 30 | 83.3 | 2255 | 4 | US-09-270-767-11388 | Sequence 11388, A |
| C 288 | 30 | 83.3 | 675 | 4 | US-09-685-166A-822 | Sequence 822, App | c 361 | 30 | 83.3 | 2256 | 4 | US-09-949-016-2903 | Sequence 2903, Ap |
| C 289 | 30 | 83.3 | 675 | 4 | US-09-679-426-822 | Sequence 822, App | c 362 | 30 | 83.3 | 2256 | 4 | US-09-949-016-2904 | Sequence 2904, Ap |
| C 290 | 30 | 83.3 | 675 | 4 | US-09-753-143-822 | Sequence 822, App | c 363 | 30 | 83.3 | 2275 | 4 | US-09-281-646B-1 | Sequence 1, Appli |
| C 291 | 30 | 83.3 | 675 | 4 | US-09-651-236-822 | Sequence 822, App | c 364 | 30 | 83.3 | 2280 | 4 | US-09-489-039A-6589 | Sequence 6589, Ap |
| C 292 | 30 | 83.3 | 735 | 1 | US-08-577-184-3 | Sequence 3, Appli | c 365 | 30 | 83.3 | 2303 | 4 | US-09-949-016-2622 | Sequence 2622, Ap |
| C 293 | 30 | 83.3 | 744 | 3 | US-09-032-215-39 | Sequence 39, Appl | c 366 | 30 | 83.3 | 2334 | 4 | US-09-248-796A-1911 | Sequence 1911, Ap |
| C 294 | 30 | 83.3 | 744 | 3 | US-09-032-215-40 | Sequence 40, Appl | c 367 | 30 | 83.3 | 2336 | 1 | US-08-577-184-5 | Sequence 5, Appli |
| C 295 | 30 | 83.3 | 764 | 6 | 5215909-7 | Patent No. 5215909 | c 368 | 30 | 83.3 | 2381 | 2 | US-08-318-826A-9 | Sequence 9, Appli |
| C 296 | 30 | 83.3 | 764 | 6 | 5215909-7 | Patent No. 5215909 | c 369 | 30 | 83.3 | 2400 | 6 | 5215909-13 | Patent No. 5215909 |
| C 297 | 30 | 83.3 | 774 | 4 | US-09-902-540-4990 | Sequence 4990, Ap | c 370 | 30 | 83.3 | 2400 | 6 | 5215909-13 | Patent No. 5215909 |
| C 298 | 30 | 83.3 | 789 | 4 | US-09-583-110-1124 | Sequence 1124, Ap | c 371 | 30 | 83.3 | 2416 | 2 | US-08-318-826A-8 | Sequence 8, Appli |
| C 299 | 30 | 83.3 | 789 | 4 | US-09-107-433-1029 | Sequence 1029, Ap | c 372 | 30 | 83.3 | 2416 | 3 | US-09-334-489-1 | Sequence 1, Appli |
| C 300 | 30 | 83.3 | 819 | 4 | US-09-601-198-45 | Sequence 45, Appl | c 373 | 30 | 83.3 | 2416 | 3 | US-09-334-489-2 | Sequence 2, Appli |
| C 301 | 30 | 83.3 | 834 | 4 | US-09-232-991A-10044 | Sequence 10044, A | c 374 | 30 | 83.3 | 2444 | 4 | US-09-949-016-5275 | Sequence 5275, Ap |
| C 302 | 30 | 83.3 | 841 | 3 | US-08-906-616-110 | Sequence 110, App | c 375 | 30 | 83.3 | 2445 | 6 | 5215909-9 | Patent No. 5215909 |
| C 303 | 30 | 83.3 | 841 | 3 | US-08-906-616-110 | Sequence 110, App | c 376 | 30 | 83.3 | 2445 | 6 | 5215909-9 | Patent No. 5215909 |
| C 304 | 30 | 83.3 | 841 | 3 | US-08-817-795-110 | Sequence 110, App | c 377 | 30 | 83.3 | 2651 | 4 | US-09-252-991A-10428 | A |

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| C 378 | 30 | 83.3 | 2688 | 4 | US-09-489-039A-5956 | Sequence 5956, Ap | 451 | 30 | 83.3 | 25375 | 4 | US-09-949-016-15880 | Sequence 15880, A |
| C 379 | 30 | 83.3 | 2769 | 3 | US-09-397-885-2 | Sequence 2, Appli | 452 | 30 | 83.3 | 27425 | 4 | US-09-524-101D-18 | Sequence 18, Appl |
| C 380 | 30 | 83.3 | 2769 | 4 | US-09-965-382-2 | Sequence 2, Appli | C 453 | 30 | 83.3 | 28805 | 4 | US-09-949-016-12825 | Sequence 12825, A |
| C 381 | 30 | 83.3 | 2990 | 4 | US-09-710-279-3899 | Sequence 3899, Ap | C 454 | 30 | 83.3 | 28864 | 4 | US-09-949-016-12250 | Sequence 12250, A |
| C 382 | 30 | 83.3 | 3001 | 4 | US-09-533-333D-115 | Sequence 115, App | C 455 | 30 | 83.3 | 28865 | 4 | US-09-949-016-13647 | Sequence 13647, A |
| C 383 | 30 | 83.3 | 3001 | 4 | US-09-533-333D-217 | Sequence 217, App | C 456 | 30 | 83.3 | 32666 | 4 | US-09-949-016-16086 | Sequence 16086, A |
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| C 385 | 30 | 83.3 | 3182 | 1 | US-08-188-582-12 | Sequence 12, Appl | 458 | 30 | 83.3 | 42988 | 4 | US-08-311-731A-128 | Sequence 128, App |
| C 386 | 30 | 83.3 | 3182 | 1 | US-08-646-715-12 | Sequence 12, Appl | 459 | 30 | 83.3 | 47698 | 4 | US-09-949-016-13514 | Sequence 13514, A |
| C 387 | 30 | 83.3 | 3505 | 4 | US-09-774-528-5 | Sequence 5, Appli | C 460 | 30 | 83.3 | 48219 | 4 | US-09-949-016-16158 | Sequence 16158, A |
| C 388 | 30 | 83.3 | 4113 | 4 | US-09-902-540-531 | Sequence 531, App | C 461 | 30 | 83.3 | 50836 | 4 | US-09-949-016-16722 | Sequence 16722, A |
| C 389 | 30 | 83.3 | 4231 | 4 | US-09-647-140B-1 | Sequence 1, Appli | C 462 | 30 | 83.3 | 53500 | 4 | US-09-266-965-76 | Sequence 76, Appl |
| C 390 | 30 | 83.3 | 4403 | 4 | US-08-956-171E-78 | Sequence 78, Appl | 463 | 30 | 83.3 | 54649 | 4 | US-09-949-016-15867 | Sequence 15867, A |
| C 391 | 30 | 83.3 | 4403 | 4 | US-08-781-986A-78 | Sequence 78, Appl | 464 | 30 | 83.3 | 54950 | 4 | US-09-949-016-14383 | Sequence 14383, A |
| C 392 | 30 | 83.3 | 4438 | 4 | US-09-949-016-13578 | Sequence 13578, A | 465 | 30 | 83.3 | 55061 | 4 | US-09-949-016-14704 | Sequence 14704, A |
| C 393 | 30 | 83.3 | 4757 | 3 | US-09-572-191-1 | Sequence 1, Appli | 466 | 30 | 83.3 | 55061 | 4 | US-09-949-016-14705 | Sequence 14705, A |
| C 394 | 30 | 83.3 | 4757 | 3 | US-09-723-262-1 | Sequence 1, Appli | 467 | 30 | 83.3 | 55061 | 4 | US-09-949-016-14706 | Sequence 14706, A |
| C 395 | 30 | 83.3 | 4757 | 3 | US-09-723-219-1 | Sequence 1, Appli | 468 | 30 | 83.3 | 55061 | 4 | US-09-949-016-14707 | Sequence 14707, A |
| C 396 | 30 | 83.3 | 5058 | 3 | US-09-889-595-1 | Sequence 1, Appli | 469 | 30 | 83.3 | 55061 | 4 | US-09-949-016-14708 | Sequence 14708, A |
| C 397 | 30 | 83.3 | 5058 | 3 | US-09-895-595-1 | Sequence 1, Appli | 470 | 30 | 83.3 | 55061 | 4 | US-09-949-016-14709 | Sequence 14709, A |
| C 398 | 30 | 83.3 | 5427 | 1 | US-08-168-917-1 | Sequence 1, Appli | 471 | 30 | 83.3 | 55195 | 4 | US-09-949-016-15854 | Sequence 15854, A |
| C 399 | 30 | 83.3 | 5427 | 2 | US-08-460-510-1 | Sequence 1, Appli | C 472 | 30 | 83.3 | 56523 | 4 | US-09-949-016-14237 | Sequence 14237, A |
| C 400 | 30 | 83.3 | 5427 | 2 | US-08-460-510-1 | Sequence 1, Appli | C 473 | 30 | 83.3 | 58593 | 4 | US-09-949-016-12232 | Sequence 12232, A |
| C 401 | 30 | 83.3 | 5427 | 3 | US-08-462-728-3 | Sequence 3, Appli | C 474 | 30 | 83.3 | 60593 | 4 | US-09-949-016-13779 | Sequence 13779, A |
| C 402 | 30 | 83.3 | 5427 | 3 | US-08-461-917-3 | Sequence 3, Appli | C 475 | 30 | 83.3 | 61042 | 4 | US-09-949-016-13224 | Sequence 13224, A |
| C 403 | 30 | 83.3 | 5427 | 4 | US-08-464-436-3 | Sequence 3, Appli | C 476 | 30 | 83.3 | 61735 | 4 | US-09-949-016-12064 | Sequence 12064, A |
| C 404 | 30 | 83.3 | 5427 | 4 | US-08-464-436-3 | Sequence 3, Appli | C 477 | 30 | 83.3 | 64813 | 4 | US-09-949-016-11957 | Sequence 11957, A |
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| C 406 | 30 | 83.3 | 5427 | 5 | PCT-US92-00862-1 | Sequence 1, Appli | C 479 | 30 | 83.3 | 67620 | 4 | US-09-949-016-16939 | Sequence 16939, A |
| C 407 | 30 | 83.3 | 5570 | 4 | US-09-023-655-1193 | Sequence 1193, Ap | 480 | 30 | 83.3 | 68667 | 4 | US-09-949-016-17017 | Sequence 17017, A |
| C 408 | 30 | 83.3 | 5727 | 3 | US-09-628-188A-1 | Sequence 1, Appli | 481 | 30 | 83.3 | 69737 | 4 | US-09-949-016-15140 | Sequence 15140, A |
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| C 410 | 30 | 83.3 | 6082 | 4 | US-09-636-215-535 | Sequence 535, App | C 483 | 30 | 83.3 | 75212 | 4 | US-09-949-016-13313 | Sequence 13313, A |
| C 411 | 30 | 83.3 | 6082 | 4 | US-09-685-166A-535 | Sequence 535, App | C 484 | 30 | 83.3 | 75212 | 4 | US-09-949-016-13314 | Sequence 13314, A |
| C 412 | 30 | 83.3 | 6082 | 4 | US-09-679-426-535 | Sequence 535, App | C 485 | 30 | 83.3 | 75212 | 4 | US-09-949-016-13315 | Sequence 13315, A |
| C 413 | 30 | 83.3 | 6082 | 4 | US-09-759-143-535 | Sequence 535, App | 486 | 30 | 83.3 | 76401 | 4 | US-09-949-016-17153 | Sequence 17153, A |
| C 414 | 30 | 83.3 | 6082 | 4 | US-09-651-236-535 | Sequence 535, App | 487 | 30 | 83.3 | 77994 | 4 | US-09-949-016-12517 | Sequence 12517, A |
| C 415 | 30 | 83.3 | 6140 | 3 | US-09-439-313-536 | Sequence 536, App | 488 | 30 | 83.3 | 77994 | 4 | US-09-949-016-16021 | Sequence 16021, A |
| C 416 | 30 | 83.3 | 6140 | 3 | US-09-636-215-536 | Sequence 536, App | C 489 | 30 | 83.3 | 80717 | 4 | US-09-949-016-14968 | Sequence 14968, A |
| C 417 | 30 | 83.3 | 6140 | 4 | US-09-685-166A-536 | Sequence 536, App | C 490 | 30 | 83.3 | 87523 | 4 | US-09-949-016-12670 | Sequence 12670, A |
| C 418 | 30 | 83.3 | 6140 | 4 | US-09-679-426-536 | Sequence 536, App | C 491 | 30 | 83.3 | 87523 | 4 | US-09-949-016-15047 | Sequence 15047, A |
| C 419 | 30 | 83.3 | 6140 | 4 | US-09-759-143-536 | Sequence 536, App | C 492 | 30 | 83.3 | 87523 | 4 | US-09-949-016-15048 | Sequence 15048, A |
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| C 421 | 30 | 83.3 | 6426 | 4 | US-09-976-594-136 | Sequence 136, App | C 494 | 30 | 83.3 | 87869 | 4 | US-09-949-016-11744 | Sequence 11744, A |
| C 422 | 30 | 83.3 | 6660 | 2 | US-08-771-602D-1 | Sequence 1, Appli | C 495 | 30 | 83.3 | 87869 | 4 | US-09-949-016-15044 | Sequence 15044, A |
| C 423 | 30 | 83.3 | 6660 | 3 | US-09-232-446B-1 | Sequence 1, Appli | C 496 | 30 | 83.3 | 87869 | 4 | US-09-949-016-15045 | Sequence 15045, A |
| C 424 | 30 | 83.3 | 8501 | 3 | US-09-298-367B-6 | Sequence 6, Appli | C 497 | 30 | 83.3 | 87869 | 4 | US-09-949-016-15046 | Sequence 15046, A |
| C 425 | 30 | 83.3 | 9622 | 4 | US-09-949-016-14643 | Sequence 14643, A | C 498 | 30 | 83.3 | 88268 | 4 | US-09-949-016-14178 | Sequence 14178, A |
| C 426 | 30 | 83.3 | 9622 | 4 | US-09-949-016-14644 | Sequence 14644, A | C 499 | 30 | 83.3 | 89625 | 4 | US-09-949-016-17012 | Sequence 17012, A |
| C 427 | 30 | 83.3 | 9623 | 4 | US-09-949-016-14362 | Sequence 14362, A | 500 | 30 | 83.3 | 92074 | 4 | US-09-949-016-17163 | Sequence 17163, A |
| C 428 | 30 | 83.3 | 10758 | 4 | US-08-956-171E-221 | Sequence 221, App | C 501 | 30 | 83.3 | 92155 | 4 | US-09-949-016-17484 | Sequence 17484, A |
| C 429 | 30 | 83.3 | 12028 | 4 | US-09-902-540-1071 | Sequence 221, App | C 502 | 30 | 83.3 | 93778 | 4 | US-09-949-016-15096 | Sequence 15096, A |
| C 430 | 30 | 83.3 | 13543 | 4 | US-10-127-862-1 | Sequence 1, Appli | C 503 | 30 | 83.3 | 97221 | 4 | US-09-949-016-12755 | Sequence 12755, A |
| C 431 | 30 | 83.3 | 15109 | 4 | US-08-956-171E-44 | Sequence 44, Appl | C 504 | 30 | 83.3 | 100468 | 4 | US-09-949-016-12511 | Sequence 12511, A |
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| C 434 | 30 | 83.3 | 16347 | 4 | US-09-949-016-14645 | Sequence 14645, A | 507 | 30 | 83.3 | 110585 | 4 | US-09-949-016-13427 | Sequence 13427, A |
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| C 436 | 30 | 83.3 | 16347 | 4 | US-09-902-540-1156 | Sequence 1156, Ap | 509 | 30 | 83.3 | 137048 | 4 | US-09-949-016-13438 | Sequence 13438, A |
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| C 439 | 30 | 83.3 | 19870 | 4 | US-09-949-016-13462 | Sequence 13462, A | 512 | 30 | 83.3 | 143173 | 4 | US-09-949-016-14513 | Sequence 14513, A |
| C 440 | 30 | 83.3 | 19307 | 3 | US-08-836-028A-10 | Sequence 10, Appl | 513 | 30 | 83.3 | 145320 | 4 | US-09-949-016-15858 | Sequence 15858, A |
| C 441 | 30 | 83.3 | 19307 | 3 | US-09-427-048A-10 | Sequence 10, Appl | 514 | 30 | 83.3 | 156617 | 4 | US-09-949-016-16131 | Sequence 16131, A |
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| C 443 | 30 | 83.3 | 20662 | 4 | US-09-949-016-15156 | Sequence 15156, A | 516 | 30 | 83.3 | 189560 | 4 | US-09-949-016-17202 | Sequence 17202, A |
| C 444 | 30 | 83.3 | 22243 | 4 | US-08-956-171E-164 | Sequence 164, App | 517 | 30 | 83.3 | 192302 | 4 | US-09-949-016-15270 | Sequence 15270, A |
| C 445 | 30 | 83.3 | 22243 | 4 | US-08-781-986A-164 | Sequence 164, App | C 518 | 30 | 83.3 | 194537 | 4 | US-09-949-016-12928 | Sequence 12928, A |
| C 446 | 30 | 83.3 | 22906 | 4 | US-09-949-016-16471 | Sequence 16471, A | C 519 | 30 | 83.3 | 201529 | 4 | US-09-949-016-12740 | Sequence 12740, A |
| C 447 | 30 | 83.3 | 23951 | 4 | US-09-902-540-1245 | Sequence 1245, Ap | C 520 | 30 | 83.3 | 239964 | 4 | US-09-949-016-15086 | Sequence 15086, A |
| C 448 | 30 | 83.3 | 24207 | 4 | US-09-949-016-14364 | Sequence 14364, A | C 521 | 30 | 83.3 | 239964 | 4 | US-09-949-016-15753 | Sequence 15753, A |
| C 449 | 30 | 83.3 | 24602 | 4 | US-09-902-540-1202 | Sequence 1202, Ap | 522 | 30 | 83.3 | 278866 | 4 | US-09-949-016-13922 | Sequence 13922, A |
| C 450 | 30 | 83.3 | 25370 | 4 | US-09-949-016-12109 | Sequence 12109, A | 523 | 30 | 83.3 | 278866 | 4 | US-09-949-016-13923 | Sequence 13923, A |

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| 670 | 29 | 80.6 | 601 | 4 | US-09-949-016-190088 | Sequence 130088, | c 743 | 29 | 80.6 | 1215 | 4 | US-09-248-796A-808 | Sequence 808, App |
| 671 | 29 | 80.6 | 601 | 4 | US-09-949-016-190089 | Sequence 130089, | 744 | 29 | 80.6 | 1248 | 4 | US-09-252-991A-4042 | Sequence 4042, App |
| c 672 | 29 | 80.6 | 601 | 4 | US-09-949-016-205013 | Sequence 250013, | c 745 | 29 | 80.6 | 1248 | 4 | US-09-248-796A-809 | Sequence 809, App |
| 673 | 29 | 80.6 | 606 | 4 | US-09-252-991A-2689 | Sequence 2689, App | 746 | 29 | 80.6 | 1251 | 4 | US-09-252-991A-8004 | Sequence 8004, App |
| c 674 | 29 | 80.6 | 609 | 4 | US-09-328-352-2228 | Sequence 2228, App | 747 | 29 | 80.6 | 1272 | 4 | US-09-252-991A-4511 | Sequence 4511, App |
| c 675 | 29 | 80.6 | 621 | 4 | US-09-902-540-9316 | Sequence 9316, App | 748 | 29 | 80.6 | 1296 | 4 | US-09-023-655-747 | Sequence 747, App |
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| c 677 | 29 | 80.6 | 627 | 4 | US-09-902-540-5753 | Sequence 5753, App | c 750 | 29 | 80.6 | 1305 | 4 | US-09-107-532A-2655 | Sequence 2655, App |
| c 678 | 29 | 80.6 | 639 | 4 | US-09-252-991A-829 | Sequence 829, App | 751 | 29 | 80.6 | 1314 | 2 | US-08-868-577-10 | Sequence 10, Appl |
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| c 680 | 29 | 80.6 | 657 | 4 | US-09-710-279-3057 | Sequence 3057, App | 753 | 29 | 80.6 | 1315 | 2 | US-08-671-320-10 | Sequence 10, Appl |
| 681 | 29 | 80.6 | 662 | 4 | US-09-710-279-3057 | Sequence 3057, App | c 754 | 29 | 80.6 | 1371 | 4 | US-09-252-991A-764 | Sequence 764, App |
| c 682 | 29 | 80.6 | 672 | 3 | US-10-101-464A-439 | Sequence 439, App | c 755 | 29 | 80.6 | 1392 | 4 | US-09-252-991A-704 | Sequence 704, App |
| c 683 | 29 | 80.6 | 687 | 4 | US-09-134-001C-1349 | Sequence 1349, App | c 756 | 29 | 80.6 | 1403 | 2 | US-08-202-044-1 | Sequence 1, Appli |
| c 684 | 29 | 80.6 | 696 | 4 | US-09-328-352-752 | Sequence 752, App | c 757 | 29 | 80.6 | 1403 | 3 | US-08-751-344B-1 | Sequence 1, Appli |
| c 685 | 29 | 80.6 | 696 | 4 | US-09-252-991A-647 | Sequence 647, App | c 758 | 29 | 80.6 | 1403 | 4 | US-09-920-868A-1 | Sequence 1, Appli |
| c 686 | 29 | 80.6 | 699 | 3 | US-08-476-102A-6 | Sequence 6, Appli | c 759 | 29 | 80.6 | 1407 | 4 | US-09-920-868A-1 | Sequence 1, Appli |
| c 687 | 29 | 80.6 | 702 | 4 | US-09-252-991A-8108 | Sequence 8108, App | c 760 | 29 | 80.6 | 1407 | 4 | US-09-489-039A-7152 | Sequence 7152, App |
| c 688 | 29 | 80.6 | 714 | 3 | US-09-134-001C-2794 | Sequence 2794, App | c 761 | 29 | 80.6 | 1444 | 4 | US-09-958-969-1 | Sequence 1, Appli |
| c 689 | 29 | 80.6 | 726 | 4 | US-09-252-991A-3106 | Sequence 3106, App | c 762 | 29 | 80.6 | 1455 | 4 | US-09-489-039A-2724 | Sequence 2724, App |
| c 690 | 29 | 80.6 | 738 | 4 | US-09-252-991A-8362 | Sequence 8362, App | c 763 | 29 | 80.6 | 1476 | 4 | US-09-248-796A-4380 | Sequence 83, Appl |
| c 691 | 29 | 80.6 | 744 | 4 | US-09-902-540-8000 | Sequence 8000, App | c 764 | 29 | 80.6 | 1476 | 4 | US-09-248-796A-4380 | Sequence 4380, App |
| c 692 | 29 | 80.6 | 765 | 4 | US-09-252-991A-10992 | Sequence 10992, A | c 765 | 29 | 80.6 | 1482 | 4 | US-09-902-540-3526 | Sequence 3526, App |
| c 693 | 29 | 80.6 | 801 | 4 | US-09-813-453B-26 | Sequence 26, Appl | c 766 | 29 | 80.6 | 1488 | 4 | US-09-252-991A-10930 | Sequence 10930, A |
| c 694 | 29 | 80.6 | 825 | 4 | US-09-543-681A-3188 | Sequence 3188, App | c 767 | 29 | 80.6 | 1488 | 4 | US-09-489-039A-943 | Sequence 943, App |
| c 695 | 29 | 80.6 | 834 | 4 | US-09-489-039A-5870 | Sequence 5870, App | c 768 | 29 | 80.6 | 1491 | 2 | US-08-949-637-1 | Sequence 1, Appli |
| c 696 | 29 | 80.6 | 837 | 4 | US-09-134-000C-3336 | Sequence 3336, App | c 769 | 29 | 80.6 | 1491 | 3 | US-09-291-488-1 | Sequence 1, Appli |
| c 697 | 29 | 80.6 | 852 | 4 | US-09-902-540-5089 | Sequence 5089, App | c 770 | 29 | 80.6 | 1509 | 4 | US-09-252-991A-6819 | Sequence 6819, App |
| c 698 | 29 | 80.6 | 858 | 4 | US-09-252-991A-1260 | Sequence 1260, App | c 771 | 29 | 80.6 | 1515 | 4 | US-09-902-540-6888 | Sequence 6888, App |
| c 699 | 29 | 80.6 | 861 | 4 | US-09-252-991A-16287 | Sequence 16287, A | c 772 | 29 | 80.6 | 1524 | 3 | US-09-902-540-6888 | Sequence 1, Appli |
| c 700 | 29 | 80.6 | 867 | 4 | US-09-925-637-63 | Sequence 63, Appl | c 773 | 29 | 80.6 | 1525 | 2 | US-09-153-277-3 | Sequence 3, Appli |
| c 701 | 29 | 80.6 | 882 | 3 | US-09-276-873-1 | Sequence 10672, A | c 774 | 29 | 80.6 | 1533 | 4 | US-09-006-535-1 | Sequence 1, Appli |
| c 702 | 29 | 80.6 | 897 | 2 | US-09-006-535-2 | Sequence 2, Appli | c 775 | 29 | 80.6 | 1563 | 4 | US-09-949-016-730 | Sequence 730, App |
| c 703 | 29 | 80.6 | 897 | 2 | US-09-006-535-7 | Sequence 7, Appli | c 776 | 29 | 80.6 | 1563 | 4 | US-09-949-016-4161 | Sequence 4161, App |
| c 704 | 29 | 80.6 | 897 | 2 | US-09-252-991A-1170 | Sequence 1170, App | c 777 | 29 | 80.6 | 1563 | 4 | US-09-949-016-4161 | Sequence 370, App |
| c 705 | 29 | 80.6 | 900 | 4 | US-09-710-279-1887 | Sequence 1887, App | c 778 | 29 | 80.6 | 1578 | 4 | US-09-134-001C-521 | Sequence 521, App |
| c 706 | 29 | 80.6 | 903 | 4 | US-09-489-039A-6547 | Sequence 6547, App | c 779 | 29 | 80.6 | 1584 | 3 | US-09-902-540-5836 | Sequence 5836, App |
| c 707 | 29 | 80.6 | 912 | 3 | US-09-221-017B-763 | Sequence 763, App | c 780 | 29 | 80.6 | 1611 | 4 | US-09-902-540-5836 | Sequence 128, App |
| c 708 | 29 | 80.6 | 921 | 4 | US-09-902-540-8162 | Sequence 8162, App | c 781 | 29 | 80.6 | 1612 | 1 | US-08-583-672-1 | Sequence 1, Appli |
| c 709 | 29 | 80.6 | 930 | 3 | US-09-134-001C-2830 | Sequence 2830, App | c 782 | 29 | 80.6 | 1634 | 4 | US-09-328-352-3270 | Sequence 3270, App |
| c 710 | 29 | 80.6 | 933 | 4 | US-09-252-991A-810 | Sequence 810, App | c 783 | 29 | 80.6 | 1677 | 4 | US-09-489-039A-5200 | Sequence 5200, App |
| c 711 | 29 | 80.6 | 936 | 4 | US-09-248-796A-5402 | Sequence 5402, App | c 784 | 29 | 80.6 | 1695 | 4 | US-09-252-991A-10758 | Sequence 10758, A |
| c 712 | 29 | 80.6 | 945 | 4 | US-09-252-991A-3092 | Sequence 3092, App | c 785 | 29 | 80.6 | 1701 | 3 | US-09-134-001C-594 | Sequence 594, App |
| c 713 | 29 | 80.6 | 954 | 2 | US-08-336-198C-2 | Sequence 2, Appli | c 786 | 29 | 80.6 | 1719 | 4 | US-09-252-991A-8515 | Sequence 8515, App |
| c 714 | 29 | 80.6 | 954 | 4 | US-09-184-965-2 | Sequence 2, Appli | c 787 | 29 | 80.6 | 1752 | 3 | US-09-022-949-1 | Sequence 1, Appli |
| c 715 | 29 | 80.6 | 963 | 4 | US-09-248-796A-10655 | Sequence 10655, A | c 788 | 29 | 80.6 | 1755 | 2 | US-08-317-785-1 | Sequence 1, Appli |
| c 716 | 29 | 80.6 | 978 | 4 | US-09-252-991A-2878 | Sequence 2878, App | c 789 | 29 | 80.6 | 1761 | 4 | US-09-248-796A-6859 | Sequence 6859, App |
| c 717 | 29 | 80.6 | 981 | 4 | US-09-489-039A-4121 | Sequence 4121, App | c 790 | 29 | 80.6 | 1761 | 4 | US-09-902-540-3727 | Sequence 3727, App |
| c 718 | 29 | 80.6 | 990 | 4 | US-09-248-796A-2160 | Sequence 2160, App | c 791 | 29 | 80.6 | 1811 | 4 | US-09-902-540-396 | Sequence 396, App |
| c 719 | 29 | 80.6 | 996 | 4 | US-09-543-681A-1915 | Sequence 1915, App | c 792 | 29 | 80.6 | 1836 | 4 | US-09-248-796A-10454 | Sequence 10454, A |
| c 720 | 29 | 80.6 | 1023 | 4 | US-09-328-352-3716 | Sequence 3716, App | c 793 | 29 | 80.6 | 1836 | 4 | US-09-461-325-23 | Sequence 23, Appl |
| c 721 | 29 | 80.6 | 1024 | 3 | US-09-615-192A-135 | Sequence 135, App | c 794 | 29 | 80.6 | 1839 | 4 | US-10-012-542-23 | Sequence 23, Appl |
| c 722 | 29 | 80.6 | 1024 | 4 | US-08-975-316-72 | Sequence 135, App | c 795 | 29 | 80.6 | 1839 | 4 | US-10-115-123-23 | Sequence 23, Appl |
| c 723 | 29 | 80.6 | 1038 | 2 | US-08-975-316-72 | Sequence 72, Appl | c 796 | 29 | 80.6 | 1893 | 4 | US-08-986-171E-155 | Sequence 155, App |
| c 724 | 29 | 80.6 | 1038 | 3 | US-09-615-192A-72 | Sequence 72, Appl | c 797 | 29 | 80.6 | 1893 | 4 | US-08-781-986A-155 | Sequence 155, App |
| c 725 | 29 | 80.6 | 1038 | 4 | US-09-252-991A-15754 | Sequence 15754, A | c 798 | 29 | 80.6 | 2055 | 4 | US-09-248-796A-5691 | Sequence 5691, App |
| c 726 | 29 | 80.6 | 1038 | 4 | US-09-169-789-72 | Sequence 72, Appl | c 799 | 29 | 80.6 | 2055 | 4 | US-09-107-433-779 | Sequence 779, App |
| c 727 | 29 | 80.6 | 1059 | 4 | US-09-489-039A-1125 | Sequence 1125, App | c 799 | 29 | 80.6 | 2061 | 4 | US-09-583-110-1876 | Sequence 1876, App |
| c 728 | 29 | 80.6 | 1059 | 4 | US-09-902-540-8205 | Sequence 8205, App | c 799 | 29 | 80.6 | 2106 | 4 | US-09-252-991A-869 | Sequence 869, App |
| c 729 | 29 | 80.6 | 1083 | 4 | US-09-252-991A-849 | Sequence 849, App | c 800 | 29 | 80.6 | 2142 | 4 | US-09-853-533A-1 | Sequence 1, Appli |
| c 730 | 29 | 80.6 | 1094 | 4 | US-09-270-767-13736 | Sequence 13736, A | c 801 | 29 | 80.6 | 2148 | 4 | US-09-949-016-2145 | Sequence 2145, App |
| c 731 | 29 | 80.6 | 1107 | 4 | US-09-252-991A-1881 | Sequence 1881, App | c 802 | 29 | 80.6 | 2148 | 4 | US-09-158-232-50 | Sequence 50, Appl |
| c 732 | 29 | 80.6 | 1116 | 4 | US-09-248-796A-10969 | Sequence 10969, App | c 803 | 29 | 80.6 | 2172 | 1 | US-08-611-928-50 | Sequence 50, Appl |
| c 733 | 29 | 80.6 | 1137 | 4 | US-09-934-868-49 | Sequence 49, Appl | c 804 | 29 | 80.6 | 2172 | 3 | US-08-173-891-50 | Sequence 50, Appl |
| c 734 | 29 | 80.6 | 1143 | 4 | US-09-710-279-701 | Sequence 701, App | c 805 | 29 | 80.6 | 2172 | 4 | US-09-853-533A-9 | Sequence 9, Appli |
| c 735 | 29 | 80.6 | 1146 | 4 | US-09-134-000C-1824 | Sequence 1824, App | c 806 | 29 | 80.6 | 2172 | 4 | US-09-153-277-1 | Sequence 1, Appli |
| c 736 | 29 | 80.6 | 1155 | 4 | US-09-252-991A-412 | Sequence 412, App | c 807 | 29 | 80.6 | 2235 | 3 | US-09-700-993-2 | Sequence 2, Appli |
| c 737 | 29 | 80.6 | 1158 | 4 | US-09-902-540-5745 | Sequence 5745, App | c 808 | 29 | 80.6 | 2254 | 3 | US-08-552-369-1 | Sequence 1, Appli |
| c 738 | 29 | 80.6 | 1161 | 4 | US-09-710-279-2299 | Sequence 2299, App | c 809 | 29 | 80.6 | 2286 | 4 | US-09-252-991A-10566 | Sequence 10566, A |
| c 739 | 29 | 80.6 | 1161 | 4 | US-09-977-554-1 | Sequence 1, Appli | c 810 | 29 | 80.6 | 2286 | 4 | US-09-270-767-12223 | Sequence 12223, A |
| c 740 | 29 | 80.6 | 1182 | 2 | US-09-225-967-1 | Sequence 1, Appli | c 811 | 29 | 80.6 | 2295 | 4 | US-09-184-748-1 | Sequence 1, Appli |
| c 741 | 29 | 80.6 | 1182 | 3 | US-09-227-806-1 | Sequence 1, Appli | c 812 | 29 | 80.6 | 2344 | 4 | US-09-700-993-1 | Sequence 1, Appli |
| c 742 | 29 | 80.6 | 1191 | 4 | US-09-252-991A-15593 | Sequence 15593, A | c 813 | 29 | 80.6 | 2369 | 4 | US-09-710-279-4438 | Sequence 4438, App |
| | | | | | | | c 814 | 29 | 80.6 | 2389 | 4 | US-09-710-279-4438 | Sequence 1, Appli |
| | | | | | | | c 815 | 29 | 80.6 | 2414 | 6 | 5248599-1 | Patent No. 5248599 |

| | | | | | | | | | | | | | |
|-------|----|------|------|---|----------------------|--------------------|-------|----|------|-------|---|---------------------|--------------------|
| 816 | 29 | 80.6 | 2414 | 6 | 5248599-1 | Patent No. 5248599 | C 889 | 29 | 80.6 | 5049 | 1 | US-08-336-345-2 | Sequence 2, Appli |
| 817 | 29 | 80.6 | 2433 | 1 | US-07-710-279-4350 | Sequence 4350, Ap | C 890 | 29 | 80.6 | 5049 | 2 | US-08-647-655-1 | Sequence 1, Appli |
| C 818 | 29 | 80.6 | 2468 | 1 | US-07-779-049-2 | Sequence 2, Appli | C 891 | 29 | 80.6 | 5049 | 2 | US-08-647-655-2 | Sequence 2, Appli |
| C 819 | 29 | 80.6 | 2468 | 1 | US-08-080-240-2 | Sequence 2, Appli | C 892 | 29 | 80.6 | 5211 | 1 | US-09-902-540-846 | Sequence 846, App |
| C 820 | 29 | 80.6 | 2472 | 4 | US-09-252-991A-8197 | Sequence 8197, Ap | C 893 | 29 | 80.6 | 5308 | 4 | US-09-902-540-750 | Sequence 750, App |
| C 821 | 29 | 80.6 | 2496 | 4 | US-09-252-991A-8330 | Sequence 8330, Ap | C 894 | 29 | 80.6 | 5433 | 3 | US-09-157-021-35 | Sequence 35, Appl |
| C 822 | 29 | 80.6 | 2505 | 4 | US-09-907-744A-176 | Sequence 176, App | C 895 | 29 | 80.6 | 5433 | 3 | US-09-156-842-35 | Sequence 35, Appl |
| C 823 | 29 | 80.6 | 2505 | 4 | US-09-905-125A-176 | Sequence 176, App | C 896 | 29 | 80.6 | 5433 | 3 | US-09-023-655-1363 | Sequence 1363, Ap |
| C 824 | 29 | 80.6 | 2505 | 4 | US-09-902-775A-176 | Sequence 176, App | C 897 | 29 | 80.6 | 5433 | 4 | US-09-591-514-35 | Sequence 35, Appl |
| C 825 | 29 | 80.6 | 2505 | 4 | US-09-906-700A-176 | Sequence 176, App | C 898 | 29 | 80.6 | 5574 | 4 | US-09-620-312D-253 | Sequence 253, App |
| C 826 | 29 | 80.6 | 2505 | 4 | US-09-903-620A-176 | Sequence 176, App | C 899 | 29 | 80.6 | 5656 | 4 | US-09-902-540-694 | Sequence 694, App |
| C 827 | 29 | 80.6 | 2505 | 4 | US-09-904-920A-176 | Sequence 176, App | C 900 | 29 | 80.6 | 5854 | 4 | US-09-902-540-191 | Sequence 191, App |
| C 828 | 29 | 80.6 | 2505 | 4 | US-09-903-064A-176 | Sequence 176, App | C 901 | 29 | 80.6 | 6060 | 4 | US-08-956-171E-534 | Sequence 534, App |
| C 829 | 29 | 80.6 | 2505 | 4 | US-09-905-381A-176 | Sequence 176, App | C 902 | 29 | 80.6 | 6060 | 4 | US-08-956-171E-534 | Sequence 534, App |
| C 830 | 29 | 80.6 | 2505 | 4 | US-09-906-618-176 | Sequence 176, App | C 903 | 29 | 80.6 | 6261 | 4 | US-08-956-171E-12 | Sequence 12, Appl |
| C 831 | 29 | 80.6 | 2517 | 3 | US-09-149-476-227 | Sequence 227, App | C 904 | 29 | 80.6 | 6261 | 4 | US-08-781-986A-12 | Sequence 12, Appl |
| C 832 | 29 | 80.6 | 2520 | 3 | US-08-961-527-14 | Sequence 14, Appl | C 905 | 29 | 80.6 | 6644 | 4 | US-09-949-016-13771 | Sequence 13771, A |
| C 833 | 29 | 80.6 | 2523 | 4 | US-09-252-991A-2990 | Sequence 2990, Ap | C 906 | 29 | 80.6 | 6663 | 4 | US-09-335-011-15 | Sequence 15, Appl |
| C 834 | 29 | 80.6 | 2625 | 3 | US-09-453-702B-210 | Sequence 210, App | C 907 | 29 | 80.6 | 6851 | 4 | US-09-902-540-838 | Sequence 838, App |
| C 835 | 29 | 80.6 | 2637 | 4 | US-09-949-016-5313 | Sequence 5313, Ap | C 908 | 29 | 80.6 | 6873 | 4 | US-09-553-690-5 | Sequence 5, Appli |
| C 836 | 29 | 80.6 | 2682 | 4 | US-09-949-016-5604 | Sequence 5604, Ap | C 909 | 29 | 80.6 | 7151 | 4 | US-09-902-540-861 | Sequence 861, App |
| C 837 | 29 | 80.6 | 2690 | 4 | US-09-949-016-298 | Sequence 298, App | C 910 | 29 | 80.6 | 7223 | 4 | US-09-335-011-8 | Sequence 8, Appli |
| C 838 | 29 | 80.6 | 2815 | 4 | US-09-710-279-3819 | Sequence 3819, Ap | C 911 | 29 | 80.6 | 7404 | 4 | US-09-902-540-3115 | Sequence 3115, Ap |
| C 839 | 29 | 80.6 | 2888 | 3 | US-09-149-476-61 | Sequence 61, Appl | C 912 | 29 | 80.6 | 7588 | 4 | US-08-956-171E-142 | Sequence 142, App |
| C 840 | 29 | 80.6 | 2967 | 3 | US-08-637-823B-26 | Sequence 26, Appl | C 913 | 29 | 80.6 | 7588 | 4 | US-08-781-986A-142 | Sequence 142, App |
| C 841 | 29 | 80.6 | 2967 | 4 | US-09-614-937D-26 | Sequence 26, Appl | C 914 | 29 | 80.6 | 7698 | 4 | US-09-902-540-812 | Sequence 812, App |
| C 842 | 29 | 80.6 | 3012 | 4 | US-09-489-039A-5186 | Sequence 5186, Ap | C 915 | 29 | 80.6 | 8401 | 4 | US-09-949-016-16280 | Sequence 16280, A |
| C 843 | 29 | 80.6 | 3029 | 4 | US-09-949-016-4552 | Sequence 4552, Ap | C 916 | 29 | 80.6 | 8536 | 4 | US-08-956-171E-278 | Sequence 278, App |
| 844 | 29 | 80.6 | 3124 | 4 | US-09-710-279-4128 | Sequence 4128, Ap | C 917 | 29 | 80.6 | 8536 | 4 | US-08-781-986A-278 | Sequence 278, App |
| C 845 | 29 | 80.6 | 3147 | 4 | US-09-248-796A-4508 | Sequence 4508, Ap | C 918 | 29 | 80.6 | 9139 | 3 | US-09-322-478-22 | Sequence 22, Appl |
| C 846 | 29 | 80.6 | 3148 | 4 | US-09-710-279-3800 | Sequence 3800, Ap | C 919 | 29 | 80.6 | 9139 | 4 | US-09-586-106D-22 | Sequence 22, Appl |
| 847 | 29 | 80.6 | 3150 | 4 | US-09-489-039A-5843 | Sequence 5843, Ap | C 920 | 29 | 80.6 | 9638 | 4 | US-09-949-016-12472 | Sequence 12472, A |
| 848 | 29 | 80.6 | 3183 | 4 | US-09-220-132-16 | Sequence 16, Appl | C 921 | 29 | 80.6 | 9969 | 4 | US-09-949-016-15903 | Sequence 15903, A |
| C 849 | 29 | 80.6 | 3255 | 4 | US-09-601-198-108 | Sequence 108, App | C 922 | 29 | 80.6 | 9985 | 4 | US-09-949-016-16340 | Sequence 16340, A |
| C 850 | 29 | 80.6 | 3336 | 2 | US-08-977-554-7 | Sequence 7, Appli | C 923 | 29 | 80.6 | 10482 | 3 | US-09-322-478-23 | Sequence 23, Appl |
| C 851 | 29 | 80.6 | 3336 | 3 | US-08-978-456-7 | Sequence 7, Appli | C 924 | 29 | 80.6 | 10554 | 4 | US-09-586-106D-23 | Sequence 23, Appl |
| C 852 | 29 | 80.6 | 3336 | 3 | US-09-225-967-7 | Sequence 7, Appli | C 925 | 29 | 80.6 | 10554 | 4 | US-09-949-016-12320 | Sequence 12320, A |
| C 853 | 29 | 80.6 | 3336 | 3 | US-09-369-700-7 | Sequence 7, Appli | C 926 | 29 | 80.6 | 10554 | 4 | US-09-949-016-16084 | Sequence 16084, A |
| C 854 | 29 | 80.6 | 3336 | 3 | US-09-227-806-7 | Sequence 7, Appli | C 927 | 29 | 80.6 | 11272 | 4 | US-09-341-461-1 | Sequence 1, Appli |
| C 855 | 29 | 80.6 | 3336 | 3 | US-09-491-916-5 | Sequence 5, Appli | C 928 | 29 | 80.6 | 11792 | 4 | US-09-902-540-995 | Sequence 995, App |
| C 856 | 29 | 80.6 | 3336 | 3 | US-08-977-866-7 | Sequence 7, Appli | C 929 | 29 | 80.6 | 12785 | 4 | US-09-553-690-1 | Sequence 1, Appli |
| C 857 | 29 | 80.6 | 3341 | 2 | US-08-868-577-18 | Sequence 18, Appl | C 930 | 29 | 80.6 | 12785 | 4 | US-09-949-016-13573 | Sequence 13573, A |
| C 858 | 29 | 80.6 | 3341 | 4 | US-09-207-914-18 | Sequence 18, Appl | C 931 | 29 | 80.6 | 14255 | 4 | US-09-949-016-16875 | Sequence 16875, A |
| C 859 | 29 | 80.6 | 3362 | 4 | US-09-620-312D-469 | Sequence 469, App | C 932 | 29 | 80.6 | 14367 | 4 | US-09-902-540-1113 | Sequence 1113, Ap |
| C 860 | 29 | 80.6 | 3402 | 4 | US-09-252-991A-15560 | Sequence 15560, A | C 933 | 29 | 80.6 | 14462 | 4 | US-09-902-540-1090 | Sequence 1090, Ap |
| C 861 | 29 | 80.6 | 3430 | 3 | US-09-462-561B-9 | Sequence 9, Appli | C 934 | 29 | 80.6 | 14462 | 4 | US-09-902-540-9597 | Sequence 9597, Ap |
| C 862 | 29 | 80.6 | 3450 | 3 | US-09-462-561B-10 | Sequence 10, Appl | C 935 | 29 | 80.6 | 14561 | 4 | US-09-322-478-23 | Sequence 23, Appl |
| C 863 | 29 | 80.6 | 3452 | 4 | US-09-902-540-5745 | Sequence 5745, App | C 936 | 29 | 80.6 | 16605 | 4 | US-09-949-016-17023 | Sequence 17023, A |
| C 864 | 29 | 80.6 | 3453 | 4 | US-09-902-540-545 | Sequence 545, App | C 937 | 29 | 80.6 | 16645 | 4 | US-09-949-016-12459 | Sequence 12459, A |
| C 865 | 29 | 80.6 | 3465 | 3 | US-08-914-999-5 | Sequence 5, Appli | C 938 | 29 | 80.6 | 17710 | 3 | US-08-976-259-70 | Sequence 70, Appl |
| C 866 | 29 | 80.6 | 3467 | 3 | US-08-972-719-1 | Sequence 1, Appli | C 939 | 29 | 80.6 | 17710 | 4 | US-09-956-004-70 | Sequence 70, Appl |
| C 867 | 29 | 80.6 | 3467 | 3 | US-08-753-038-1 | Sequence 1, Appli | C 940 | 29 | 80.6 | 18000 | 4 | US-09-657-346A-17 | Sequence 17, Appl |
| C 868 | 29 | 80.6 | 3467 | 3 | US-09-530-175-1 | Sequence 1, Appli | C 941 | 29 | 80.6 | 18000 | 4 | US-09-949-016-17055 | Sequence 17055, A |
| C 869 | 29 | 80.6 | 3579 | 4 | US-09-902-540-7318 | Sequence 7318, Ap | C 942 | 29 | 80.6 | 18120 | 4 | US-09-949-016-13260 | Sequence 13260, A |
| C 870 | 29 | 80.6 | 3606 | 4 | US-09-252-991A-15688 | Sequence 15688, A | C 943 | 29 | 80.6 | 18538 | 4 | US-09-902-540-1169 | Sequence 1169, Ap |
| C 871 | 29 | 80.6 | 3621 | 2 | US-09-019-201A-1 | Sequence 1, Appli | C 944 | 29 | 80.6 | 18572 | 4 | US-09-949-016-17183 | Sequence 17183, Ap |
| C 872 | 29 | 80.6 | 3643 | 4 | US-09-710-279-4194 | Sequence 4194, Ap | C 945 | 29 | 80.6 | 18601 | 4 | US-09-949-016-17560 | Sequence 17560, A |
| C 873 | 29 | 80.6 | 3769 | 4 | US-09-710-279-4106 | Sequence 4106, Ap | C 946 | 29 | 80.6 | 18809 | 4 | US-09-902-540-1141 | Sequence 1141, Ap |
| C 874 | 29 | 80.6 | 3793 | 4 | US-09-902-540-587 | Sequence 587, App | C 947 | 29 | 80.6 | 19112 | 4 | US-09-902-540-1181 | Sequence 1181, Ap |
| C 875 | 29 | 80.6 | 3836 | 4 | US-09-976-534-59 | Sequence 534, App | C 948 | 29 | 80.6 | 20030 | 4 | US-09-949-016-13316 | Sequence 13316, A |
| C 876 | 29 | 80.6 | 4017 | 4 | US-09-710-279-3428 | Sequence 3428, Ap | C 949 | 29 | 80.6 | 23292 | 4 | US-09-949-016-12100 | Sequence 12100, A |
| C 877 | 29 | 80.6 | 4039 | 4 | US-09-710-279-3797 | Sequence 3797, Ap | C 950 | 29 | 80.6 | 23292 | 4 | US-09-949-016-13205 | Sequence 13205, A |
| C 878 | 29 | 80.6 | 4179 | 4 | US-09-902-540-2511 | Sequence 2511, Ap | C 951 | 29 | 80.6 | 24405 | 4 | US-09-949-016-12040 | Sequence 12040, A |
| C 879 | 29 | 80.6 | 4249 | 4 | US-09-710-279-4133 | Sequence 4133, Ap | C 952 | 29 | 80.6 | 24405 | 4 | US-09-949-016-17346 | Sequence 17346, A |
| C 880 | 29 | 80.6 | 4266 | 3 | US-09-651-011A-3 | Sequence 3, Appli | C 953 | 29 | 80.6 | 24602 | 4 | US-09-902-540-1202 | Sequence 1202, Ap |
| C 881 | 29 | 80.6 | 4344 | 3 | US-09-462-561B-11 | Sequence 11, Appl | C 954 | 29 | 80.6 | 24735 | 4 | US-09-949-016-12850 | Sequence 12850, A |
| C 882 | 29 | 80.6 | 4440 | 3 | US-07-792-600-1 | Sequence 1, Appli | C 955 | 29 | 80.6 | 24922 | 4 | US-09-949-016-13921 | Sequence 13921, A |
| C 883 | 29 | 80.6 | 4440 | 3 | US-09-157-021-1 | Sequence 1, Appli | C 956 | 29 | 80.6 | 25194 | 4 | US-09-949-016-13887 | Sequence 13887, A |
| C 884 | 29 | 80.6 | 4440 | 3 | US-09-156-842-1 | Sequence 1, Appli | C 957 | 29 | 80.6 | 26354 | 4 | US-09-949-016-12746 | Sequence 12746, A |
| C 885 | 29 | 80.6 | 4440 | 3 | US-09-591-514-1 | Sequence 1, Appli | C 958 | 29 | 80.6 | 26355 | 4 | US-09-949-016-12995 | Sequence 12995, A |
| C 886 | 29 | 80.6 | 4693 | 3 | US-09-462-561B-8 | Sequence 8, Appli | C 959 | 29 | 80.6 | 26416 | 4 | US-09-949-016-14266 | Sequence 14266, A |
| C 887 | 29 | 80.6 | 4992 | 4 | US-09-377-497-5 | Sequence 5, Appli | C 960 | 29 | 80.6 | 26896 | 4 | US-09-949-016-16800 | Sequence 16800, A |
| C 888 | 29 | 80.6 | 5049 | 1 | US-08-336-345-1 | Sequence 1, Appli | C 961 | 29 | 80.6 | 27056 | 4 | US-09-949-016-12200 | Sequence 12200, A |

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962 29 80.6 27057 4 US-09-949-016-13115 Sequence 13115, A
963 29 80.6 28194 4 US-09-902-540-1250 Sequence 1250, Ap
964 29 80.6 23103 4 US-09-902-540-1236 Sequence 1236, Ap
c 965 29 80.6 33353 4 US-09-949-016-17285 Sequence 1285, A
c 966 29 80.6 34279 4 US-09-536-002-26 Sequence 26, Appl
c 967 29 80.6 35725 4 US-09-949-016-13172 Sequence 13172, A
968 29 80.6 36470 4 US-08-311-731A-123 Sequence 123, Appl
c 969 29 80.6 36519 3 US-08-923-137-2 Sequence 2, Appl
c 970 29 80.6 37622 4 US-09-949-016-12294 Sequence 12294, A
c 971 29 80.6 37622 4 US-09-949-016-15726 Sequence 15726, A
c 972 29 80.6 38239 4 US-09-949-016-12348 Sequence 12348, A
c 973 29 80.6 38252 4 US-09-949-016-13570 Sequence 13570, A
974 29 80.6 38261 4 US-09-949-016-13802 Sequence 13802, A
c 975 29 80.6 40000 3 US-09-780-049-18 Sequence 18, Appl
c 976 29 80.6 40138 3 US-09-231-899-12 Sequence 12, Appl
c 977 29 80.6 40586 4 US-09-949-016-16965 Sequence 16965, A
978 29 80.6 43255 4 US-09-949-016-11909 Sequence 11909, A
c 979 29 80.6 43981 4 US-09-949-016-16294 Sequence 16294, A
980 29 80.6 47683 4 US-09-949-016-16460 Sequence 16460, A
981 29 80.6 52494 4 US-09-949-016-16498 Sequence 16498, A
982 29 80.6 52494 4 US-09-949-016-16498 Sequence 16498, A
983 29 80.6 54816 4 US-09-902-540-1272 Sequence 1272, Ap
c 984 29 80.6 54816 4 US-09-949-016-16069 Sequence 16069, A
985 29 80.6 56714 4 US-09-949-016-11960 Sequence 11960, A
c 986 29 80.6 57280 4 US-09-949-016-11796 Sequence 11796, A
c 987 29 80.6 57280 4 US-09-949-016-12843 Sequence 12843, A
c 988 29 80.6 57280 4 US-09-949-016-12844 Sequence 12844, A
c 989 29 80.6 57280 4 US-09-949-016-12846 Sequence 12846, A
c 990 29 80.6 57280 4 US-09-949-016-13542 Sequence 13542, A
c 991 29 80.6 57280 4 US-09-949-016-13543 Sequence 13543, A
c 992 29 80.6 57280 4 US-09-949-016-13544 Sequence 13544, A
c 993 29 80.6 57280 4 US-09-949-016-13545 Sequence 13545, A
c 994 29 80.6 57280 4 US-09-949-016-14633 Sequence 14633, A
c 995 29 80.6 57280 4 US-09-949-016-14634 Sequence 14634, A
c 996 29 80.6 57280 4 US-09-949-016-14635 Sequence 14635, A
c 997 29 80.6 57280 4 US-09-949-016-14636 Sequence 14636, A
c 998 29 80.6 57280 4 US-09-949-016-14637 Sequence 14637, A
c 999 29 80.6 57280 4 US-09-949-016-14638 Sequence 14638, A
c1000 29 80.6 57280 4 US-09-949-016-14639 Sequence 14639, A
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ALIGNMENTS

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RESULT 1
US-09-313-294A-3256
; Sequence 3256, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 3256
; LENGTH: 266
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700611205H1
; NAME/KEY: unsure
; LOCATION: 262
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-3256
Alignment Scores:
Pred. No.: 34.5 Length: 266
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0

RESULT 2
US-09-313-294A-1966
; Sequence 1966, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 1966
; LENGTH: 291
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700551823H1
; NAME/KEY: unsure
; LOCATION: 256
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-1966
Alignment Scores:
Pred. No.: 38.2 Length: 291
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-313-294A-1966 (1-291)
Qy 1 PheGlnIleGluHisHis 6
Db 228 TTCAGATTGAGCACCAT 245

RESULT 3
US-09-702-705-355/c
; Sequence 355, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 355
; LENGTH: 347
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
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US-10-029-756-20 (1-6) x US-09-313-294A-3256 (1-266)

Qy 1 PheGlnIleGluHisHis 6

Db 78 TTCAGATTGAGCACCAT 95

RESULT 2

US-09-313-294A-1966

; Sequence 1966, Application US/09313294A

; Patent No. 6476212

; GENERAL INFORMATION:

; APPLICANT: Lalgudi, Raghunath V.

; APPLICANT: Ito, Laura Y.

; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR

; FILE REFERENCE: PL-0017 US

; CURRENT APPLICATION NUMBER: US/09/313,294A

; CURRENT FILING DATE: 1999-05-14

; NUMBER OF SEQ ID NOS: 7600

; SOFTWARE: PERL Program

; SEQ ID NO 1966

; LENGTH: 291

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No. 6476212 700551823H1

; NAME/KEY: unsure

; LOCATION: 256

; OTHER INFORMATION: a, t, c, g, or other

US-09-313-294A-1966

Alignment Scores:

Pred. No.: 38.2 Length: 291

Score: 36.00 Matches: 6

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-313-294A-1966 (1-291)

Qy 1 PheGlnIleGluHisHis 6

Db 228 TTCAGATTGAGCACCAT 245

RESULT 3

US-09-702-705-355/c

; Sequence 355, Application US/09702705

; Patent No. 6504010

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Lodes, Michael A.

; APPLICANT: Fanger, Gary

; APPLICANT: Vedvick, Tom

; APPLICANT: Carter, Darrick

; APPLICANT: Retter, Marc

; APPLICANT: Mannion, Jane

; APPLICANT: Fan, Liqun

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.478C14

; CURRENT APPLICATION NUMBER: US/09/702,705

; CURRENT FILING DATE: 2000-10-30

; NUMBER OF SEQ ID NOS: 1833

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 355

; LENGTH: 347

Alignment Scores:

Pred. No.: 34.5 Length: 266

Score: 36.00 Matches: 6

Percent Similarity: 100.00% Conservative: 0


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; TYPE: DNA
; ORGANISM: Homo sapien
US-09-702-705-355

Alignment Scores:
Pred. No.: 46.6 Length: 347
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-702-705-355 (1-347)

Qy 1 PheGlnIleGluHis 6
Db 284 TTCAGATCGAGCACCAC 267

RESULT 4
US-09-736-457-355/c
; Sequence 355, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 355
; LENGTH: 347
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-355

Alignment Scores:
Pred. No.: 46.6 Length: 347
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-736-457-355 (1-347)

Qy 1 PheGlnIleGluHis 6
Db 284 TTCAGATCGAGCACCAC 267

RESULT 5
US-09-614-124B-355/c
; Sequence 355, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 355
; LENGTH: 347
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-614-124B-355

Alignment Scores:
Pred. No.: 46.6 Length: 347
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-614-124B-355 (1-347)

Qy 1 PheGlnIleGluHis 6
Db 284 TTCAGATCGAGCACCAC 267

RESULT 6
US-09-671-325-355/c
; Sequence 355, Application US/09671325
; Patent No. 6867154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 355
; LENGTH: 347
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-671-325-355

Alignment Scores:
Pred. No.: 46.6 Length: 347
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-671-325-355 (1-347)

Qy 1 PheGlnIleGluHis 6
Db 284 TTCAGATCGAGCACCAC 267

RESULT 7
US-09-589-184-355/c
; Sequence 355, Application US/09589184
; Patent No. 6866447
; GENERAL INFORMATION:
```

```

; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaityanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C8
; CURRENT APPLICATION NUMBER: US/09/589,184
; CURRENT FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 827
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 355
; LENGTH: 347
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-589-184-355

Alignment Scores:
Pred. No.: 46.6 Length: 347
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-589-184-355 (1-347)

Qy 1 PheGlnIleGluHisHis 6
Db 284 TTCCAGATCGAGCACCAC 267

RESULT 8
US-09-658-824-355/c
; Sequence 355, Application US/09658824
; Patent No. 6746846
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaityanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C11
; CURRENT APPLICATION NUMBER: US/09/658,824
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 1788
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 355
; LENGTH: 347
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-658-824-355

Alignment Scores:
Pred. No.: 46.6 Length: 347
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-658-824-355 (1-347)

Qy 1 PheGlnIleGluHisHis 6
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Db 284 TTCCAGATCGAGCACCAC 267

RESULT 9
US-09-710-279-1855/c
; Sequence 1855, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1855
; LENGTH: 372
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-1855

Alignment Scores:
Pred. No.: 50.4 Length: 372
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-710-279-1855 (1-372)

Qy 1 PheGlnIleGluHisHis 6
Db 154 TTTCANATCGAGCACCAT 137

RESULT 10
US-09-134-001C-1672/c
; Sequence 1672, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1672
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1672

Alignment Scores:
Pred. No.: 55.5 Length: 405
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-134-001C-1672 (1-405)

Qy 1 PheGlnIleGluHisHis 6
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Db 187 TTTCAATGAGCACCAT 170
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RESULT 11
US-09-439-261-38
; Sequence 38, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)..(5)
; OTHER INFORMATION: k = g or t/u at position 5
; NAME/KEY: misc_feature
; LOCATION: (6)..(6)
; OTHER INFORMATION: m = a or c at position 6
US-09-439-261-38

Alignment Scores:
Pred. No.: 62.4 Length: 449
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-439-261-38 (1-449)
Qy 1 PheGlnIleGluHis 6
|||||
Db 248 TTCCAGATTGAGCACCAT 265
|||||

RESULT 12
US-09-227-613-37
; Sequence 37, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-227-613-37
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Alignment Scores:
Pred. No.: 62.4 Length: 449
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-227-613-37 (1-449)
Qy 1 PheGlnIleGluHis 6
|||||
Db 248 TTCCAGATTGAGCACCAT 265
|||||

RESULT 13
US-09-439-261-37
; Sequence 37, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-261-37

Alignment Scores:
Pred. No.: 66.2 Length: 473
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-439-261-37 (1-473)
Qy 1 PheGlnIleGluHis 6
|||||
Db 279 TTCCAGATTGAGCACCAT 296
|||||

RESULT 14
US-09-227-613-36
; Sequence 36, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 473
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```

; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-227-613-36

Alignment Scores:
Pred. No.: 473
Score: 66.2
Percent Similarity: 100.00%
Conservative: 6
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 100.00%
Indels: 0
Gaps: 0
DB: 3

US-10-029-756-20 (1-6) x US-09-227-613-36 (1-473)

QY 1 PheGlnIleGluHis 6
DB 279 TTCCAGATTGAGCACCAC 296

RESULT 15
US-09-439-261-3
; Sequence 3, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 655
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-261-3

Alignment Scores:
Pred. No.: 95.7
Score: 36.00
Percent Similarity: 100.00%
Conservative: 6
Best Local Similarity: 100.00%
Mismatch: 0
Query Match: 100.00%
Indels: 0
Gaps: 0
DB: 3

US-10-029-756-20 (1-6) x US-09-439-261-3 (1-655)

QY 1 PheGlnIleGluHis 6
DB 242 TTCCAGATTGAGCACCAC 259

RESULT 16
US-09-227-613-3
; Sequence 3, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11

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; CURRENT APPLICATION NUMBER: US/09/227.613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows version 3.0
; SEQ ID NO 13
; LENGTH: 864
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-227-613-13

Alignment Scores:
Pred. No.: 131 Length: 864
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-227-613-13 (1-864)

Qy 1 PheGlnIleGluHis 6
Db 670 TTCGATTGAGCACCAT 687

RESULT 19

US-09-248-796A-2259/c
; Sequence 2259, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 2259
; LENGTH: 876
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-2259

Alignment Scores:
Pred. No.: 133 Length: 876
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-248-796A-2259 (1-876)

Qy 1 PheGlnIleGluHis 6
Db 478 TTCGATTGAGCACCAT 461

RESULT 20

US-09-710-279-4425
; Sequence 4425, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3490US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258

; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4425
; LENGTH: 1132
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-4425

Alignment Scores:
Pred. No.: 178 Length: 1132
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-710-279-4425 (1-1132)

Qy 1 PheGlnIleGluHis 6
Db 359 TTTCAGATCGAGCACCAT 376

RESULT 21

US-09-769-863-28
; Sequence 28, Application US/09769863
; Patent No. 6635451
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Dae, Tapas
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
; FILE REFERENCE: 6763 US.O1
; CURRENT APPLICATION NUMBER: US/09/769,863
; CURRENT FILING DATE: 2001-01-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 1320
; TYPE: DNA
; ORGANISM: Thraustochytrium aureum
US-09-769-863-28

Alignment Scores:
Pred. No.: 212 Length: 1320
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-769-863-28 (1-1320)

Qy 1 PheGlnIleGluHis 6
Db 1123 TTTCAGATCGAGCACCAC 1140

RESULT 22

US-09-439-261-1
; Sequence 1, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF

```
; FILE REFERENCE: 6295.US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-261-1

Alignment Scores:
Pred. No.: 214 Length: 1335
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-439-261-1 (1-1335)

Qy 1 PheGlnIleGluHisHis 6
Db 1141 TTCCAGATTGACCCAT 1158

RESULT 23
US-09-227-613-1
; Sequence 1, Application US/09/227613A
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Pradip
; APPLICANT: LEONARD, Amanda B.
; APPLICANT: HUANG, Yung-Sheng.
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295.US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-227-613-1

Alignment Scores:
Pred. No.: 214 Length: 1335
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-227-613-1 (1-1335)

Qy 1 PheGlnIleGluHisHis 6
Db 1141 TTCCAGATTGACCCAT 1158

RESULT 24
US-09-148-545-63
; Sequence 63, Application US/09148545
; Patent No. 6590075
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
```

; EARLIER FILING DATE: 1997-04-11
 ; EARLIER APPLICATION NUMBER: 60/043,311
 ; EARLIER FILING DATE: 1997-04-11
 ; EARLIER APPLICATION NUMBER: 60/043,671
 ; EARLIER FILING DATE: 1997-04-11
 ; EARLIER APPLICATION NUMBER: 60/043,674
 ; EARLIER FILING DATE: 1997-04-11
 ; EARLIER APPLICATION NUMBER: 60/043,669
 ; EARLIER FILING DATE: 1997-04-11
 ; EARLIER APPLICATION NUMBER: 60/043,312
 ; EARLIER FILING DATE: 1997-04-11
 ; EARLIER APPLICATION NUMBER: 60/043,313
 ; EARLIER FILING DATE: 1997-04-11
 ; EARLIER APPLICATION NUMBER: 60/043,672
 ; EARLIER FILING DATE: 1997-04-11
 ; EARLIER APPLICATION NUMBER: 60/043,315
 ; EARLIER FILING DATE: 1997-04-11
 ; EARLIER APPLICATION NUMBER: 60/048,974
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/056,886
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,877
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,889
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,893
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,630
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,878
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,662
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,872
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,882
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,637
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,903
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,888
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,879
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,880
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,894
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,911
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,636
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,874
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,910
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,864
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,631
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,845
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,892
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/047,595
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/057,761
 ; EARLIER FILING DATE: 05-Sep-1997
 ; EARLIER APPLICATION NUMBER: 60/047,599
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,588
 ; EARLIER FILING DATE: 1997-05-23

; EARLIER APPLICATION NUMBER: 60/047,585
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,586
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,590
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,594
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,589
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,593
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/047,614
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/043,578
 ; EARLIER FILING DATE: 1997-04-11
 ; EARLIER APPLICATION NUMBER: 60/043,576
 ; EARLIER FILING DATE: 1997-04-11
 ; EARLIER APPLICATION NUMBER: 60/047,501
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: 60/043,670
 ; EARLIER FILING DATE: 1997-04-11
 ; EARLIER APPLICATION NUMBER: 60/056,632
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,664
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,876
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,881
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,909
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,875
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,862
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,887
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/056,908
 ; EARLIER FILING DATE: 1997-08-22
 ; EARLIER APPLICATION NUMBER: 60/048,964
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/057,650
 ; EARLIER FILING DATE: 1997-09-05
 ; EARLIER APPLICATION NUMBER: 60/056,884
 ; EARLIER FILING DATE: 1997-08-22
 ; NUMBER OF SEQ ID NOS: 280
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 63
 ; LENGTH: 1478

Alignment Scores:
 Pred. No.: 241 Length: 1478
 Score: 36.00 Matches: 6
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-148-545-63 (1-1478)

Qy 1 PheGlnIleGluHis 6
 |||||
 Db 947 TTCCAGATCGAGACCAC 964

RESULT 25
 US-08-831-570-1
 ; Sequence 1, Application US/08831570
 ; Patent No. 5959175
 ; GENERAL INFORMATION:
 ; APPLICANT: Thomas, Terry L.
 ; APPLICANT: Nunberg, Andrew N.
 ; APPLICANT: Beremand, Phillip D.

TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1685 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-366-779-4

Alignment Scores:
Pred. No.: 279 Length: 1685
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x US-08-366-779-4 (1-1685)

Qy 1 PheGlnIleGluHisHis 6
|||||
Db 1157 TTCCAATTGAGCATCAT 1174

RESULT 28

US-08-789-936-4
; Sequence 4, Application US/08789936
; Patent No. 5789220
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; APPLICANT: Reddy, Avutu S.
; APPLICANT: Nuccio, Michael
; APPLICANT: Preyasinet, Georges L.
; APPLICANT: Nunberg, Andrew N.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; TITLE OF INVENTION: DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/789,936
; FILING DATE: 28-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/366,779
; FILING DATE: 30-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 83832YXW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1685 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

US-08-789-936-4
Alignment Scores:
Pred. No.: 279 Length: 1685
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-10-029-756-20 (1-6) x US-08-789-936-4 (1-1685)

Qy 1 PheGlnIleGluHisHis 6
|||||
Db 1157 TTCCAATTGAGCATCAT 1174

RESULT 29

US-08-934-254-4
; Sequence 4, Application US/08934254
; Patent No. 6355861
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; TITLE OF INVENTION: DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,254
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 83832YXWVU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1685 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-934-254-4

Alignment Scores:
Pred. No.: 279 Length: 1685
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-08-934-254-4 (1-1685)

Qy 1 PheGlnIleGluHisHis 6
|||||
Db 1157 TTCCAATTGAGCATCAT 1174

RESULT 30

US-09-685-775-4
; Sequence 4, Application US/09685775
; Patent No. 6683232
; GENERAL INFORMATION:
APPLICANT: Thomas, Terry L.
TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A DELTA 6-DESATURASE

NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSES: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/685,775
FILING DATE: 10-Oct-2000
CLASSIFICATION: <Unknown>
PRIORITY CLAIMING DATA:
APPLICATION NUMBER: US/08/934,254
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 8383ZYXWVU

TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO.: 4:
SEQUENCE CHARACTERISTICS:
-- LENGTH: 1685 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-685-775-4

Alignment Scores:
Pred. No.: 279 Length: 1685
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-10-029-756-20 (1-6) x US-09-685-775-4 (1-1685)

Oy 1 PheGlnIleGlutHis 6
|||||
Db 1157 TTCCAAATGGAGCATCAT 1174

RESULT 31
US-09-439-261-6
Sequence 6, Application US/09439261
Patent No. 6428990
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Mukerji, Pradip
APPLICANT: Leonard, Amanda E.
APPLICANT: Huang, Yung-Sheng
TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
FILE REFERENCE: 6295.US.P2
CURRENT APPLICATION NUMBER: US/09/439,261
CURRENT FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: US 08/833,610


```
;
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/048,888
; FILING DATE: Filed Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Certone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0494 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1717 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: ENDANOT01
; CLONE: 2451043
; US-09-048-888-2

Alignment Scores:
Pred. No.: 285 Length: 1717
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-048-888-2 (1-1717)

Qy 1 PheGlnIleGluHisHis 6
Db 1218 TTCCAGATCGAGCACCAC 1235

RESULT 34
US-09-949-016-4904
; Sequence 4904, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4904
; LENGTH: 1758
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;
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-4904

Alignment Scores:
Pred. No.: 293 Length: 1758
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-949-016-4904 (1-1758)

Qy 1 PheGlnIleGluHisHis 6
Db 1277 TTCCAGATCGAGCACCAC 1294

RESULT 35
US-09-439-261-7
; Sequence 7, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1843
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-439-261-7

Alignment Scores:
Pred. No.: 309 Length: 1843
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-439-261-7 (1-1843)

Qy 1 PheGlnIleGluHisHis 6
Db 691 TTCCAGATCGAGCACCAC 708

RESULT 36
US-09-227-613-7
; Sequence 7, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: Mukerji, Pradip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
```

; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 1843
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-227-613-7

Alignment Scores: 309 Length: 1843
Pred. No.: 36.00 Matches: 6
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 3

US-10-029-756-20 (1-6) x US-09-227-613-7 (1-1843)

Qy 1 PheGlnIleGluHis 6
Db 691 TTCAGATTGAGCACCAC 708

RESULT 37
US-09-048-888-4
; Sequence 4, Application US/09048888
; Patent No. 6492108
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DELTA-6-DESATURASE HOMOLOGS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/048,888
; FILING DATE: Filed Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0494 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1928 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BEPNOT01
; CLONE: 2056310
US-09-048-888-4

Alignment Scores: 325 Length: 1928
Pred. No.: 36.00 Matches: 6
Score:

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-048-888-4 (1-1928)

Qy 1 PheGlnIleGluHis 6
Db 1224 TTCAGATTGAGCACCAT 1241

RESULT 38
US-09-148-545-119
; Sequence 119, Application US/09148545
; Patent No. 6590075
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: PZ001P1
; CURRENT APPLICATION NUMBER: US/09/148,545
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/US98/04482
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,161
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,582
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,596
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,612
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,632
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,601
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,580
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,568
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,314
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,569
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,311
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,671
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,674
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,669
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,312
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,313
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,672
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,315
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,877
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,889
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,893
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,630
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,878
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,662
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,872
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,882
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,637
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,903
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,888
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,879
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,880
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,894
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,911
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,636
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,874
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,910

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,864
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,631
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,845
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,892
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047,595
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/057,761
EARLIER FILING DATE: 05-Sep-1997
EARLIER APPLICATION NUMBER: 60/047,599
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,588
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,585
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,586
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,590
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,594
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,589
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,593
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 280
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 119
LENGTH: 2016

Alignment Scores:
Pred. No.: 342
Score: 36.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Length: 2016
Matches: 6
Conservative: 0
Mismatch: 0

Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-029-756-20 (1-6) x US-09-148-545-119 (1-2016)
Qy 1 PheGlnIleGluHis 6
Db 1498 TTCAGATCGAGCACCAC 1515
RESULT 39
US-09-439-261-8
; Sequence 8, Application US/09439261
; Patent No. 6428990
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Paridip
; APPLICANT: Leonard, Amanda E.
; APPLICANT: Huang, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US.P2
; CURRENT APPLICATION NUMBER: US/09/439,261
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 08/833,610
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: PCT/US98/07422
; PRIOR FILING DATE: 1998-04-10
; PRIOR APPLICATION NUMBER: US 09/227,613
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 2257
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-261-8
Alignment Scores:
Pred. No.: 389 Length: 2257
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-029-756-20 (1-6) x US-09-439-261-8 (1-2257)
Qy 1 PheGlnIleGluHis 6
Db 1105 TTCAGATTGAGCACCAC 1122
RESULT 40
US-09-227-613-8
; Sequence 8, Application US/09227613A
; Patent No. 6432684
; GENERAL INFORMATION:
; APPLICANT: MUKERJI, Paridip
; APPLICANT: LEONARD, Amanda E.
; APPLICANT: HUANG, Yung-Sheng
; TITLE OF INVENTION: HUMAN DESATURASE GENE AND USES THEREOF
; FILE REFERENCE: 6295 US.P1
; CURRENT APPLICATION NUMBER: US/09/227,613A
; CURRENT FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 08/833,610
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 2257
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-227-613-8
Alignment Scores:
Pred. No.: 444 Length: 2254
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-029-756-20 (1-6) x US-09-023-655-295 (1-2540)
Qy 1 PheGlnIleGluHis 6

Pred. No.: 389 Length: 2257
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-10-029-756-20 (1-6) x US-09-227-613-8 (1-2257)
Qy 1 PheGlnIleGluHis 6
Db 1105 TTCAGATTGAGCACCAC 1122
RESULT 41
US-09-023-655-295
; Sequence 295, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 295:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2540 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PROSNOT11
; CLONE: 1346478
US-09-023-655-295
Alignment Scores:
Pred. No.: 444 Length: 2540
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-10-029-756-20 (1-6) x US-09-023-655-295 (1-2540)
Qy 1 PheGlnIleGluHis 6

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Db      674  TTTCCAGATTGAGCACCAC 691
RESULT 42
US-09-949-016-4613
; Sequence 4613, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4613
; LENGTH: 3158
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4613
Alignment Scores:
Pred. No.:      569      Length:      3158
Score:          36.00    Matches:      6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:     4      Indels:      0
DB:              Gaps:      0
US-10-029-756-20 (1-6) x US-09-949-016-4613 (1-3158)
Qy      1  PheGlnIleGluHisHis 6
Db      1305  TTTCCAGATTGAGCACCAC 1322
RESULT 43
US-09-710-279-4180
; Sequence 4180, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4180
; LENGTH: 4103
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-710-279-4180
Alignment Scores:
Pred. No.:      765      Length:      4103
Score:          36.00    Matches:      6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:     4      Indels:      0
DB:              Gaps:      0
US-10-029-756-20 (1-6) x US-09-949-016-16077 (1-15595)
Qy      1  PheGlnIleGluHisHis 6
Db      14170  TTTCCAGATGAGCATCAC 14187
RESULT 45
US-09-949-016-15109
; Sequence 15109, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15109
; LENGTH: 26684
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(26684)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15109
US-10-029-756-20 (1-6) x US-09-949-016-16077 (1-15595)
Qy      1  PheGlnIleGluHisHis 6
Db      14170  TTTCCAGATGAGCATCAC 14187
RESULT 45
US-09-949-016-15109
; Sequence 15109, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15109
; LENGTH: 26684
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(26684)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15109
```

Alignment Scores: Length: 26684
Pred. No.: 6.38e+03 Matches: 6
Score: 36.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-949-016-15109 (1-26684)

Qy 1 PheGlnIleGluHisHis 6
Db 349 TTCAGATAGACATCAC 366

RESULT 46

US-09-949-016-15110
Sequence 15110, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 15110

LENGTH: 26684

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(26684)

OTHER INFORMATION: n = A,T,C or G

US-09-949-016-15110

Alignment Scores: Length: 26684
Pred. No.: 6.38e+03 Matches: 6
Score: 36.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-949-016-15110 (1-26684)

Qy 1 PheGlnIleGluHisHis 6
Db 349 TTCAGATAGACATCAC 366

RESULT 47

US-09-949-016-17409

Sequence 17409, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17409
LENGTH: 26684
TYPE: DNA
ORGANISM: Human
FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(26684)

OTHER INFORMATION: n = A,T,C or G

US-09-949-016-17409

Alignment Scores: Length: 26684
Pred. No.: 6.38e+03 Matches: 6
Score: 36.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-949-016-17409 (1-26684)

Qy 1 PheGlnIleGluHisHis 6
Db 349 TTCAGATAGACATCAC 366

RESULT 48

US-09-949-016-17410

Sequence 17410, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 17410

LENGTH: 26684

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(26684)

OTHER INFORMATION: n = A,T,C or G

US-09-949-016-17410

Alignment Scores: Length: 26684
Pred. No.: 6.38e+03 Matches: 6
Score: 36.00
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-949-016-17410 (1-26684)

Qy 1 PheGlnIleGluHisHis 6
Db 349 TTCAGATAGACATCAC 366

RESULT 49

US-09-949-016-16089

; Sequence 16089, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16089
; LENGTH: 175265
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(175265)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16089

Alignment Scores:
Pred. No.: 5,31e+04 Length: 175265
Score: 36.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-949-016-16089 (1-175265)

Qy 1 PheGlnIleGluHisHis 6
|||||:|||||
Db 161293 TTTCAGTTCGAGCATCAT 161310

RESULT 50
US-09-672-265-7/c
; Sequence 7, Application US/09672265
; Patent No. 6812019
; GENERAL INFORMATION:
; APPLICANT: Roche Diagnostics GmbH
; TITLE OF INVENTION: Process for the recombinant production of holo-citrate lyase
; FILE REFERENCE: BMID 9975 US
; CURRENT APPLICATION NUMBER: US/09/672,265
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: DE 99119404.4
; PRIOR FILING DATE: 1999-09-30
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 5593
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-672-265-7

Alignment Scores:
Pred. No.: 1,74e+03 Length: 5593
Score: 35.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 97.22% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-672-265-7 (1-5593)

Qy 1 PheGlnIleGluHisHis 6
|||||:|||||

Db 1576 TTCCAGTTCGAGCATCATC 1559

RESULT 51

US-09-415-522-5/c
; Sequence 5, Application US/09415522A
; Patent No. 6291660
; GENERAL INFORMATION:
; APPLICANT: Gaffney, Thomas
; APPLICANT: Wendland, Juergen
; APPLICANT: Philippsen, Peter
; TITLE OF INVENTION: No. 6291660el Fungal Genes Required For No. 6291660mal Growth And
; TITLE OF INVENTION: Development
; FILE REFERENCE: CGC2046
; CURRENT APPLICATION NUMBER: US/09/415,522A
; CURRENT FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 6216
; TYPE: DNA
; ORGANISM: Ashbya gossypii
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(6216)
US-09-415-522-5

Alignment Scores:
Pred. No.: 1,97e+03 Length: 6216
Score: 35.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 97.22% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-415-522-5 (1-6216)

Qy 1 PheGlnIleGluHisHis 6
|||||:|||||

Db 3547 TTTCAGTTCGAGCATCAT 3530

RESULT 52

US-08-834-655-14/c
; Sequence 14, Application US/08834655
; Patent No. 5968809
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,655
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER, BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.124.00US

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 328-4400
; TELEFAX: (650) 328-4477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-834-655-14

Alignment Scores:
Pred. No.: 8.37 Length: 33
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 94.44% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x US-08-834-655-14 (1-33)

Qy 1 PheGlnIleGluHis 6
Db 30 TTTCAGCTTGAGCATCAT 13

RESULT 53
US-08-834-033A-22/c
; Sequence 22, Application US/08834033A
; Patent No. 6075183
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MUKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,033A
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-300.USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-834-033A-22

Alignment Scores:
Pred. No.: 8.37 Length: 33
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 94.44% Indels: 0
DB: 2 Gaps: 0

US-10-029-756-20 (1-6) x US-08-834-655-14 (1-33)

Qy 1 PheGlnIleGluHis 6
Db 30 TTTCAGCTTGAGCATCAT 13

RESULT 54
US-09-363-574-14/c
; Sequence 14, Application US/09363574
; Patent No. 6136574
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MUKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/363,574
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38,651
; REFERENCE/DOCKET NUMBER: CGAB-202 USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-09-363-574-14

Alignment Scores:
Pred. No.: 8.37 Length: 33
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 94.44% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-363-574-14 (1-33)

Qy 1 PheGlnIleGluHis 6
Db 30 TTTCAGCTTGAGCATCAT 13
```


RESULT 55
US-09-363-526-14/c
; Sequence 14, Application US/09363526
; Patent No. 6410288
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/363.526
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: WARD, MICHAEL R.
; REGISTRATION NUMBER: 38.651
; REFERENCE/DOCKET NUMBER: CGAB-201 USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-09-363-526-14
Alignment Scores:
Pred. No.: 8.37 Length: 33
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 94.44% Indels: 0
DB: 3 Gaps: 0
US-10-029-756-20 (1-6) x US-09-363-526-14 (1-33)
Qy 1 PheGlnIleGluHis 6
Db 30 TTTCAGCTTGAGCATCAT 13
RESULT 56
US-09-489-039A-5096/c
; Sequence 5096, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489.039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 5096
; LENGTH: 315
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-5096
Alignment Scores:
Pred. No.: 108 Length: 315
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 94.44% Indels: 0
DB: 4 Gaps: 0
US-10-029-756-20 (1-6) x US-09-489-039A-5096 (1-315)
Qy 1 PheGlnIleGluHis 6
Db 31 TTTCAGCTTGAGCATCAC 14
RESULT 57
US-08-836-075A-3
; Sequence 3, Application US/08836075A
; Patent No. 6180768
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; APPLICANT: STUYVER, LIEVEN
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
; TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836.075A
; FILING DATE: 21 Apr 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/04155
; FILING DATE: 23 Oct 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94870166.9
; FILING DATE: 21 Oct 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95870076.7
; FILING DATE: 28 Jun 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:004
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-836-075A-3
Alignment Scores:

Pred. No.: 160 Length: 447
 Score: 34.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 83.33% Mismatches: 0
 Query Match: 94.44% Indels: 0
 DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-08-836-075A-3 (1-447)

Qy 1 PheGlnIleGluHis 6
 Db 144 TTCCAACGAGCATCAT 161

RESULT 58

US-08-836-075A-7
 ; Sequence 7, Application US/08836075A
 ; Patent No. 6180768
 ; GENERAL INFORMATION:
 ; APPLICANT: MAERTENS, GEERT
 ; APPLICANT: STUYVER, LIEVEN
 ; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
 ; TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
 ; TITLE OF INVENTION: AGENTS
 ; NUMBER OF SEQUENCES: 207
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ARNOLD, WHITE & DURKEE
 ; STREET: P.O. BOX 4433
 ; CITY: HOUSTON
 ; STATE: TEXAS
 ; COUNTRY: USA
 ; ZIP: 77210-4433
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Microsoft Word 6.0 / ASCII text output
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/836.075A
 ; FILING DATE: 21 Apr 1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/EP95/04155
 ; FILING DATE: 23 Oct 1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 94870166.9
 ; FILING DATE: 21 Oct 1994
 ; APPLICATION DATA:
 ; APPLICATION NUMBER: EP 95870076.7
 ; FILING DATE: 28 Jun 1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KAMMERER, PATRICIA A.
 ; REGISTRATION NUMBER: 29,775
 ; REFERENCE/DOCKET NUMBER: INNS:004
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 447 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; US-08-836-075A-7

Alignment Scores:
 Pred. No.: 160 Length: 447
 Score: 34.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 83.33% Mismatches: 0
 Query Match: 94.44% Indels: 0
 DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-08-836-075A-7 (1-447)

Qy 1 PheGlnIleGluHis 6
 Db 144 TTCCAACGAGCATCAT 161

RESULT 59

US-09-949-016-202174/c
 ; Sequence 202174, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 202174
 ; LENGTH: 601
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-202174

Alignment Scores:
 Pred. No.: 224 Length: 601
 Score: 34.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 83.33% Mismatches: 0
 Query Match: 94.44% Indels: 0
 DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-949-016-202174 (1-601)

Qy 1 PheGlnIleGluHis 6
 Db 369 TTCCAACGAGCATCAT 352

RESULT 60

US-09-949-016-202175/c
 ; Sequence 202175, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 202175
 ; LENGTH: 601
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-202175

Alignment Scores:
 Pred. No.: 224 Length: 601
 Score: 34.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 1
 Best Local Similarity: 83.33% Mismatches: 0

Query Match: 94.44% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-949-016-202175 (1-601)

Qy 1 PheGlnIleGluHis 6
Db 430 TTCCAACTTGAACATCAT 413

RESULT 61

US-09-949-016-202176/c
; Sequence 202176, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 202176
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-202176

Alignment Scores:

Pred. No.: 224 Length: 601
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 94.44% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-949-016-202176 (1-601)

Qy 1 PheGlnIleGluHis 6
Db 585 TTCCAACTTGAACATCAT 568

RESULT 62

US-09-578-063-34/c
; Sequence 34, Application US/09578063
; Patent No. 6764677
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A
; APPLICANT: Barnes, Thomas M
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
; PREVENTIVE, THERAPEUTIC, AND OTHER USES
; FILE REFERENCE: 210147.0023/6U1
; CURRENT APPLICATION NUMBER: US/09/578,063
; CURRENT FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-578-063-34

Alignment Scores:

Pred. No.: 567 Length: 1365
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 94.44% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-578-063-34 (1-1365)

Qy 1 PheGlnIleGluHis 6
Db 139 TTCACGCTTGAACCAT 122

RESULT 63

US-08-934-254-26
; Sequence 26, Application US/08934254
; Patent No. 6355861
; GENERAL INFORMATION:
; APPLICANT: Thomas, Terry L.
; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
; TITLE OF INVENTION: DELTA 6-DESATURASE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/934,254
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 83832YXWVU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1702 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 48..1406
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 48..1406
US-08-934-254-26

Alignment Scores:

Pred. No.: 728 Length: 1702
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 94.44% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-08-934-254-26 (1-1702)

Qy 1 PheGlnIleGluHis 6
|||||:|||||

Db 1164 TTCAGTTGGAGCACCAC 1181

RESULT 64

US-09-685-775-26

; Sequence 26, Application US/09685775

; Patent No. 6683232

; GENERAL INFORMATION:

; APPLICANT: Thomas, Terry L.

; TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A DELTA 6-DESATURASE

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Scully, Scott, Murphy & Presser

; STREET: 400 Garden City Plaza

; CITY: Garden City

; STATE: New York

; COUNTRY: United States

; ZIP: 11530

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/685,775

; FILING DATE: 10-Oct-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/934,254

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Presser, Leopold

; REGISTRATION NUMBER: 19,827

; REFERENCE/DOCKET NUMBER: 8383ZYXWU

; TELEPHONE: (516) 742-4343

; TELEFAX: (516) 742-4366

; TELEX: 230 901 SANS UR

; INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 1702 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 48..1406

FEATURE:

NAME/KEY: CDS

LOCATION: 48..1406

SEQUENCE DESCRIPTION: SEQ ID NO: 26:

US-09-685-775-26

Alignment Scores:

Pred. No.: 728 Length: 1702

Score: 34.00 Matches: 5

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 83.33% Mismatches: 0

Query Match: 94.44% Indels: 0

DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-685-775-26 (1-1702)

Qy 1 PheGlnIleGluHis 6

Db 1164 TTCAGTTGGAGCACCAC 1181

RESULT 65

US-09-578-063-33/c

; Sequence 33, Application US/09578063

; Patent No. 6764677

; GENERAL INFORMATION:

; APPLICANT: McCarthy, Sean A

; APPLICANT: Barnes, Thomas M

; APPLICANT: Fraser, Christopher C

; APPLICANT: Sharp, John D

; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,

; FILE REFERENCE: 210147.0023/6U1

; PREVENTIVE, THERAPEUTIC, AND OTHER USES

; CURRENT APPLICATION NUMBER: US/09/578,063

; CURRENT FILING DATE: 2000-05-24

; PRIOR APPLICATION NUMBER: US 09/333,159

; PRIOR FILING DATE: 1999-06-14

; NUMBER OF SEQ ID NOS: 79

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 33

; LENGTH: 1980

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-578-063-33

Alignment Scores:

Pred. No.: 864 Length: 1980

Score: 34.00 Matches: 5

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 83.33% Mismatches: 0

Query Match: 94.44% Indels: 0

DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-578-063-33 (1-1980)

Qy 1 PheGlnIleGluHis 6

Db 271 TTCAGCTTGACACCAT 254

RESULT 66

US-09-489-039A-5328/c

; Sequence 5328, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Garty Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

; FILE REFERENCE: 2709.2004001

; PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

; CURRENT APPLICATION NUMBER: US/09/489,039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 5328

; LENGTH: 2688

; TYPE: DNA

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-5328

Alignment Scores:

Pred. No.: 1,22e+03 Length: 2688

Score: 34.00 Matches: 5

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 83.33% Mismatches: 0

Query Match: 94.44% Indels: 0

DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-489-039A-5328 (1-2688)

Qy 1 PheGlnIleGluHis 6

Db 1455 TTCAGCTTGACATCAC 1438

RESULT 67

US-08-956-171E-186

; Sequence 186, Application US/08956171E

; Patent No. 6593114

; GENERAL INFORMATION:

; APPLICANT: Charles Kunsch

;;
;; Gil H. Choi
;; Patrick S. Dillion
;; Craig A. Rosen
;; Steven C. Barash
;; Michael R. Fannon
;;
;; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;; NUMBER OF SEQUENCES: 5256
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Human Genome Sciences, Inc.
;; STREET: 9410 Key West Avenue
;; CITY: Rockville
;; STATE: Maryland
;; COUNTRY: USA
;; ZIP: 20850
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;; COMPUTER: HP Vectra 486/33
;; OPERATING SYSTEM: MSDOS version 6.2
;; SOFTWARE: ASCII Text
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/956,171E
;; FILING DATE: 20-Oct-1997
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/009,861
;; FILING DATE: January 5, 1996
;; APPLICATION NUMBER: 08/781,986
;; FILING DATE: January 3, 1997
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mark J. Hyman
;; REGISTRATION NUMBER: 46,789
;; REFERENCE/DOCKET NUMBER: PB248P1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (240) 314-1224
;; TELEFAX: (301) 309-8439
;;
;; INFORMATION FOR SEQ ID NO: 186:
;;
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6876 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;;
;; SEQUENCE DESCRIPTION: SEQ ID NO: 186:
US-08-956-171E-186

Alignment Scores:
Pred. No.: 3,54e+03 Length: 6876
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 94.44% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-08-956-171E-186 (1-6876)

Qy 1 PheGlnIleGluHisHis 6
|||||:|||||
Db 1425 TTCCAACTCGAACACCAT 1442

RESULT 68
US-08-956-186
; Sequence 186, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850

;;
;; Gil H. Choi
;; Patrick S. Dillion
;; Craig A. Rosen
;; Steven C. Barash
;; Michael R. Fannon
;;
;; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;; NUMBER OF SEQUENCES: 5256
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Human Genome Sciences, Inc.
;; STREET: 9410 Key West Avenue
;; CITY: Rockville
;; STATE: Maryland
;; COUNTRY: USA
;; ZIP: 20850
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;; COMPUTER: HP Vectra 486/33
;; OPERATING SYSTEM: MSDOS version 6.2
;; SOFTWARE: ASCII Text
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/956,171E
;; FILING DATE: 20-Oct-1997
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/009,861
;; FILING DATE: January 5, 1996
;; APPLICATION NUMBER: 08/781,986
;; FILING DATE: January 3, 1997
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mark J. Hyman
;; REGISTRATION NUMBER: 46,789
;; REFERENCE/DOCKET NUMBER: PB248P1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (240) 314-1224
;; TELEFAX: (301) 309-8439
;;
;; INFORMATION FOR SEQ ID NO: 186:
;;
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6876 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;;
;; SEQUENCE DESCRIPTION: SEQ ID NO: 186:
US-08-956-171E-186

Alignment Scores:
Pred. No.: 3,54e+03 Length: 6876
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 94.44% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-08-956-171E-186 (1-6876)

Qy 1 PheGlnIleGluHisHis 6
|||||:|||||
Db 1425 TTCCAACTCGAACACCAT 1442

RESULT 68
US-08-956-186
; Sequence 186, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850

;;
;; Gil H. Choi
;; Patrick S. Dillion
;; Craig A. Rosen
;; Steven C. Barash
;; Michael R. Fannon
;;
;; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
;; NUMBER OF SEQUENCES: 5256
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Human Genome Sciences, Inc.
;; STREET: 9410 Key West Avenue
;; CITY: Rockville
;; STATE: Maryland
;; COUNTRY: USA
;; ZIP: 20850
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
;; COMPUTER: HP Vectra 486/33
;; OPERATING SYSTEM: MSDOS version 6.2
;; SOFTWARE: ASCII Text
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/781,986A
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Benson, Bob
;; REGISTRATION NUMBER: 30,446
;; REFERENCE/DOCKET NUMBER: PB248PP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (301) 309-8504
;; TELEFAX: (301) 309-8512
;; INFORMATION FOR SEQ ID NO: 186:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6876 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;;
;; US-08-781-986A-186

Alignment Scores:
Pred. No.: 3,54e+03 Length: 6876
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 94.44% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-08-781-986A-186 (1-6876)

Qy 1 PheGlnIleGluHisHis 6
|||||:|||||
Db 1425 TTCCAACTCGAACACCAT 1442

RESULT 69
US-09-949-016-17411
; Sequence 17411, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17411
; LENGTH: 99580
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17411

Alignment Scores:
Pred. No.: 7,2e+04 Length: 99580
Score: 34.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 94.44% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-949-016-17411 (1-99580)

Qy 1 PheGlnIleGluHis 6

Db 92428 TTCCAACCTGGAACATCAT 92445

RESULT 70

US-09-949-016-12805/c

; Sequence 12805, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12805

; LENGTH: 421491

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(421491)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-12805

Alignment Scores:

Pred. No.: 3.47e+05 Length: 421491

Score: 34.00 Matches: 5

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 83.33% Mismatches: 0

Query Match: 94.44% Indels: 0

DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-949-016-12805 (1-421491)

Qy 1 PheGlnIleGluHis 6

Db 192589 TTCCAACCTGGAACATCAT 192572

RESULT 71

US-09-949-016-14060/c

; Sequence 14060, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 14060

; LENGTH: 421494

; TYPE: DNA

; ORGANISM: Human

; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(421494)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14060

Alignment Scores:

Pred. No.: 3.47e+05 Length: 421494

Score: 34.00 Matches: 5

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 83.33% Mismatches: 0

Query Match: 94.44% Indels: 0

DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-949-016-14060 (1-421494)

Qy 1 PheGlnIleGluHis 6

Db 192589 TTCCAACCTGGAACATCAT 192572

RESULT 72

US-09-134-001C-2030/c

; Sequence 2030, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 2030

; LENGTH: 249

; TYPE: DNA

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-2030

Alignment Scores:

Pred. No.: 133 Length: 249

Score: 33.00 Matches: 5

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 83.33% Mismatches: 0

Query Match: 91.67% Indels: 0

DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-134-001C-2030 (1-249)

Qy 1 PheGlnIleGluHis 6

Db 67 TTTCATAATACACATCATC 50

RESULT 73

US-09-248-796A-9501/c

; Sequence 9501, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstein et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

; FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 9501


```
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/111,301
; PRIOR FILING DATE: 1998-12-07
; PRIOR APPLICATION NUMBER: PCT/US99/28655
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 1281
; TYPE: DNA
; ORGANISM: Euglena gracilis
US-09-857-583B-3

Alignment Scores:
Pred. No.:      848      Length:      1281
Score:          33.00    Matches:      5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match:     91.67% Indels:      0
DB:              4      Gaps:        0

US-10-029-756-20 (1-6) x US-09-857-583B-3 (1-1281)

Qy      1 PheGlnIleGluHis 6
Db      1079 TACCAGATCGAGCACCAT 1096

RESULT 78
US-09-857-583B-1
; Sequence 1, Application US/09857583B
; Patent No. 6825017
; GENERAL INFORMATION:
; APPLICANT: WASHINGTON STATE UNIVERSITY RESEARCH FOUNDATION
; APPLICANT: Browse, John A
; APPLICANT: Wallis, James G
; APPLICANT: Watts, Jennifer L.
; TITLE OF INVENTION: DESATURASES AND METHODS OF USING THEM FOR SYNTHESIS OF
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS
; FILE REFERENCE: 4630-58963
; CURRENT APPLICATION NUMBER: US/09/857,583B
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/111,301
; PRIOR FILING DATE: 1998-12-07
; PRIOR APPLICATION NUMBER: PCT/US99/28655
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1461
; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-09-857-583B-1

Alignment Scores:
Pred. No.:      984      Length:      1461
Score:          33.00    Matches:      5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match:     91.67% Indels:      0
DB:              4      Gaps:        0

US-10-029-756-20 (1-6) x US-09-857-583B-1 (1-1461)

Qy      1 PheGlnIleGluHis 6
Db      1189 TATCAGATTGAGCACCAT 1206

RESULT 79
US-08-834-655-1
; Sequence 1, Application US/08834655
; Patent No. 5968809
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
```

```
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,655
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER, BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.124.00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 328-4400
; TELEFAX: (650) 328-4477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1617 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-834-655-1

Alignment Scores:
Pred. No.:      11e+03    Length:      1617
Score:          33.00    Matches:      5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match:     91.67% Indels:      0
DB:              2      Gaps:        0

US-10-029-756-20 (1-6) x US-08-834-655-1 (1-1617)

Qy      1 PheGlnIleGluHis 6
Db      1250 TATCAGATCGAGCACCAC 1267

RESULT 80
US-08-834-033A-1
; Sequence 1, Application US/08834033A
; Patent No. 6075183
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; TITLE OF INVENTION: OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LIMBACH AND LIMBACH, L.L.P.
; STREET: 2001 FERRY BUILDING
; CITY: SAN FRANCISCO
; STATE: CA
; COUNTRY: USA
```


ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,033A
FILING DATE: 11-APR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-300.USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1617 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-834-033A-1

Alignment Scores:
Pred. No.: 1,1e+03 Length: 1617
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 91.67% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-08-834-033A-1 (1-1617)

QY 1 PheGlnIleGluHis 6
:::|||||

Db 1250 TATCAGATCGAGCACCAC 1267

RESULT 81
US-09-363-574-1
Sequence 1, Application US/09363574
Patent No. 6136574
GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,574
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651

REFERENCE/DOCKET NUMBER: CGAB-202 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1617 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
US-09-363-574-1

Alignment Scores:
Pred. No.: 1,1e+03 Length: 1617
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 91.67% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-363-574-1 (1-1617)

QY 1 PheGlnIleGluHis 6
:::|||||

Db 1250 TATCAGATCGAGCACCAC 1267

RESULT 82
US-09-363-526-1
Sequence 1, Application US/09363526
Patent No. 6410288
GENERAL INFORMATION:
APPLICANT: KNUTZON, DEBORAH
APPLICANT: MURKERJI, PRADIP
APPLICANT: HUANG, YUNG-SHENG
APPLICANT: THURMOND, JENNIFER
APPLICANT: CHAUDHARY, SUNITA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: LIMBACH AND LIMBACH L.L.P.
STREET: 2001 FERRY BUILDING
CITY: SAN FRANCISCO
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/363,526
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WARD, MICHAEL R.
REGISTRATION NUMBER: 38,651
REFERENCE/DOCKET NUMBER: CGAB-201 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 433-4150
TELEFAX: (415) 433-8716
TELEX: N/A
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1617 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
US-09-363-526-1

Alignment Scores:
Pred. No.: 1.1e+03 Length: 1617
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 91.67% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-363-526-1 (1-1617)

Qy 1 PheGlnIleGluHis 6
:::|||||
Db 1250 TATCAGATCGAGCACCAC 1267

RESULT 83
US-09-330-235-17
; Sequence 17, Application US/09330235
; Patent No. 6459018
; GENERAL INFORMATION:
; APPLICANT: Knutson, Debbie
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN PLANTS
; FILE REFERENCE: MOCO.156.00US
; CURRENT APPLICATION NUMBER: US/09/330,235
; CURRENT FILING DATE: 1999-06-10
; PRIOR APPLICATION NUMBER: 60/089,043
; PRIOR FILING DATE: 1998-06-12
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 1617
; TYPE: DNA
; ORGANISM: Mortierella alpina
US-09-330-235-17

Alignment Scores:
Pred. No.: 1.1e+03 Length: 1617
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 91.67% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-330-235-17 (1-1617)

Qy 1 PheGlnIleGluHis 6
:::|||||
Db 1250 TATCAGATCGAGCACCAC 1267

RESULT 84
US-09-710-279-1595/c
; Sequence 1595, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1595
; LENGTH: 1980
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-1595

Alignment Scores:

Pred. No.: 1.39e+03 Length: 1980
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 91.67% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-710-279-1595 (1-1980)

Qy 1 PheGlnIleGluHis 6
|||||
Db 622 TTTCAAATTGACCAT 605

RESULT 85
US-09-134-001C-2101/c
; Sequence 2101, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2101
; LENGTH: 2073
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2101

Alignment Scores:
Pred. No.: 1.46e+03 Length: 2073
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 91.67% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-09-134-001C-2101 (1-2073)

Qy 1 PheGlnIleGluHis 6
|||||
Db 715 TTTCAAATTGACCAT 698

RESULT 86
US-09-710-279-4299
; Sequence 4299, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4299
; LENGTH: 3004
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-4299

Alignment Scores:

Pred. No.: 2.23e+03 Length: 3004
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 91.67% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-710-279-4299 (1-3004)

Qy 1 PheGlnIleGluHis 6
Db 183 TTTCAAATGATCACCAT 200

RESULT 87

US-09-710-279-3717/c
; Sequence 3717, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3717
; LENGTH: 3177
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-3717

Alignment Scores:
Pred. No.: 2.37e+03 Length: 3177
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 91.67% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-710-279-3717 (1-3177)

Qy 1 PheGlnIleGluHis 6
Db 864 TTTCAAATGATCACCAT 847

RESULT 88

US-09-710-279-3649/c
; Sequence 3649, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3649
; LENGTH: 3320
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-3649

Alignment Scores:
Pred. No.: 2.49e+03 Length: 3320
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 91.67% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-710-279-3649 (1-3320)

Qy 1 PheGlnIleGluHis 6
Db 2542 TTTCAAATGATCACCAT 2525

RESULT 89

US-09-016-434-1363
; Sequence 1363, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1363:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3459 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9425220
US-09-016-434-1363

Alignment Scores:
Pred. No.: 2.61e+03 Length: 3459
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 91.67% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-016-434-1363 (1-3459)

Qy 1 PheGlnIleGluHis 6


```
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15249 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-102

Alignment Scores:
Pred. No.: 1.4e+04 Length: 15249
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 91.67% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-08-781-986A-102 (1-15249)

Qy 1 PheGlnIleGluHis 6
Db 10238 TATCAATAGACCAACCAC 10255

RESULT 94
US-09-949-016-16231
; Sequence 16231, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16231
; LENGTH: 30053
; TYPE: DNA
; ORGANISM: Human
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US-09-949-016-16231

Alignment Scores:
Pred. No.: 3e+04 Length: 30053
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 91.67% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-949-016-16231 (1-30053)

Qy 1 PheGlnIleGluHis 6
Db 12299 TTTCAGATTGACCACCAC 12316

RESULT 95
US-08-920-422-17
; Sequence 17, Application US/08920422A
; Patent No. 6255473
; GENERAL INFORMATION:
; APPLICANT: Vitek, Michael P.
; APPLICANT: Mitsuda, No. 6255473iaki
; APPLICANT: Roses, Allen D.
; TITLE OF INVENTION: Presenilin-1 Gene Promoter
; FILE REFERENCE: VITEKPRESENTLIN
; CURRENT APPLICATION NUMBER: US/08/920,422A
; CURRENT FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 48974
; TYPE: DNA
; ORGANISM: Mus musculus
US-08-920-422-17

Alignment Scores:
Pred. No.: 5.2e+04 Length: 48974
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 91.67% Indels: 0
DB: 3 Gaps: 0

US-10-029-756-20 (1-6) x US-08-920-422-17 (1-48974)

Qy 1 PheGlnIleGluHis 6
Db 1500 TTTCAGATACCAACCACAT 1517

RESULT 96
US-09-949-016-14094
; Sequence 14094, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14094
; LENGTH: 69752
; TYPE: DNA
; ORGANISM: Human
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(69752)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14094

Alignment Scores:
Pred. No.: 7.71e+04 Length: 69752
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 91.67% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-949-016-14094 (1-69752)

Qy 1 PheGlnIleGluHis 6
|||||:|||||
Db 68492 TTTCAGATTGATCATCAT 68509

RESULT 97
US-09-949-016-12147/c
; Sequence 12147, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-04-14, 755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12147
; LENGTH: 767677
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(767677)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12147

Alignment Scores:
Pred. No.: 9.36e+05 Length: 767677
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 91.67% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-949-016-12147 (1-767677)

Qy 1 PheGlnIleGluHis 6
|||||:|||||
Db 22102 TTTCAGATTGATCATCAT 22085

RESULT 98
US-09-949-016-17361/c
; Sequence 17361, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
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; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17361
; LENGTH: 767677
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(767677)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17361

Alignment Scores:
Pred. No.: 9.36e+05 Length: 767677
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 91.67% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-949-016-17361 (1-767677)

Qy 1 PheGlnIleGluHis 6
|||||:|||||
Db 22102 TTTCAGATTGATCATCAT 22085

RESULT 99
US-09-751-389-3
; Sequence 3, Application US/09751389
; Patent No. 6630334
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; THEREOF
; FILE REFERENCE: CL001067
; CURRENT APPLICATION NUMBER: US/09/751,389
; CURRENT FILING DATE: 2001-01-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 786431
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(786431)
; OTHER INFORMATION: n = A,T,C or G
US-09-751-389-3

Alignment Scores:
Pred. No.: 9.55e+05 Length: 786431
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 91.67% Indels: 0
DB: 4 Gaps: 0

US-10-029-756-20 (1-6) x US-09-751-389-3 (1-786431)

Qy 1 PheGlnIleGluHis 6
|||||:|||||
Db 665664 TTTCAGATTGATCATCAT 665681

RESULT 100
US-08-916-421B-1/c
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Sequence 1, Application US/08916421B
Patent No. 6503729
GENERAL INFORMATION:
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococcus
Patent No. 6503729
TITLE OF INVENTION: jannaschii
FILE REFERENCE: PB275
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1664976
TYPE: DNA
ORGANISM: Methanococcus jannaschii
FEATURE:
NAME/KEY: misc feature
LOCATION: (28222)..(28222)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a, t, c, or g
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NAME/KEY: misc feature
LOCATION: (231980)..(231980)
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NAME/KEY: misc feature
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NAME/KEY: misc feature
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NAME/KEY: misc feature
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NAME/KEY: misc feature
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NAME/KEY: misc feature
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NAME/KEY: misc feature
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NAME/KEY: misc feature
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NAME/KEY: misc feature
LOCATION: (657081)..(657081)
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NAME/KEY: misc feature
LOCATION: (657203)..(657203)
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NAME/KEY: misc feature
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NAME/KEY: misc feature
LOCATION: (682442)..(682442)
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NAME/KEY: misc feature
LOCATION: (713652)..(713652)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature
LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a, t, c, or g
NAME/KEY: misc feature

Thu Jun 9 15:54:35 2005

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; LOCATION: (1310988)..(1310988)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1313224)..(1313224)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1349473)..(1349473)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1349491)..(1349491)
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; NAME/KEY: misc_feature
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; NAME/KEY: misc_feature
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; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1602912)..(1602912)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1603734)..(1603734)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1637998)..(1637998)
; OTHER INFORMATION: n equals a, t, c, or g
; NAME/KEY: misc_feature
; LOCATION: (1664854)..(1664855)
; OTHER INFORMATION: n equals a, t, c, or g
US-08-916-421B-1
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Alignment Scores:
Pred. No.: 1.67e+06 Length: 1664976
Score: 33.00 Matches: 5
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 83.33% Mismatches: 0
Query Match: 91.67% Indels: 0
DB: 4 Gaps: 0
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US-10-029-756-20 (1-6) x US-08-916-421B-1 (1-1664976)

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Oy 1 PheGlnIleGluHisHis 6
Db 1586301 TTCCAAATACACACCAT 1586284
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Search completed: June 8, 2005, 15:36:06
Job time : 493.579 secs